Schreiber, David

From: Schultz, James
Sent: Tuesday, June 01, 2004 8:52 PM
To: Schreiber, David
Subject: RE: length over score search 10/023,782

Hi David,
I need a length over score nucleotide sequence search on SEQ ID NO:3 in the above entitled case. I need the lower and upper limits to be 8 and 50, respectively, I need any hits that are above 65% complementarity, and please transfer as many hits into the excel program as possible. Please do not search the interference databases at this time.
Thanks,
Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

04

contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 47 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCM6 row: E column: 5
High quality sequence stop: 40.

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FEATURES             Location/Qualifiers
     source          1. .47
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                     /clone="IMAGE:2821228"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
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  Query Match              1.1%;  Score 30.8;  DB 1;  Length 47;
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  Matches   35;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              ||||||| || ||||||||||||||||||||    ||| | |
Db          2 TTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTCACA 43
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RESULT 19
CF321993
LOCUS       CF321993                47 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--13-G24.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--13-G24, mRNA sequence.
ACCESSION   CF321993
VERSION     CF321993.1  GI:33693754
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--13-G24"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
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  Query Match              1.1%;  Score 30.8;  DB 1;  Length 47;
  Best Local Similarity   83.3%;  Pred. No. 52;
  Matches   35;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  ||||||||||||||||||||| | |||
Db          6 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTTT 47
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RESULT 20
CF314394
LOCUS       CF314394                46 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--02-O10.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--02-O10, mRNA sequence.
ACCESSION   CF314394
VERSION     CF314394.1  GI:33686155
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--02-O10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
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  Query Match              1.1%;  Score 30.6;  DB 1;  Length 46;
  Best Local Similarity   80.0%;  Pred. No. 53;
  Matches   36;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAA 2195
              ||  ||||||| |  ||||||||||||||||||||    ||| ||
Db          2 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAA 46
```

```
RESULT 21
CF301565
LOCUS       CF301565                47 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-H17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-H17, mRNA sequence.
ACCESSION   CF301565
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VERSION     CF301565.1  GI:33673326
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--06-H17"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.1%;  Score 30.6;  DB 1;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 58;
  Matches   36;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2148 TGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              || ||  ||||||| |  ||||||||||||||||||||    |||
Db          1 TGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 45


RESULT 22
CF305473
LOCUS       CF305473                 44 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  CLD1--01-M22.b1 Rice cold treated leaf plasmid cDNA library (CLD1)
            Oryza sativa cDNA clone CLD1--01-M22, mRNA sequence.
ACCESSION   CF305473
VERSION     CF305473.1  GI:33677234
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="CLD1--01-M22"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice cold treated leaf plasmid cDNA library
                     (CLD1)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was
                     incubated at 4 C(360uM/m-2sec-1) for 2hrs. Oligo-capped
                     mRNA was reverse transcribed and then used for PCR."

  Query Match             1.1%;  Score 30.4;  DB 1;  Length 44;
  Best Local Similarity   85.0%;  Pred. No. 50;
  Matches   34;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              | ||||||| |  ||||||||||||||||||||  ||||
Db          3 GTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTT 42


RESULT 23
BX554654
LOCUS       BX554654                 43 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX554654 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse16f07_p1c, mRNA sequence.
ACCESSION   BX554654
VERSION     BX554654.1  GI:33378726
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse16f07_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             1.1%;  Score 30.2;  DB 1;  Length 43;
  Best Local Similarity   81.4%;  Pred. No. 50;
  Matches   35;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2144 CTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||   ||| | ||||||| |  ||||||||||||||||||||
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Db          1 CTCTAGATAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 43


RESULT 24
CF302691
LOCUS       CF302691                 43 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-H12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-H12, mRNA sequence.
ACCESSION   CF302691
VERSION     CF302691.1  GI:33674452
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .43
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                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="7LEAF--08-H12"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.1%;  Score 30.2;  DB 1;  Length 43;
  Best Local Similarity   81.4%;  Pred. No. 50;
  Matches   35;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||  ||||||| |  ||||||||||||||||||||    ||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTG 43


RESULT 25
CF298596
LOCUS       CF298596                 44 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--02-A24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--02-A24, mRNA sequence.
ACCESSION   CF298596
VERSION     CF298596.1  GI:33670357
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
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                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
                     /clone="7LEAF--02-A24"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.1%;  Score 30.2;  DB 1;  Length 44;
  Best Local Similarity   81.4%;  Pred. No. 55;
  Matches   35;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
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Db          2 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTG 44


RESULT 26
CF331239
LOCUS       CF331239                 44 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-E14.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-E14, mRNA sequence.
ACCESSION   CF331239
VERSION     CF331239.1  GI:33810702
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
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                     /db_xref="taxon:4530"
                     /clone="NACL--07-E14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.1%;  Score 30.2;  DB 1;  Length 44;
  Best Local Similarity   81.4%;  Pred. No. 55;
  Matches   35;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTTGAAAG 2197
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Db              1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAG 43


RESULT 27
AW249952
LOCUS       AW249952                 45 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821663.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821663 3',
            mRNA sequence.
ACCESSION   AW249952
VERSION     AW249952.1  GI:6592945
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821663.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 40
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 45 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM7  row: G  column: 8
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821663"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             1.1%;  Score 30.2;  DB 1;  Length 45;
  Best Local Similarity   81.4%;  Pred. No. 60;
  Matches   35;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAG 2197
              |||||||     ||||||||||||||||||||   ||| ||||
Db          3 TTTTTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAG 45


RESULT 28
BQ589206
LOCUS       BQ589206                 46 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S014009-024-015-K16-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-015-K16 3-PRIME, mRNA sequence.
ACCESSION   BQ589206
VERSION     BQ589206.1  GI:26118789
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 46   Std Error: 0.00
            Plate: 15  row: K  column: 16
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:187865"
                     /db_xref="taxon:161934"
                     /clone="024-015-K16"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             1.1%;  Score 30.2;  DB 1;  Length 46;
  Best Local Similarity   81.4%;  Pred. No. 64;
  Matches   35;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||  ||||||  | ||||||||||||||||||||||   ||||
Db          4 TTTTTTTTTTATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTG 46


RESULT 29
BQ591313
LOCUS       BQ591313                 46 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012712-024-017-M21-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-M21 3-PRIME, mRNA sequence.
ACCESSION   BQ591313
VERSION     BQ591313.1  GI:26120896
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
```

```
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 46   Std Error: 0.00
            Plate: 17  row: M  column: 21
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188804"
                     /db_xref="taxon:161934"
                     /clone="024-017-M21"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             1.1%;  Score 30.2;  DB 1;  Length 46;
  Best Local Similarity   81.4%;  Pred. No. 64;
  Matches   35;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||  ||||||| |  ||||||||||||||||||||   ||||
Db          2 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTG 44


RESULT 30
TA116F09P
LOCUS       TA116F09P               39 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 116f09, forward sequence,
            genomic survey sequence.
ACCESSION   AL462533
VERSION     AL462533.1  GI:11832371
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="116f09"

  Query Match             1.1%;  Score 30;  DB 1;  Length 39;
  Best Local Similarity   86.8%;  Pred. No. 39;
  Matches   33;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  |||||||||| ||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTTTCTTTTTTTTTTAATTTT 38


RESULT 31
CF298283
LOCUS       CF298283                46 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-J16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-J16, mRNA sequence.
ACCESSION   CF298283
VERSION     CF298283.1  GI:33670044
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--01-J16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.1%;  Score 30;  DB 1;  Length 46;
  Best Local Similarity   78.3%;  Pred. No. 71;
  Matches   36;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              ||  ||||||| |  ||||||||||||||||||||   ||  |||
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```
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACAAA 46


RESULT 32
CF316388/c
LOCUS       CF316388                 44 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-K14.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--05-K14, mRNA sequence.
ACCESSION   CF316388
VERSION     CF316388.1  GI:33688149
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--05-K14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.1%;  Score 29.8;  DB 1;  Length 44;
  Best Local Similarity   82.9%;  Pred. No. 66;
  Matches   34;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTT 2191
                ||| ||||||| |  ||||||||||||||||||||    ||
Db         41 TTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 33
CF334384
LOCUS       CF334384                 44 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-K14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-K14, mRNA sequence.
ACCESSION   CF334384
VERSION     CF334384.1  GI:33817097
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--03-K14"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.1%;  Score 29.8;  DB 1;  Length 44;
  Best Local Similarity   82.9%;  Pred. No. 66;
  Matches   34;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTT 2191
                ||  ||||||| |  ||||||||||||||||||||  |||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTT 44


RESULT 34
BE894682/c
LOCUS       BE894682                 36 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
            mRNA sequence.
ACCESSION   BE894682
VERSION     BE894682.1  GI:10357319
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9753  row: a  column: 08
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3920911"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
```

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  Query Match             1.1%;  Score 29.6;  DB 1;  Length 36;
  Best Local Similarity   88.9%;  Pred. No. 35;
  Matches   32;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||| ||||||| |  ||||||||||||||||||||
Db         36 TTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 35
AZ773771
LOCUS       AZ773771                 38 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0001B04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0001B04 R, genomic survey sequence.
ACCESSION   AZ773771
VERSION     AZ773771.1  GI:12898489
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0001  row: B  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 38.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0001B04"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.1%;  Score 29.6;  DB 1;  Length 38;
  Best Local Similarity   88.9%;  Pred. No. 43;
  Matches   32;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| ||| ||||||||||||||||||||
Db          3 TTTTTTTTTTTTCCCTTTTTTTTTTTTTTTTTTT 38


RESULT 36
CF319510/c
LOCUS       CF319510                 39 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-A16.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-A16, mRNA sequence.
ACCESSION   CF319510
VERSION     CF319510.1  GI:33691271
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-A16"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.1%;  Score 29.6;  DB 1;  Length 39;
  Best Local Similarity   88.9%;  Pred. No. 47;
  Matches   32;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||| ||||||| |  ||||||||||||||||||||
Db         36 TTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 37
CF302032
LOCUS       CF302032                 41 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-C22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-C22, mRNA sequence.
ACCESSION   CF302032
VERSION     CF302032.1  GI:33673793
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
```

```
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-C22"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.1%;  Score 29.6;  DB 1;  Length 41;
  Best Local Similarity   88.9%;  Pred. No. 57;
  Matches   32;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| | ||||||||||||||||||||
Db          2 TTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTT 37


RESULT 38
CF336692
LOCUS       CF336692                 42 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-N12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-N12, mRNA sequence.
ACCESSION   CF336692
VERSION     CF336692.1  GI:33821756
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--06-N12"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.1%;  Score 29.6;  DB 1;  Length 42;
  Best Local Similarity   88.9%;  Pred. No. 62;
  Matches   32;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| | ||||||||||||||||||||
Db          7 TTTTTTTTTTTTTACTTTTTTTTTTTTTTTTTTTT 42


RESULT 39
BG117508/c
LOCUS       BG117508                 44 bp    mRNA    linear   EST 30-JAN-2001
DEFINITION  602347636F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4442553 5',
            mRNA sequence.
ACCESSION   BG117508
VERSION     BG117508.1  GI:12611014
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10215  row: h  column: 10
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4442553"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_90"
                     /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.7 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."

  Query Match             1.1%;  Score 29.6;  DB 1;  Length 44;
  Best Local Similarity   79.5%;  Pred. No. 73;
  Matches   35;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2143 CCTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              |||  |  ||  ||||||| |  ||||||||||||||||||||
Db         44 CCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 40
CF305383
LOCUS       CF305383                 44 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  CLD1--01-I24.b1 Rice cold treated leaf plasmid cDNA library (CLD1)
            Oryza sativa cDNA clone CLD1--01-I24, mRNA sequence.
ACCESSION   CF305383
VERSION     CF305383.1  GI:33677144
```

```
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="CLD1--01-I24"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice cold treated leaf plasmid cDNA library
                     (CLD1)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was
                     incubated at 4 C(360uM/m-2sec-1) for 2hrs. Oligo-capped
                     mRNA was reverse transcribed and then used for PCR."

  Query Match             1.1%;  Score 29.6;  DB 1;  Length 44;
  Best Local Similarity   79.5%;  Pred. No. 73;
  Matches   35;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTGA 2194
              ||  ||||||| |  ||||||||||||||||||||    ||| |
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTTTAA 44


RESULT 41
AL587540
LOCUS       AL587540                 45 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587540 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS058F08, mRNA sequence.
ACCESSION   AL587540
VERSION     AL587540.1  GI:13192574
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS058F08"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                     Clonetech (*6854-1)"

  Query Match             1.1%;  Score 29.6;  DB 1;  Length 45;
  Best Local Similarity   79.5%;  Pred. No. 79;
  Matches   35;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2143 CCTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTT 2186
              | | | | ||  ||||||| |  ||||||||||||||||||||
Db          2 CTTCCAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 45


RESULT 42
BF525658/c
LOCUS       BF525658                 45 bp    mRNA    linear   EST 11-DEC-2000
DEFINITION  602069777F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212594
            5', mRNA sequence.
ACCESSION   BF525658
VERSION     BF525658.1  GI:11613019
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9783  row: j  column: 19
            High quality sequence stop: 45.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4212594"
                     /tissue_type="glioblastoma with EGFR amplification"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Brn64"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.57 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."

  Query Match             1.1%;  Score 29.6;  DB 1;  Length 45;
  Best Local Similarity   79.5%;  Pred. No. 79;
  Matches   35;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2143 CCTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||  ||  ||||||| |  ||||||||||||||||||||
Db         45 CCCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 43
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```
AZ467950/c
LOCUS       AZ467950                 45 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0279L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0279L07 R, genomic survey sequence.
ACCESSION   AZ467950
VERSION     AZ467950.1  GI:10626075
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0279  row: L  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 45.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0279L07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.1%;  Score 29.6;  DB 1;  Length 45;
  Best Local Similarity   88.9%;  Pred. No. 79;
  Matches   32;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACT 2190
              |||||||  |  |||||||||||||||||||| |||
Db         38 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGACT 3


RESULT 44
CF301837
LOCUS       CF301837                 41 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-N13.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-N13, mRNA sequence.
ACCESSION   CF301837
VERSION     CF301837.1  GI:33673598
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--06-N13"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29.4;  DB 1;  Length 41;
  Best Local Similarity   84.6%;  Pred. No. 62;
  Matches   33;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||  |  ||||||||||||||||||||   ||||
Db          3 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTG 41


RESULT 45
AL587884
LOCUS       AL587884                 43 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587884 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS064G06, mRNA sequence.
ACCESSION   AL587884
VERSION     AL587884.1  GI:13192918
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
```

```
          Seq primer: M13F.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS064G06"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                     Clonetech (*6854-1)"

  Query Match             1.0%;  Score 29.4;  DB 1;  Length 43;
  Best Local Similarity   84.6%;  Pred. No. 74;
  Matches   33;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||||||||  |  ||||||||||||||||||||   |||
Db          2 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 40


RESULT 46
CF316064
LOCUS       CF316064                 45 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-D11.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--05-D11, mRNA sequence.
ACCESSION   CF316064
VERSION     CF316064.1  GI:33687825
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--05-D11"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 29.4;  DB 1;  Length 45;
  Best Local Similarity   84.6%;  Pred. No. 87;
  Matches   33;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2148 TGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                ||  ||  |||||||  |  ||||||||||||||||||||
Db          7 TGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 45


RESULT 47
CF331757
LOCUS       CF331757                 45 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-A04, mRNA sequence.
ACCESSION   CF331757
VERSION     CF331757.1  GI:33811741
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-A04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29.4;  DB 1;  Length 45;
  Best Local Similarity   84.6%;  Pred. No. 87;
  Matches   33;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAAC 2189
                ||  |||||||  |  ||||||||||||||||||| |
Db          5 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATC 43


RESULT 48
BE894837/c
LOCUS       BE894837                 35 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601434018F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919061 5',
            mRNA sequence.
ACCESSION   BE894837
VERSION     BE894837.1  GI:10357627
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
```

```
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM9748  row: d  column: 06
           High quality sequence start: 4
           High quality sequence stop: 35.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3919061"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 35;
  Best Local Similarity   91.2%;  Pred. No. 39;
  Matches   31;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAA 2188
                ||||||| |  ||||||||||||||||||||||
Db         35 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAA 2

RESULT 49
CF328866
LOCUS       CF328866                 37 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-P15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-P15, mRNA sequence.
ACCESSION   CF328866
VERSION     CF328866.1  GI:33805974
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--03-P15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 37;
  Best Local Similarity   91.2%;  Pred. No. 47;
  Matches   31;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAA 2188
                ||||||| |  ||||||||||||||||||||||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAA 37

RESULT 50
AW334133
LOCUS       AW334133                 42 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  S30H7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION   AW334133
VERSION     AW334133.1  GI:6830490
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
  ORGANISM  Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Pneumocystis carinii"
                     /mol_type="mRNA"
                     /db_xref="taxon:4754"
                     /lab_host="E. coli"
                     /clone_lib="AGS-1"
                     /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                     P. carinii organisms (3x10e9) from a single rat (99-1-6,
                     sacrificed on 3/17/99)  at Cincinnati VA facilities.
                     Trizol extracted RNA.  Oligo dT priming, standard
                     conditions described by  vendor, Stratagene. Further
                     details see www.uky.edu/Project/Pneumocystis/"

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 42;
  Best Local Similarity   81.0%;  Pred. No. 75;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||  ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42

RESULT 51
CF292085
LOCUS       CF292085                 42 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-M10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-M10, mRNA sequence.
ACCESSION   CF292085
VERSION     CF292085.1  GI:33661118
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
```

```
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-M10"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 42;
  Best Local Similarity   81.0%;  Pred. No. 75;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAG 2197
              |||||| |  ||||||||||||||||||||    ||| | ||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAG 42


RESULT 52
CF318962
LOCUS       CF318962                42 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--09-E19.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--09-E19, mRNA sequence.
ACCESSION   CF318962
VERSION     CF318962.1  GI:33690723
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--09-E19"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 42;
  Best Local Similarity   81.0%;  Pred. No. 75;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 53
CF319867
LOCUS       CF319867                42 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-I15.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-I15, mRNA sequence.
ACCESSION   CF319867
VERSION     CF319867.1  GI:33691628
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-I15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 42;
  Best Local Similarity   81.0%;  Pred. No. 75;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 54
CF320056/c
LOCUS       CF320056                42 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-M17.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-M17, mRNA sequence.
ACCESSION   CF320056
VERSION     CF320056.1  GI:33691817
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .42
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="HD--10-M17"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                      /lab_host="E.coli DH10B"
                      /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                      cDNA library (HD)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                      treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                      reverse transcribed and then used for PCR. mRNA was
                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 42;
  Best Local Similarity   81.0%;  Pred. No. 75;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||  |||||||  |  ||||||||||||||||||||   |||
Db         42 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 55
CF332408
LOCUS       CF332408                 42 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-O12.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-O12, mRNA sequence.
ACCESSION   CF332408
VERSION     CF332408.1  GI:33813036
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .42
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="NACL--08-O12"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 42;
  Best Local Similarity   81.0%;  Pred. No. 75;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||  |||||||  |  ||||||||||||||||||||   |||
Db         1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 56
BG028362/c
LOCUS       BG028362                 43 bp    mRNA    linear   EST 24-JAN-2001
DEFINITION  602295420F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4389940 5',
            mRNA sequence.
ACCESSION   BG028362
VERSION     BG028362.1  GI:12417456
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10078  row: h  column: 05
            High quality sequence stop: 40.
FEATURES              Location/Qualifiers
     source           1. .43
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4389940"
                      /tissue_type="osteosarcoma, cell line"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_86"
                      /note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                      Average insert size 1.533 kb. Library enriched for
                      full-length clones and constructed by Life Technologies.
                      Note: this is a NIH_MGC Library."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 43;
  Best Local Similarity   81.0%;  Pred. No. 82;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||  |||||||  |  ||||||||||||||||||||   |||
Db         42 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 57
CF302744
LOCUS       CF302744                 43 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-I23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-I23, mRNA sequence.
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ACCESSION   CF302744
VERSION     CF302744.1  GI:33674505
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--08-I23"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 43;
  Best Local Similarity   81.0%;  Pred. No. 82;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||  ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 58
CF334344/c
LOCUS       CF334344                43 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-J17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-J17, mRNA sequence.
ACCESSION   CF334344
VERSION     CF334344.1  GI:33817016
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--03-J17"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 43;
  Best Local Similarity   81.0%;  Pred. No. 82;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||  ||||||| |  ||||||||||||||||||||   |||
Db         43 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 59
AZ355703
LOCUS       AZ355703                43 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0095D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0095D02 R, genomic survey sequence.
ACCESSION   AZ355703
VERSION     AZ355703.1  GI:10468288
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0095  row: D  column: 02
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 43.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0095D02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
```

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 29.2; DB 1; Length 43;
Best Local Similarity 81.0%; Pred. No. 82;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42
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RESULT 60
BQ587867/c
LOCUS BQ587867 44 bp mRNA linear EST 06-DEC-2002
DEFINITION S013709-024-009-023-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-009-023 3-PRIME, mRNA sequence.
ACCESSION BQ587867
VERSION BQ587867.1 GI:26117449
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 44)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 44 Std Error: 0.00
Plate: 9 row: O column: 23
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .44
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:184993"
/db_xref="taxon:161934"
/clone="024-009-023"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 1.0%; Score 29.2; DB 1; Length 44;
Best Local Similarity 81.0%; Pred. No. 89;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
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Db         44 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3
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RESULT 61
CF313794
LOCUS CF313794 44 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-B06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-B06, mRNA sequence.
ACCESSION CF313794
VERSION CF313794.1 GI:33685555
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 44)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .44
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--02-B06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.0%; Score 29.2; DB 1; Length 44;
Best Local Similarity 81.0%; Pred. No. 89;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42
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RESULT 62
CF318325
LOCUS CF318325 44 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--08-G14.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-G14, mRNA sequence.
ACCESSION CF318325
VERSION CF318325.1 GI:33690086
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--08-G14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 89;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  |||||||  |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 63
CF321724
LOCUS       CF321724                  44 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--13-B07.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--13-B07, mRNA sequence.
ACCESSION   CF321724
VERSION     CF321724.1  GI:33693485
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--13-B07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 89;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  |||||||  |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 64
CF330416
LOCUS       CF330416                  44 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-B23.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-B23, mRNA sequence.
ACCESSION   CF330416
VERSION     CF330416.1  GI:33809063
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-B23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 89;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  |||||||  |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 65
CF331035
LOCUS       CF331035                  44 bp    mRNA    linear   EST 18-AUG-2003
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```
DEFINITION  NACL--07-A01.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-A01, mRNA sequence.
ACCESSION   CF331035
VERSION     CF331035.1  GI:33810287
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--07-A01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 89;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 66
CF331425
LOCUS       CF331425                44 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-I19.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-I19, mRNA sequence.
ACCESSION   CF331425
VERSION     CF331425.1  GI:33811069
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--07-I19"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 89;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 67
CF332339
LOCUS       CF332339                44 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-M24.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-M24, mRNA sequence.
ACCESSION   CF332339
VERSION     CF332339.1  GI:33812903
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-M24"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 89;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 68
CF332388
```

```
LOCUS       CF332388                 44 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-O02.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-O02, mRNA sequence.
ACCESSION   CF332388
VERSION     CF332388.1  GI:33812996
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-O02"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 89;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 69
CF337983
LOCUS       CF337983                 44 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--08-K11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--08-K11, mRNA sequence.
ACCESSION   CF337983
VERSION     CF337983.1  GI:33824332
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--08-K11"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 89;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 70
AW333985
LOCUS       AW333985                 38 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  S28H9 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION   AW333985
VERSION     AW333985.1  GI:6830342
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
  ORGANISM  Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Pneumocystis carinii"
                     /mol_type="mRNA"
                     /db_xref="taxon:4754"
                     /lab_host="E. coli"
                     /clone_lib="AGS-1"
                     /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                     P. carinii organisms (3x10e9) from a single rat (99-1-6,
                     sacrificed on 3/17/99)  at Cincinnati VA facilities.
                     Trizol extracted RNA.  Oligo dT priming, standard
                     conditions described by  vendor, Stratagene. Further
                     details see www.uky.edu/Project/Pneumocystis/"

  Query Match             1.0%;  Score 29;  DB 1;  Length 38;
  Best Local Similarity   86.5%;  Pred. No. 57;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||||  ||||||||||||||||||||   |||
Db          1 TTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTT 37


RESULT 71
```

```
CF316791/c
LOCUS       CF316791                38 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--06-D18.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--06-D18, mRNA sequence.
ACCESSION   CF316791
VERSION     CF316791.1  GI:33688552
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--06-D18"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 29;  DB 1;  Length 38;
  Best Local Similarity   86.5%;  Pred. No. 57;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTT 2186
              | || ||||||| |  ||||||||||||||||||||
Db         37 AGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 72
CF330901
LOCUS       CF330901                42 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-N01.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-N01, mRNA sequence.
ACCESSION   CF330901
VERSION     CF330901.1  GI:33810020
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-N01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 29;  DB 1;  Length 42;
  Best Local Similarity   86.5%;  Pred. No. 82;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTT 2186
              | || ||||||| |  ||||||||||||||||||||
Db          5 AGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 41


RESULT 73
AZ374531/c
LOCUS       AZ374531                43 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0127B19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0127B19 F, genomic survey sequence.
ACCESSION   AZ374531
VERSION     AZ374531.1  GI:10488231
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0127  row: B  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 43.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0127B19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
```

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 29; DB 1; Length 43;
Best Local Similarity 86.5%; Pred. No. 90;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||  |  ||||||||||||||||||||||  |||
Db         43 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTTT 7
```

RESULT 74
CF310325
LOCUS CF310325 44 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--04-O14.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--04-O14, mRNA sequence.
ACCESSION CF310325
VERSION CF310325.1 GI:33682086
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 44)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .44
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--04-O14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 1.0%; Score 29; DB 1; Length 44;
Best Local Similarity 86.5%; Pred. No. 97;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              | || ||||||| |  ||||||||||||||||||||
Db          5 AGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 41
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RESULT 75
BF343329/c
LOCUS BF343329 42 bp mRNA linear EST 22-NOV-2000
DEFINITION 602015993F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151542 5', mRNA sequence.
ACCESSION BF343329
VERSION BF343329.1 GI:11290489
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 42)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9416 row: j column: 23
High quality sequence stop: 39.
FEATURES Location/Qualifiers
source 1. .42
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4151542"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

Query Match 1.0%; Score 28.8; DB 1; Length 42;
Best Local Similarity 82.5%; Pred. No. 91;
Matches 33; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy       2147 CTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||  ||  ||||||| |  ||||||||||||||||||||
Db         41 CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2
```

RESULT 76
BG292448/c
LOCUS BG292448 42 bp mRNA linear EST 21-FEB-2001
DEFINITION 602386574F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4515403 5', mRNA sequence.
ACCESSION BG292448
VERSION BG292448.1 GI:13051253
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 42)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

```
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10405  row: c  column: 20
            High quality sequence stop: 42.
FEATURES              Location/Qualifiers
     source           1. .42
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4515403"
                      /tissue_type="transitional cell papilloma, cell line"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_93"
                      /note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                      Average insert size 1.7 kb. Library enriched for
                      full-length clones and constructed by Life Technologies.
                      Note: this is a NIH_MGC Library."

  Query Match             1.0%;  Score 28.8;  DB 1;  Length 42;
  Best Local Similarity   82.5%;  Pred. No. 91;
  Matches   33;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2147 CTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||  ||||||| |  ||||||||||||||||||||
Db         40 CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 77
BI908698/c
LOCUS       BI908698                 43 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603066333F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215376 5',
            mRNA sequence.
ACCESSION   BI908698
VERSION     BI908698.1  GI:16171728
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11541  row: a  column: 09
            High quality sequence stop: 43.
FEATURES              Location/Qualifiers
     source           1. .43
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5215376"
                      /tissue_type="leukocyte"
                      /lab_host="DH10B"
                      /clone_lib="NIH_MGC_118"
                      /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                      (destroyed); RNA source leukocytes from anonymous pool of
                      non-activated  adult donors.  Library is oligo-dT primed
                      and directionally cloned  (EcoRV site is destroyed upon
                      cloning).  Average insert size 1.7 kb, insert size range
                      1.2-3.3 kb.  Library is normalized and enriched for
                      full-length clones and was constructed by C. Gruber
                      (Invitrogen).  Research Genetics tracking code 027. Note:
                      this is a NIH_MGC Library."

  Query Match             1.0%;  Score 28.8;  DB 1;  Length 43;
  Best Local Similarity   82.5%;  Pred. No. 99;
  Matches   33;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2147 CTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||  ||||||| |  ||||||||||||||||||||
Db         41 CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 78
CF302212
LOCUS       CF302212                 44 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-I14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-I14, mRNA sequence.
ACCESSION   CF302212
VERSION     CF302212.1  GI:33673973
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .44
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="7LEAF--07-I14"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             1.0%;  Score 28.8;  DB 1;  Length 44;
  Best Local Similarity   82.5%;  Pred. No. 1.1e+02;
  Matches   33;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACT 2190
              ||  ||||||| |  ||||||||||||||||||  |||
Db          2 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTACT 41


RESULT 79
BJ054011/c
LOCUS       BJ054011                 37 bp    mRNA    linear   EST 29-SEP-2003
DEFINITION  BJ054011 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL048p20 3', mRNA sequence.
ACCESSION   BJ054011
VERSION     BJ054011.1  GI:17499017
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
```

```
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL048p20"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"

  Query Match             1.0%;  Score 28.6;  DB 1;  Length 37;
  Best Local Similarity   88.6%;  Pred. No. 63;
  Matches   31;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAAC 2189
              ||||||| |  |||||||||||||||||||| |||
Db         36 TTTTTTTTTGGTTTTTTTTTTTTTTTTTTCAAC 2


RESULT 80
CF291807/c
LOCUS       CF291807                37 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G07.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G07, mRNA sequence.
ACCESSION   CF291807
VERSION     CF291807.1  GI:33660840
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-G07"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.6;  DB 1;  Length 37;
  Best Local Similarity   88.6%;  Pred. No. 63;
  Matches   31;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2152 TGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              || ||||||| |  |||||||||||||||||||
Db         36 TGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 81
CF309581
LOCUS       CF309581                40 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-N04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-N04, mRNA sequence.
ACCESSION   CF309581
VERSION     CF309581.1  GI:33681342
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--03-N04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             1.0%;  Score 28.6;  DB 1;  Length 40;
  Best Local Similarity   88.6%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAAC 2189
              ||||||| |  |||||||||||||||||||| ||
Db          3 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAC 37


RESULT 82
CF291176
LOCUS       CF291176                38 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--01-I01.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--01-I01, mRNA sequence.
ACCESSION   CF291176
```

```
VERSION     CF291176.1  GI:33660209
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--01-I01"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 76;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 83
CF301164
LOCUS       CF301164                38 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-O13.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-O13, mRNA sequence.
ACCESSION   CF301164
VERSION     CF301164.1  GI:33672925
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-O13"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 76;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 84
CF301819
LOCUS       CF301819                38 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-N03.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-N03, mRNA sequence.
ACCESSION   CF301819
VERSION     CF301819.1  GI:33673580
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--06-N03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 76;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 85
CF315184
LOCUS       CF315184                38 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-A04.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--04-A04, mRNA sequence.
```

```
ACCESSION   CF315184
VERSION     CF315184.1  GI:33686945
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--04-A04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 76;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||||||  |  ||||||||||||||||||||   ||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTG 38


RESULT 86
CF321261
LOCUS       CF321261                38 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--12-H08.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--12-H08, mRNA sequence.
ACCESSION   CF321261
VERSION     CF321261.1  GI:33693022
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--12-H08"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 76;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              |||||||  |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 87
CF328351/c
LOCUS       CF328351                38 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-D10.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-D10, mRNA sequence.
ACCESSION   CF328351
VERSION     CF328351.1  GI:33804947
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--03-D10"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 76;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              |||||||  |  ||||||||||||||||||||   |||
Db         38 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1
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RESULT 88
CF329605
LOCUS       CF329605                38 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-P21.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-P21, mRNA sequence.
ACCESSION   CF329605
VERSION     CF329605.1  GI:33807458
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-P21"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 76;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 89
CF329690/c
LOCUS       CF329690                38 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-B17.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-B17, mRNA sequence.
ACCESSION   CF329690
VERSION     CF329690.1  GI:33807593
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--05-B17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 76;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          38 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 90
CF329730
LOCUS       CF329730                38 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--05-C15.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--05-C15, mRNA sequence.
ACCESSION   CF329730
VERSION     CF329730.1  GI:33807676
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--05-C15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 76;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
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Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 91
AZ785034
LOCUS       AZ785034                38 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0028I06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0028I06 R, genomic survey sequence.
ACCESSION   AZ785034
VERSION     AZ785034.1  GI:12921371
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0028  row: I  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 38.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0028I06"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 38;
  Best Local Similarity   84.2%;  Pred. No. 76;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 92
BE891613/c
LOCUS       BE891613                39 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601434505F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919584 5',
            mRNA sequence.
ACCESSION   BE891613
VERSION     BE891613.1  GI:10351110
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9749  row: j  column: 01
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3919584"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 39;
  Best Local Similarity   84.2%;  Pred. No. 84;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db         39 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 93
BF032623/c
LOCUS       BF032623                39 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601453114F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857019 5',
            mRNA sequence.
ACCESSION   BF032623
VERSION     BF032623.1  GI:10740335
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

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            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM9586  row: k  column: 04
           High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3857019"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_66"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies.  "

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 39;
  Best Local Similarity   84.2%;  Pred. No. 84;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db         39 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 94
CF298508
LOCUS       CF298508                 39 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--01-O19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--01-O19, mRNA sequence.
ACCESSION   CF298508
VERSION     CF298508.1  GI:33670269
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--01-O19"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 39;
  Best Local Similarity   84.2%;  Pred. No. 84;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 95
CF302356
LOCUS       CF302356                 39 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-M16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-M16, mRNA sequence.
ACCESSION   CF302356
VERSION     CF302356.1  GI:33674117
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-M16"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 39;
  Best Local Similarity   84.2%;  Pred. No. 84;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 96
CF315736
LOCUS       CF315736                 39 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-M06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--04-M06, mRNA sequence.
ACCESSION   CF315736
VERSION     CF315736.1  GI:33687497
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
```

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            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES                Location/Qualifiers
     source             1. .39
                        /organism="Oryza sativa"
                        /mol_type="mRNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:4530"
                        /clone="HD--04-M06"
                        /tissue_type="callus"
                        /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                        /lab_host="E.coli DH10B"
                        /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                        cDNA library (HD)"
                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                        treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                        reverse transcribed and then used for PCR. mRNA was
                        derived from rice Histone Deacetylase overexpression
                        line."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 39;
  Best Local Similarity   84.2%;  Pred. No. 84;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 97
CF321323
LOCUS       CF321323                39 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--12-I17.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--12-I17, mRNA sequence.
ACCESSION   CF321323
VERSION     CF321323.1  GI:33693084
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES                Location/Qualifiers
     source             1. .39
                        /organism="Oryza sativa"
                        /mol_type="mRNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:4530"
                        /clone="HD--12-I17"
                        /tissue_type="callus"
                        /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                        /lab_host="E.coli DH10B"
                        /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                        cDNA library (HD)"
                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                        treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                        reverse transcribed and then used for PCR. mRNA was
                        derived from rice Histone Deacetylase overexpression
                        line."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 39;
  Best Local Similarity   84.2%;  Pred. No. 84;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 98
CF330732
LOCUS       CF330732                39 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-J06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-J06, mRNA sequence.
ACCESSION   CF330732
VERSION     CF330732.1  GI:33809685
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES                Location/Qualifiers
     source             1. .39
                        /organism="Oryza sativa"
                        /mol_type="mRNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:4530"
                        /clone="NACL--06-J06"
                        /tissue_type="callus"
                        /dev_stage="proliferated callus on 2N6 media for 30 days"
                        /lab_host="E.coli DH10B"
                        /clone_lib="Rice callus plasmid cDNA library (NACL)"
                        /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 39;
  Best Local Similarity   84.2%;  Pred. No. 84;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 99
AZ639088
LOCUS       AZ639088                39 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0499A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0499A20 F, genomic survey sequence.
ACCESSION   AZ639088
VERSION     AZ639088.1  GI:11762488
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE   1  (bases 1 to 39)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0499  row: A  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0499A20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 39;
  Best Local Similarity   84.2%;  Pred. No. 84;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 100
AL449576
LOCUS       AL449576                 40 bp    mRNA    linear   EST 15-NOV-2000
DEFINITION  AL449576 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   AL449576
VERSION     AL449576.1  GI:11181211
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Stavrides,G.S., Huckle,E.J. and Deloukas,P.
  TITLE     Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Stavrides GS
            The Sanger Centre
            Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: humquery@sanger.ac.uk
            Sanger Centre name : sccd3232.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="20"
                     /tissue_type="Testis"
                     /clone_lib="Homo sapiens Testis (Stavrides GS)"
                     /note="cDNA fragment isolated using a cDNA end rescue
                     technique"

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 92;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2149 GATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  | |||||||  |  ||||||||||||||||||||
Db          1 GAGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 101
CF311814
LOCUS       CF311814                 40 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--07-D23.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-D23, mRNA sequence.
ACCESSION   CF311814
VERSION     CF311814.1  GI:33683575
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--07-D23"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 92;
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  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 102
CF327027
LOCUS       CF327027                 40 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-F11.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-F11, mRNA sequence.
ACCESSION   CF327027
VERSION     CF327027.1  GI:33802307
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--01-F11"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 92;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 103
CF328199
LOCUS       CF328199                 40 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-P21.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-P21, mRNA sequence.
ACCESSION   CF328199
VERSION     CF328199.1  GI:33804646
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--02-P21"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 92;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 104
CF328306/c
LOCUS       CF328306                 40 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-C09.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-C09, mRNA sequence.
ACCESSION   CF328306
VERSION     CF328306.1  GI:33804858
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--03-C09"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
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  Best Local Similarity   84.2%;  Pred. No. 92;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db         40 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 105
CF332441
LOCUS       CF332441                  40 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-P05.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-P05, mRNA sequence.
ACCESSION   CF332441
VERSION     CF332441.1  GI:33813099
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .40
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 92;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||  |||| |
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAAACTCT 38


RESULT 106
CF334545
LOCUS       CF334545                  40 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-O02.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-O02, mRNA sequence.
ACCESSION   CF334545
VERSION     CF334545.1  GI:33817420
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--03-O02"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 92;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 107
CF336399
LOCUS       CF336399                  40 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-H01.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-H01, mRNA sequence.
ACCESSION   CF336399
VERSION     CF336399.1  GI:33821186
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--06-H01"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
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was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 1.0%; Score 28.4; DB 1; Length 40;
Best Local Similarity 84.2%; Pred. No. 92;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTT 38
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RESULT 108
AZ831983/c
LOCUS AZ831983 40 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0112K02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0112K02 F, genomic survey sequence.
ACCESSION AZ831983
VERSION AZ831983.1 GI:13001891
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 40)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: K column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 40.
FEATURES Location/Qualifiers
source 1. .40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0112K02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 28.4; DB 1; Length 40;
Best Local Similarity 84.2%; Pred. No. 92;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db         40 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3
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RESULT 109
CF291539
LOCUS CF291539 41 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-A03.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-A03, mRNA sequence.
ACCESSION CF291539
VERSION CF291539.1 GI:33660572
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 41)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .41
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-A03"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.0%; Score 28.4; DB 1; Length 41;
Best Local Similarity 84.2%; Pred. No. 1e+02;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38
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RESULT 110
CF305364
LOCUS CF305364 41 bp mRNA linear EST 15-AUG-2003
DEFINITION CLD1--01-I05.b1 Rice cold treated leaf plasmid cDNA library (CLD1) Oryza sativa cDNA clone CLD1--01-I05, mRNA sequence.
ACCESSION CF305364
VERSION CF305364.1 GI:33677125
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="CLD1--01-I05"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice cold treated leaf plasmid cDNA library
                     (CLD1)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was
                     incubated at 4 C(360uM/m-2sec-1) for 2hrs. Oligo-capped
                     mRNA was reverse transcribed and then used for PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 41;
  Best Local Similarity   84.2%;  Pred. No. 1e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||| |||||  ||||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTGTTTTTTCTTT 41


RESULT 111
CF318677
LOCUS       CF318677                 41 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-O09.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--08-O09, mRNA sequence.
ACCESSION   CF318677
VERSION     CF318677.1  GI:33690438
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--08-O09"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 41;
  Best Local Similarity   84.2%;  Pred. No. 1e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||| |||||  ||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTGTTTTTTCTTT 38


RESULT 112
CF320203
LOCUS       CF320203                 41 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-P19.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-P19, mRNA sequence.
ACCESSION   CF320203
VERSION     CF320203.1  GI:33691964
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-P19"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 41;
  Best Local Similarity   84.2%;  Pred. No. 1e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||| |||||  ||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTGTTTTTTCTTT 38


RESULT 113
CF330464
LOCUS       CF330464                 41 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-D01.b1 Rice callus plasmid cDNA library (NACL) Oryza
```

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          sativa cDNA clone NACL--06-D01, mRNA sequence.
ACCESSION   CF330464
VERSION     CF330464.1  GI:33809160
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-D01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 41;
  Best Local Similarity   84.2%;  Pred. No. 1e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 114
CF334638
LOCUS       CF334638                 41 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--04-A03.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--04-A03, mRNA sequence.
ACCESSION   CF334638
VERSION     CF334638.1  GI:33817610
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--04-A03"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 41;
  Best Local Similarity   84.2%;  Pred. No. 1e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 115
AZ775066/c
LOCUS       AZ775066                 41 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0007I01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0007I01 F, genomic survey sequence.
ACCESSION   AZ775066
VERSION     AZ775066.1  GI:12901172
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0007  row: I  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0007I01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
```

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
  Query Match             1.0%;  Score 28.4;  DB 1;  Length 41;
  Best Local Similarity   84.2%;  Pred. No. 1e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db         41 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 4


RESULT 116
AZ827008/c
LOCUS       AZ827008                 41 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0103I07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0103I07 F, genomic survey sequence.
ACCESSION   AZ827008
VERSION     AZ827008.1  GI:12996916
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0103  row: I  column: 07
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0103I07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
```

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
  Query Match             1.0%;  Score 28.4;  DB 1;  Length 41;
  Best Local Similarity   84.2%;  Pred. No. 1e+02;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||   |||
Db         41 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 4


RESULT 117
AL587609
LOCUS       AL587609                 33 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587609 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS059G05, mRNA sequence.
ACCESSION   AL587609
VERSION     AL587609.1  GI:13192643
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS059G05"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                     Clonetech (*6854-1)"

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 33;
  Best Local Similarity   90.9%;  Pred. No. 50;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 33
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RESULT 118
AL587876
LOCUS       AL587876                 34 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587876 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS064F10, mRNA sequence.
ACCESSION   AL587876
VERSION     AL587876.1  GI:13192910
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="ROS064F10"
                     /tissue_type="Brain"
                     /dev_stage="Unknown"
                     /lab_host="DH10B"
                     /clone_lib="BP Chicken Brain Library"
                     /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                     unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                     5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                     GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                     Clonetech (*6854-1)"

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 34;
  Best Local Similarity   90.9%;  Pred. No. 56;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              |||||||| |  ||||||||||||||||||||
Db          1 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 33


RESULT 119
AZ345610/c
LOCUS       AZ345610                 34 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080C24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080C24 F, genomic survey sequence.
ACCESSION   AZ345610
VERSION     AZ345610.1  GI:10424847
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: C  column: 24
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 34.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080C24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 34;
  Best Local Similarity   90.9%;  Pred. No. 56;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTAA 2188
              |||||| |  ||||||||||||||||||||||
Db         34 TTTTTTTTTTTTTTTTTTTTTTTTTTTTAA 2


RESULT 120
AL587891
LOCUS       AL587891                 36 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587891 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS064H03, mRNA sequence.
ACCESSION   AL587891
VERSION     AL587891.1  GI:13192925
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
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            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES              Location/Qualifiers
     source           1. .36
                      /organism="Gallus gallus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9031"
                      /clone="ROS064H03"
                      /tissue_type="Brain"
                      /dev_stage="Unknown"
                      /lab_host="DH10B"
                      /clone_lib="BP Chicken Brain Library"
                      /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                      unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                      5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                      GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                      Clonetech (*6854-1)"

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 36;
  Best Local Similarity   90.9%;  Pred. No. 69;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              |||||||| |  ||||||||||||||||||||
Db          1 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 33


RESULT 121
AZ945733
LOCUS       AZ945733                36 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0207B13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0207B13 F, genomic survey sequence.
ACCESSION   AZ945733
VERSION     AZ945733.1  GI:13812542
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0207  row: B  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES              Location/Qualifiers
     source           1. .36
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0207B13"
                      /sex="Female"
                      /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC2M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (female) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 36;
  Best Local Similarity   90.9%;  Pred. No. 69;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              ||  ||||||| ||||||||||||||||||||
Db          4 TTTTTTTTTTTTTCCTTTTTTTTTTTTTTTTT 36


RESULT 122
CF329026
LOCUS       CF329026                37 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-D06.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-D06, mRNA sequence.
ACCESSION   CF329026
VERSION     CF329026.1  GI:33806289
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .37
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="NACL--04-D06"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 37;
  Best Local Similarity   90.9%;  Pred. No. 76;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTA 2187
              ||||||| |  ||||||||||||||||||||||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTA 36


RESULT 123
CF300591
LOCUS       CF300591                 39 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--05-C03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--05-C03, mRNA sequence.
ACCESSION   CF300591
VERSION     CF300591.1  GI:33672352
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--05-C03"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 39;
  Best Local Similarity   90.9%;  Pred. No. 92;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTA 2187
              ||||||| |  ||||||||||||||||||||||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTA 36


RESULT 124
CF318540
LOCUS       CF318540                 42 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--08-L07.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--08-L07, mRNA sequence.
ACCESSION   CF318540
VERSION     CF318540.1  GI:33690301
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--08-L07"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 42;
  Best Local Similarity   80.5%;  Pred. No. 1.2e+02;
  Matches   33;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTT 2191
              ||  ||||||| |  ||||||||||||||||||||   ||
Db          2 TTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 125
BE876160/c
LOCUS       BE876160                 36 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601485659F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888015 5',
            mRNA sequence.
ACCESSION   BE876160
VERSION     BE876160.1  GI:10324936
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9667  row: f  column: 16
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3888015"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_69"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
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  Query Match             1.0%;  Score 28;  DB 1;  Length 36;
  Best Local Similarity   86.1%;  Pred. No. 76;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  |||||||  |  ||||||||||||||||||||
Db         36 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 126
CF317028
LOCUS       CF317028                 36 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--06-J02.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--06-J02, mRNA sequence.
ACCESSION   CF317028
VERSION     CF317028.1  GI:33688789
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--06-J02"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 28;  DB 1;  Length 36;
  Best Local Similarity   86.1%;  Pred. No. 76;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  |||||||  |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 127
CF331983
LOCUS       CF331983                 36 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-F01.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-F01, mRNA sequence.
ACCESSION   CF331983
VERSION     CF331983.1  GI:33812186
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-F01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28;  DB 1;  Length 36;
  Best Local Similarity   86.1%;  Pred. No. 76;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  |||||||  |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 128
AZ470916
LOCUS       AZ470916                 36 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0285E23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0285E23 F, genomic survey sequence.
ACCESSION   AZ470916
VERSION     AZ470916.1  GI:10629041
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0285  row: E  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0285E23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28;  DB 1;  Length 36;
  Best Local Similarity   86.1%;  Pred. No. 76;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 129
AZ628484
LOCUS       AZ628484                36 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0480B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0480B08 R, genomic survey sequence.
ACCESSION   AZ628484
VERSION     AZ628484.1  GI:11750674
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0480  row: B  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0480B08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28;  DB 1;  Length 36;
  Best Local Similarity   86.1%;  Pred. No. 76;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 130
AZ793484
LOCUS       AZ793484                36 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0046G15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0046G15 R, genomic survey sequence.
ACCESSION   AZ793484
VERSION     AZ793484.1  GI:12938483
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0046  row: G  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0046G15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28;  DB 1;  Length 36;
  Best Local Similarity   86.1%;  Pred. No. 76;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                ||  |||||||  |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 131
AZ949866
LOCUS       AZ949866                36 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0213H10R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0213H10 R, genomic survey sequence.
ACCESSION   AZ949866
VERSION     AZ949866.1  GI:13821093
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0213  row: H  column: 10
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0213H10"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28;  DB 1;  Length 36;
  Best Local Similarity   86.1%;  Pred. No. 76;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                ||  |||||||  |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 132
AZ957867
LOCUS       AZ957867                36 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0224G19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0224G19 R, genomic survey sequence.
ACCESSION   AZ957867
VERSION     AZ957867.1  GI:13829094
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0224  row: G  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
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                     /clone="UUGC2M0224G19"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28;  DB 1;  Length 36;
  Best Local Similarity   86.1%;  Pred. No. 76;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                ||  |||||||  |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 133
BG033620/c
LOCUS       BG033620                37 bp    mRNA    linear   EST 24-JAN-2001
DEFINITION  602301748F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4403554 5',
            mRNA sequence.
ACCESSION   BG033620
VERSION     BG033620.1  GI:12426095
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10113  row: o  column: 11
            High quality sequence stop: 37.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4403554"
                     /tissue_type="mammary adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_87"
                     /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                ||  |||||||  |  ||||||||||||||||||||
Db         37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 134
CF291818
LOCUS       CF291818                37 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-G14.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-G14, mRNA sequence.
ACCESSION   CF291818
VERSION     CF291818.1  GI:33660851
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
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Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 135
CF293279
LOCUS       CF293279                37 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  30DGS--02-G15.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--02-G15, mRNA sequence.
ACCESSION   CF293279
VERSION     CF293279.1  GI:33662312
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
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REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="30DGS--02-G15"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTTAA 2201
              ||||||||||||||||||||||  |  ||| | ||
Db          2 TTTTTTTTTTTTTTTTTTTTAACCTAAAAATTAAA 37


RESULT 136
CF300002/c
LOCUS       CF300002                37 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-D21.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-D21, mRNA sequence.
ACCESSION   CF300002
VERSION     CF300002.1  GI:33671763
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  |||||||  |  ||||||||||||||||||||
Db         37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 137
CF300328/c
LOCUS       CF300328                37 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-K23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-K23, mRNA sequence.
ACCESSION   CF300328
VERSION     CF300328.1  GI:33672089
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  |||||||  |  ||||||||||||||||||||
Db         36 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 138
CF301864
LOCUS       CF301864                37 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-O03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-O03, mRNA sequence.
ACCESSION   CF301864
VERSION     CF301864.1  GI:33673625
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /tissue_type="leaf"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 139
CF307971
LOCUS       CF307971                37 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--01-J16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-J16, mRNA sequence.
ACCESSION   CF307971
VERSION     CF307971.1  GI:33679732
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 140
CF316114/c
LOCUS       CF316114                37 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-E13.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--05-E13, mRNA sequence.
ACCESSION   CF316114
VERSION     CF316114.1  GI:33687875
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db         37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 141
CF321294/c
LOCUS       CF321294                37 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--12-I01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--12-I01, mRNA sequence.
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ACCESSION   CF321294
VERSION     CF321294.1  GI:33693055
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
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RESULT 142
CF326975
LOCUS       CF326975                 37 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-E08.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-E08, mRNA sequence.
ACCESSION   CF326975
VERSION     CF326975.1  GI:33802205
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
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RESULT 143
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LOCUS       CF333624                 37 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--02-J14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--02-J14, mRNA sequence.
ACCESSION   CF333624
VERSION     CF333624.1  GI:33815543
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
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  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
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RESULT 144
CF336769
LOCUS       CF336769                 37 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-P04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-P04, mRNA sequence.
ACCESSION   CF336769
VERSION     CF336769.1  GI:33821918
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /clone="JMT--06-P04"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  |||||||  |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 145
AZ321759/c
LOCUS       AZ321759                 37 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0042P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0042P22 F, genomic survey sequence.
ACCESSION   AZ321759
VERSION     AZ321759.1  GI:10374820
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0042  row: P  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 37.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0042P22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  |||||||  |  ||||||||||||||||||||
Db         37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 146
AZ463801
LOCUS       AZ463801                 37 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0272E23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0272E23 R, genomic survey sequence.
ACCESSION   AZ463801
VERSION     AZ463801.1  GI:10621926
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
```

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            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0272  row: E  column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 37.
FEATURES              Location/Qualifiers
     source           1. .37
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0272E23"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                ||  ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 147
AZ831214/c
LOCUS       AZ831214                 37 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0110P16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0110P16 R, genomic survey sequence.
ACCESSION   AZ831214
VERSION     AZ831214.1  GI:13001122
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0110  row: P  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 37.
FEATURES              Location/Qualifiers
     source           1. .37
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0110P16"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                ||  ||||||| |  ||||||||||||||||||||
Db         37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 148
DR102P24T
LOCUS       DR102P24T                37 bp    DNA     linear   GSS 21-NOV-2002
DEFINITION  Danio rerio genomic clone DKEY-102P24, genomic survey sequence.
ACCESSION   AL977144
VERSION     AL977144.1  GI:25173875
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Humphray,S.J., Huckle,E. and Hunt,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 102P24. 102P24
            is part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene.
            Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES              Location/Qualifiers
     source           1. .37
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                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-102P24"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 149
DR102P2T/c
LOCUS       DR102P2T                  37 bp    DNA     linear   GSS 21-NOV-2002
DEFINITION  Danio rerio genomic clone DKEY-102P2, genomic survey sequence.
ACCESSION   AL985556
VERSION     AL985556.1  GI:25173839
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Humphray,S.J., Huckle,E. and Hunt,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 102P2. 102P2 is
            part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene.
            Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-102P2"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 84;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db         37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 150
BF526154/c
LOCUS       BF526154                  38 bp    mRNA    linear   EST 11-DEC-2000
DEFINITION  602071057F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213910
            5', mRNA sequence.
ACCESSION   BF526154
VERSION     BF526154.1  GI:11613430
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9787  row: a  column: 15
            High quality sequence stop: 38.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4213910"
                     /tissue_type="glioblastoma with EGFR amplification"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Brn64"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.57 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."

  Query Match             1.0%;  Score 28;  DB 1;  Length 38;
  Best Local Similarity   86.1%;  Pred. No. 93;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db         36 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 151
BG287495/c
LOCUS       BG287495                  39 bp    mRNA    linear   EST 21-FEB-2001
DEFINITION  602384505F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4513609 5',
            mRNA sequence.
ACCESSION   BG287495
VERSION     BG287495.1  GI:13041394
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10400  row: i  column: 02
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4513609"
                     /tissue_type="transitional cell papilloma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_93"
                     /note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.7 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
```

```
                    Note: this is a NIH_MGC Library."

  Query Match             1.0%;  Score 28;  DB 1;  Length 39;
  Best Local Similarity   86.1%;  Pred. No. 1e+02;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db         37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 152
CNS004NT
LOCUS       CNS004NT                   39 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR10D12 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL054298
VERSION     AL054298.1  GI:4931806
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR10D12"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"

  Query Match             1.0%;  Score 28;  DB 1;  Length 39;
  Best Local Similarity   86.1%;  Pred. No. 1e+02;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db          4 TTTTTTTTTTTTTTGTTTTTTTTTTTTTTTTTTTT 39


RESULT 153
BG166502/c
LOCUS       BG166502                   40 bp    mRNA    linear   EST 06-FEB-2001
DEFINITION  602339795F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4447702 5',
            mRNA sequence.
ACCESSION   BG166502
VERSION     BG166502.1  GI:12673205
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10228  row: n  column: 23
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4447702"
                     /tissue_type="hypernephroma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_89"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.3 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."

  Query Match             1.0%;  Score 28;  DB 1;  Length 40;
  Best Local Similarity   86.1%;  Pred. No. 1.1e+02;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db         37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 154
BJ082856/c
LOCUS       BJ082856                   40 bp    mRNA    linear   EST 29-SEP-2003
DEFINITION  BJ082856 NIBB Mochii normalized Xenopus tailbud library Xenopus
            laevis cDNA clone XL083e12 3', mRNA sequence.
ACCESSION   BJ082856
VERSION     BJ082856.1  GI:17577666
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Xenopus laevis"
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                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL083e12"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 25"
                     /clone_lib="NIBB Mochii normalized Xenopus tailbud
                     library"

  Query Match             1.0%;  Score 28;  DB 1;  Length 40;
  Best Local Similarity   83.8%;  Pred. No. 1.1e+02;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAAC 2189
              | ||||||| |   |||||||||||||||||||| |||
Db         39 GGTTTTTTTTGGNTTTTTTTTTTTTTTTTTTCAAC 3


RESULT 155
DR85H22T/c
LOCUS       DR85H22T                  40 bp    DNA     linear   GSS 22-NOV-2002
DEFINITION  Danio rerio genomic clone DKEY-85H22, genomic survey sequence.
ACCESSION   AL982088
VERSION     AL982088.1  GI:25187801
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Humphray,S.J., Huckle,E. and Hunt,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 85H22. 85H22 is
            part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene.
            Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-85H22"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"

  Query Match             1.0%;  Score 28;  DB 1;  Length 40;
  Best Local Similarity   86.1%;  Pred. No. 1.1e+02;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| | |||||||||||||||||| ||||
Db         39 TTTTTTTTTTTTTCTTTTTTTTTTTTTTTCTTTT 4


RESULT 156
CF328487/c
LOCUS       CF328487                  41 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-G18.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-G18, mRNA sequence.
ACCESSION   CF328487
VERSION     CF328487.1  GI:33805221
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--03-G18"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 28;  DB 1;  Length 41;
  Best Local Similarity   86.1%;  Pred. No. 1.2e+02;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||| |||| || |  ||||||||||||||||||||
Db         36 TTGTTTTTGTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 157
CF330825
LOCUS       CF330825                  42 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-L08.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-L08, mRNA sequence.
ACCESSION   CF330825
VERSION     CF330825.1  GI:33809873
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-L08"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
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  Query Match             1.0%;  Score 28;  DB 1;  Length 42;
  Best Local Similarity   86.1%;  Pred. No. 1.3e+02;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              || ||||||| |  ||||||||||||||||||||
Db          7 TTTTTTTTTTTTTATTTTTTTTTTTTTTTTTTTT 42


RESULT 158
T50295
LOCUS       T50295                   35 bp    mRNA    linear   EST 06-FEB-1995
DEFINITION  yb16g12.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA
            clone IMAGE:71398 3' similar to similar to gb:L19437 TRANSALDOLASE
            (HUMAN), mRNA sequence.
ACCESSION   T50295
VERSION     T50295.1  GI:652155
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
            Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
            and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
   PUBMED   8889549
COMMENT     Other_ESTs: yb16g12.r1
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence starts: 1
            High qality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -21m13
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:493063"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:71398"
                     /tissue_type="fetal spleen"
                     /dev_stage="fetal"
                     /lab_host="SOLR cells (kanamycin resistant)"
                     /clone_lib="Stratagene fetal spleen (#937205)"
                     /note="Organ: spleen; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. Pooled spleens. Average insert size: 1.0 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"

  Query Match             1.0%;  Score 27.8;  DB 1;  Length 35;
  Best Local Similarity   90.6%;  Pred. No. 76;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTATNATTTTTTTTTTTTTTTTTTT 32


RESULT 159
AW334249
LOCUS       AW334249                 34 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  S32D4 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION   AW334249
VERSION     AW334249.1  GI:6830606
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
  ORGANISM  Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Pneumocystis carinii"
                     /mol_type="mRNA"
                     /db_xref="taxon:4754"
                     /lab_host="E. coli"
                     /clone_lib="AGS-1"
                     /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                     P. carinii organisms (3x10e9) from a single rat (99-1-6,
                     sacrificed on 3/17/99)  at Cincinnati VA facilities.
                     Trizol extracted RNA.  Oligo dT priming, standard
                     conditions described by  vendor, Stratagene. Further
                     details see www.uky.edu/Project/Pneumocystis/"

  Query Match             1.0%;  Score 27.6;  DB 1;  Length 34;
  Best Local Similarity   88.2%;  Pred. No. 75;
  Matches   30;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTTTTTTTTTAACT 2190
              ||||| |  |||||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAT 34


RESULT 160
CF301560/c
LOCUS       CF301560                 37 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--06-H14.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-H14, mRNA sequence.
ACCESSION   CF301560
VERSION     CF301560.1  GI:33673321
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
```

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           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--06-H14"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.6;  DB 1;  Length 37;
  Best Local Similarity   88.2%;  Pred. No. 1e+02;
  Matches   30;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | ||||||| |  ||||||||||||||||||||
Db         37 GGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 4


RESULT 161
CF302184
LOCUS       CF302184                38 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-H22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-H22, mRNA sequence.
ACCESSION   CF302184
VERSION     CF302184.1  GI:33673945
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-H22"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.6;  DB 1;  Length 38;
  Best Local Similarity   88.2%;  Pred. No. 1.1e+02;
  Matches   30;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAA 2188
              ||||||| |  |||||||||||||||||||| |
Db          2 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGA 35


RESULT 162
CF331029
LOCUS       CF331029                40 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-P22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-P22, mRNA sequence.
ACCESSION   CF331029
VERSION     CF331029.1  GI:33810274
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-P22"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.6;  DB 1;  Length 40;
  Best Local Similarity   88.2%;  Pred. No. 1.3e+02;
  Matches   30;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAA 2188
              ||||||| |  |||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGA 34


RESULT 163
CF299167
LOCUS       CF299167                37 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-B09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-B09, mRNA sequence.
ACCESSION   CF299167
VERSION     CF299167.1  GI:33670928
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
```

```
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-B09"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.4;  DB 1;  Length 37;
  Best Local Similarity   83.8%;  Pred. No. 1.1e+02;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTT 2191
              ||||||| |  |||||||||| ||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTTTTGTTTTTTTTTTATTTT 37


RESULT 164
AW327277/c
LOCUS       AW327277                32 bp    mRNA    linear   EST 28-JAN-2000
DEFINITION  dq01d07.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846628 5', mRNA
            sequence.
ACCESSION   AW327277
VERSION     AW327277.1  GI:6797772
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Edge BioSystems
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Plate: LLCM0028  row: G  column: 13
            Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2846628"
                     /tissue_type="T cell leukemia"
                     /cell_line="MGC2"
                     /clone_lib="NIH_MGC_2"
                     /note="Organ: Blood; Vector: pOTB7a; Library prepared by
                     Edge BioSystems."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         32 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 165
CF291773
LOCUS       CF291773                32 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-F12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-F12, mRNA sequence.
ACCESSION   CF291773
VERSION     CF291773.1  GI:33660806
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-F12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 166
CF299386
LOCUS       CF299386                32 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-G07, mRNA sequence.
ACCESSION   CF299386
VERSION     CF299386.1  GI:33671147
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
```

```
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--03-G07"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 167
CF309233/c
LOCUS       CF309233                32 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-F14, mRNA sequence.
ACCESSION   CF309233
VERSION     CF309233.1  GI:33680994
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--03-F14"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         32 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 168
CF309345
LOCUS       CF309345                32 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--03-I03.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-I03, mRNA sequence.
ACCESSION   CF309345
VERSION     CF309345.1  GI:33681106
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--03-I03"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 169
CF313717
LOCUS       CF313717                32 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-P05.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--01-P05, mRNA sequence.
ACCESSION   CF313717
VERSION     CF313717.1  GI:33685478
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
```

```
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--01-P05"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 170
CF321046
LOCUS       CF321046                32 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--12-C15.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--12-C15, mRNA sequence.
ACCESSION   CF321046
VERSION     CF321046.1  GI:33692807
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--12-C15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 171
CF328471
LOCUS       CF328471                32 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-G09, mRNA sequence.
ACCESSION   CF328471
VERSION     CF328471.1  GI:33805189
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--03-G09"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 172
CF331270
LOCUS       CF331270                32 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--07-F08.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--07-F08, mRNA sequence.
ACCESSION   CF331270
VERSION     CF331270.1  GI:33810751
KEYWORDS    EST.
SOURCE      Oryza sativa
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  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .32
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="NACL--07-F08"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 30 days"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice callus plasmid cDNA library (NACL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 173
AZ459536
LOCUS       AZ459536                32 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0264M16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0264M16 F, genomic survey sequence.
ACCESSION   AZ459536
VERSION     AZ459536.1  GI:10617577
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0264  row: M  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 32.
FEATURES              Location/Qualifiers
     source           1. .32
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0264M16"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 174
AZ470832/c
LOCUS       AZ470832                32 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0285F14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0285F14 F, genomic survey sequence.
ACCESSION   AZ470832
VERSION     AZ470832.1  GI:10628957
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0285  row: F  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 32.
FEATURES              Location/Qualifiers
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    source          1. .32
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGC1M0285F14"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         32 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 175
AZ611890
LOCUS       AZ611890                32 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0438E02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0438E02 R, genomic survey sequence.
ACCESSION   AZ611890
VERSION     AZ611890.1  GI:11734080
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0438  row: E  column: 02
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 32.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0438E02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 176
AZ778018/c
LOCUS       AZ778018                32 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0012O20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0012O20 R, genomic survey sequence.
ACCESSION   AZ778018
VERSION     AZ778018.1  GI:12907220
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0012  row: O  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 32.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Mus musculus"
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0012O20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||||
Db         32 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 177
DR85L21T/c
LOCUS       DR85L21T                  32 bp    DNA     linear   GSS 22-NOV-2002
DEFINITION  Danio rerio genomic clone DKEY-85L21, genomic survey sequence.
ACCESSION   AL986044
VERSION     AL986044.1  GI:25187956
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Humphray,S.J., Huckle,E. and Hunt,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 85L21. 85L21 is
            part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene.
            Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-85L21"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   90.6%;  Pred. No. 73;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||||
Db         32 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 178
BU431798
LOCUS       BU431798                  33 bp    mRNA    linear   EST 09-SEP-2002
DEFINITION  601655890R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855694 3',
            mRNA sequence.
ACCESSION   BU431798
VERSION     BU431798.1  GI:22770280
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM570  row: c  column: 23
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3855694"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_66"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies.  "

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 33;
  Best Local Similarity   90.6%;  Pred. No. 82;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 179
CF291613
LOCUS       CF291613                  33 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-B21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-B21, mRNA sequence.
ACCESSION   CF291613
VERSION     CF291613.1  GI:33660646
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
```

```
          of Bioscience and Bioinformatics, MyongJi University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-B21"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 33;
  Best Local Similarity   90.6%;  Pred. No. 82;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 180
CF311229
LOCUS       CF311229                 33 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--06-F23.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-F23, mRNA sequence.
ACCESSION   CF311229
VERSION     CF311229.1  GI:33682990
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--06-F23"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 33;
  Best Local Similarity   90.6%;  Pred. No. 82;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 181
CF326967
LOCUS       CF326967                 33 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--01-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-E04, mRNA sequence.
ACCESSION   CF326967
VERSION     CF326967.1  GI:33802189
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--01-E04"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 33;
  Best Local Similarity   90.6%;  Pred. No. 82;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 182
CF328313/c
LOCUS       CF328313                 33 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-C14, mRNA sequence.
ACCESSION   CF328313
VERSION     CF328313.1  GI:33804873
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
```

```
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--03-C14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 33;
  Best Local Similarity   90.6%;  Pred. No. 82;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         33 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 183
CF336752
LOCUS       CF336752                33 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-O19.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-O19, mRNA sequence.
ACCESSION   CF336752
VERSION     CF336752.1  GI:33821884
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--06-O19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 33;
  Best Local Similarity   90.6%;  Pred. No. 82;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 184
CF337105
LOCUS       CF337105                33 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--07-G18.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--07-G18, mRNA sequence.
ACCESSION   CF337105
VERSION     CF337105.1  GI:33822596
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--07-G18"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 33;
  Best Local Similarity   90.6%;  Pred. No. 82;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 185
AZ486795
LOCUS       AZ486795                33 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0315P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0315P22 F, genomic survey sequence.
ACCESSION   AZ486795
VERSION     AZ486795.1  GI:10653918
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0315  row: P  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 33.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0315P22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 33;
  Best Local Similarity   90.6%;  Pred. No. 82;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 186
AZ627839
LOCUS       AZ627839                 33 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0474B02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0474B02 F, genomic survey sequence.
ACCESSION   AZ627839
VERSION     AZ627839.1  GI:11750125
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0474  row: B  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 33.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0474B02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 33;
  Best Local Similarity   90.6%;  Pred. No. 82;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 187
AV674152
LOCUS       AV674152                 34 bp    mRNA    linear   EST 05-OCT-2000
DEFINITION  AV674152 Nori Satoh unpublished cDNA library Ciona intestinalis
            cDNA clone citb14i22 5', mRNA sequence.
ACCESSION   AV674152
VERSION     AV674152.1  GI:10112151
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 34)
```

```
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="citb14i22"
                     /tissue_type="whole animal"
                     /dev_stage="tailbud"
                     /clone_lib="Nori Satoh unpublished cDNA library"

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 34;
  Best Local Similarity   90.6%;  Pred. No. 91;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTTTTTTTTTAA 2188
              ||||| |  ||||||||||||||||||||||
Db          3 TTTTTTTTTTTTTTTTTTTTTTTTTTTTAA 34


RESULT 188
BU431799
LOCUS       BU431799                34 bp    mRNA    linear   EST 09-SEP-2002
DEFINITION  601655967R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855737 3',
            mRNA sequence.
ACCESSION   BU431799
VERSION     BU431799.1  GI:22770281
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM570  row: e  column: 18
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3855737"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_66"
                     /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies.  "

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 34;
  Best Local Similarity   90.6%;  Pred. No. 91;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 189
CF302250
LOCUS       CF302250                34 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--07-J10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--07-J10, mRNA sequence.
ACCESSION   CF302250
VERSION     CF302250.1  GI:33674011
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--07-J10"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 34;
  Best Local Similarity   90.6%;  Pred. No. 91;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 190
AZ465350
LOCUS       AZ465350                34 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0275012F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0275012 F, genomic survey sequence.
ACCESSION   AZ465350
VERSION     AZ465350.1  GI:10623475
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
```

```
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0275  row: O  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 34.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0275O12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 34;
  Best Local Similarity   90.6%;  Pred. No. 91;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 191
AZ501040/c
LOCUS       AZ501040                34 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0339P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0339P09 R, genomic survey sequence.
ACCESSION   AZ501040
VERSION     AZ501040.1  GI:10682356
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0339  row: P  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 34.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0339P09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 34;
  Best Local Similarity   90.6%;  Pred. No. 91;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         34 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 192
AZ809643/c
LOCUS       AZ809643                34 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0073C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0073C14 R, genomic survey sequence.
ACCESSION   AZ809643
VERSION     AZ809643.1  GI:12976135
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
```

```
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0073  row: C  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 34.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0073C14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 34;
  Best Local Similarity   90.6%;  Pred. No. 91;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         34 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 193
BF338797/c
LOCUS       BF338797                35 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  602036229F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184167
            5', mRNA sequence.
ACCESSION   BF338797
VERSION     BF338797.1  GI:11285216
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9501  row: j  column: 08
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4184167"
                     /tissue_type="glioblastoma with EGFR amplification"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Brn64"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.57 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 35;
  Best Local Similarity   90.6%;  Pred. No. 1e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         32 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 194
CF315871/c
LOCUS       CF315871                35 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--04-P06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--04-P06, mRNA sequence.
ACCESSION   CF315871
VERSION     CF315871.1  GI:33687632
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--04-P06"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 35;
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```
  Best Local Similarity   90.6%;  Pred. No. 1e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         35 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 4


RESULT 195
CF334198
LOCUS       CF334198                 35 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--03-G09.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--03-G09, mRNA sequence.
ACCESSION   CF334198
VERSION     CF334198.1  GI:33816728
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--03-G09"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 35;
  Best Local Similarity   90.6%;  Pred. No. 1e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 196
CF335633
LOCUS       CF335633                 35 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--05-G03.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--05-G03, mRNA sequence.
ACCESSION   CF335633
VERSION     CF335633.1  GI:33819628
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--05-G03"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 35;
  Best Local Similarity   90.6%;  Pred. No. 1e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 197
AZ623128
LOCUS       AZ623128                 35 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0460D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0460D02 R, genomic survey sequence.
ACCESSION   AZ623128
VERSION     AZ623128.1  GI:11745318
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0460  row: D  column: 02
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 35.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Mus musculus"
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0460D02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 35;
  Best Local Similarity   90.6%;  Pred. No. 1e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 198
AZ803371
LOCUS       AZ803371                35 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0063C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0063C15 R, genomic survey sequence.
ACCESSION   AZ803371
VERSION     AZ803371.1  GI:12955694
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0063  row: C  column: 15
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 35.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0063C15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 35;
  Best Local Similarity   90.6%;  Pred. No. 1e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 199
BI761940/c
LOCUS       BI761940                36 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603048772F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189224 5',
            mRNA sequence.
ACCESSION   BI761940
VERSION     BI761940.1  GI:15753518
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11472  row: o  column: 17
            High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5189224"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
```

female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

Query Match 1.0%; Score 27.2; DB 1; Length 36;
Best Local Similarity 90.6%; Pred. No. 1.1e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         33 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2
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RESULT 200
CF279874
LOCUS CF279874 36 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--06-F10.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--06-F10, mRNA sequence.
ACCESSION CF279874
VERSION CF279874.1 GI:33657260
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 36)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .36
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--06-F10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.0%; Score 27.2; DB 1; Length 36;
Best Local Similarity 90.6%; Pred. No. 1.1e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32
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RESULT 201
CF331913
LOCUS CF331913 36 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--08-D12.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-D12, mRNA sequence.
ACCESSION CF331913
VERSION CF331913.1 GI:33812047
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 36)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .36
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--08-D12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.0%; Score 27.2; DB 1; Length 36;
Best Local Similarity 90.6%; Pred. No. 1.1e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32
```

RESULT 202
CF333863
LOCUS CF333863 36 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--02-O22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-O22, mRNA sequence.
ACCESSION CF333863
VERSION CF333863.1 GI:33816032
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 36)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .36
/organism="Oryza sativa"
/mol_type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-022"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 1.0%; Score 27.2; DB 1; Length 36;
Best Local Similarity 90.6%; Pred. No. 1.1e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
||||||| | ||||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 203
BF525501/c
LOCUS BF525501 38 bp mRNA linear EST 11-DEC-2000
DEFINITION 602069592F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212527 5', mRNA sequence.
ACCESSION BF525501
VERSION BF525501.1 GI:11612862
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 38)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9783 row: g column: 24
High quality sequence stop: 38.
FEATURES Location/Qualifiers
source 1. .38
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4212527"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

Query Match 1.0%; Score 27.2; DB 1; Length 38;
Best Local Similarity 90.6%; Pred. No. 1.4e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
||||||| | ||||||||||||||||||||||
Db 35 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 4

RESULT 204
BG778513/c
LOCUS BG778513 38 bp mRNA linear EST 15-MAY-2001
DEFINITION 602666730F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4806655 5', mRNA sequence.
ACCESSION BG778513
VERSION BG778513.1 GI:14048830
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 38)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1656 row: k column: 08
High quality sequence stop: 37.
FEATURES Location/Qualifiers
source 1. .38
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4806655"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

Query Match 1.0%; Score 27.2; DB 1; Length 38;
Best Local Similarity 90.6%; Pred. No. 1.4e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2158 TTTTCTCCTTTTTTTTTTTTTTTTTTTAAC 2189
|||| | ||||||||||||||||||||||
Db 37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTAAC 6

RESULT 205
BI694035/c
LOCUS BI694035 39 bp mRNA linear EST 18-SEP-2001
DEFINITION 603342221F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5369956 5', mRNA sequence.
ACCESSION BI694035
VERSION BI694035.1 GI:15656664
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 39)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

```
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11941  row: j  column: 05
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N-3"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5369956"
                     /tissue_type="tumor, biopsy sample"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam2"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 39;
  Best Local Similarity   90.6%;  Pred. No. 1.5e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         35 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 4


RESULT 206
CF327755
LOCUS       CF327755                39 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-F23.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-F23, mRNA sequence.
ACCESSION   CF327755
VERSION     CF327755.1  GI:33803761
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--02-F23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 39;
  Best Local Similarity   90.6%;  Pred. No. 1.5e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32


RESULT 207
BX562248
LOCUS       BX562248                40 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX562248 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse5e11_p1c, mRNA sequence.
ACCESSION   BX562248
VERSION     BX562248.1  GI:33372492
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse5e11_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 40;
  Best Local Similarity   80.0%;  Pred. No. 1.6e+02;
  Matches   32;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2144 CTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTT 2183
              ||   ||| | ||||||| |  ||||||||||||||||
Db          1 CTCTAGATAGTTTTTTTTTTTTTTTTTTTTTTTTTTTT 40


RESULT 208
BX567930
LOCUS       BX567930                40 bp    mRNA    linear   EST 14-OCT-2003
DEFINITION  BX567930 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse8h09_p1c, mRNA sequence.
```

```
ACCESSION   BX567930
VERSION     BX567930.1  GI:33434834
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse8h09_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 40;
  Best Local Similarity   80.0%;  Pred. No. 1.6e+02;
  Matches   32;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2144 CTGCTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              ||   ||| | ||||||| |  |||||||||||||||||
Db          1 CTCTAGATAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 40


RESULT 209
CF278363
LOCUS       CF278363                37 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-D24.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--04-D24, mRNA sequence.
ACCESSION   CF278363
VERSION     CF278363.1  GI:33655749
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--04-D24"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27;  DB 1;  Length 37;
  Best Local Similarity   85.7%;  Pred. No. 1.4e+02;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2152 TGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              || |||| || |  ||||||||||||||||||||
Db          2 TGCTTTTCTTTTTTTTTTTTTTTTTTTTTTTTT 36


RESULT 210
CF292043
LOCUS       CF292043                37 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-L12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-L12, mRNA sequence.
ACCESSION   CF292043
VERSION     CF292043.1  GI:33661076
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-L12"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27;  DB 1;  Length 37;
  Best Local Similarity   85.7%;  Pred. No. 1.4e+02;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTAACT 2190
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                 |||||| |  |||||||||||||||||||| | |
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGATT 35


RESULT 211
BJ081937/c
LOCUS       BJ081937                  39 bp    mRNA    linear   EST 29-SEP-2003
DEFINITION  BJ081937 NIBB Mochii normalized Xenopus tailbud library Xenopus
            laevis cDNA clone XL077g22 3', mRNA sequence.
ACCESSION   BJ081937
VERSION     BJ081937.1  GI:17576341
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL077g22"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 25"
                     /clone_lib="NIBB Mochii normalized Xenopus tailbud
                     library"

  Query Match             1.0%;  Score 27;  DB 1;  Length 39;
  Best Local Similarity   81.1%;  Pred. No. 1.6e+02;
  Matches   30;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTTAA 2201
                |  ||||||||||||||||||||  | ||||  ||||
Db         39 CCNTTTTTTTTTTTTTTTTTTTANATATGAATTTTAA 3


RESULT 212
AV742106/c
LOCUS       AV742106                  41 bp    mRNA    linear   EST 17-OCT-2000
DEFINITION  AV742106 CB Homo sapiens cDNA clone CBCAAC09 5', mRNA sequence.
ACCESSION   AV742106
VERSION     AV742106.1  GI:10859687
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
  TITLE     Homo sapiens CB library cDNA clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in
            Shanghai.
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CBCAAC09"
                     /tissue_type="cord blood"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /clone_lib="CB"
                     /note="Vector: pBluescript; Site_1: EcoRI; The insert is
                     cloned randomly with the EcoRI digestion"

  Query Match             1.0%;  Score 27;  DB 1;  Length 41;
  Best Local Similarity   81.1%;  Pred. No. 1.9e+02;
  Matches   30;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGA 2194
                |||| |  ||||||| ||||||||||||   |||||
Db         41 TTTTTTTTTTTTTTTNTTTTTTTTTTTTTTNTTTGA 5


RESULT 213
CF300448
LOCUS       CF300448                  41 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--04-N15.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--04-N15, mRNA sequence.
ACCESSION   CF300448
VERSION     CF300448.1  GI:33672209
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--04-N15"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 27;  DB 1;  Length 41;
  Best Local Similarity   85.7%;  Pred. No. 1.9e+02;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
                ||  ||||||| |  ||||||||||||||||||||
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Db          7 TTTTTTTTTTTTTTGTTTTTTTTTTTTTTTTTTT 41


RESULT 214
AZ785111
LOCUS       AZ785111                 31 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0028B14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0028B14 R, genomic survey sequence.
ACCESSION   AZ785111
VERSION     AZ785111.1  GI:12921525
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0028  row: B  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0028B14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 31;
  Best Local Similarity   93.3%;  Pred. No. 79;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| | ||||||||||||||||||||
Db          2 TTTTTTTTTTCTTTTTTTTTTTTTTTTTT 31
```

```
RESULT 215
DR85L9T/c
LOCUS       DR85L9T                  33 bp    DNA     linear   GSS 22-NOV-2002
DEFINITION  Danio rerio genomic clone DKEY-85L9, genomic survey sequence.
ACCESSION   AL983097
VERSION     AL983097.1  GI:25187898
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Humphray,S.J., Huckle,E. and Hunt,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 85L9. 85L9 is
            part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene.
            Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-85L9"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 33;
  Best Local Similarity   93.3%;  Pred. No. 99;
  Matches   28;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |||||||||||||| |||||||
Db         30 TTTTTTTTTCCTTTTTTTTTTTCTTTTTTT 1


RESULT 216
AZ589726
LOCUS       AZ589726                 38 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0398I24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0398I24 R, genomic survey sequence.
ACCESSION   AZ589726
VERSION     AZ589726.1  GI:11711916
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0398  row: I  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
```

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            Class: plasmid ends
            High quality sequence stop: 38.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0398I24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 38;
  Best Local Similarity   81.6%;  Pred. No. 1.6e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||||||| |  ||||||||||||||| ||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTCTTTTTTTTT 38


RESULT 217
AW247125
LOCUS       AW247125                 39 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819775.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819775 3',
            mRNA sequence.
ACCESSION   AW247125
VERSION     AW247125.1  GI:6590118
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819775.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 13
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 39 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM2  row: H  column: 16
            High quality sequence stop: 13.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819775"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 39;
  Best Local Similarity   81.6%;  Pred. No. 1.8e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||||||| |  ||||||||||||||| ||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTCTTTTTTTTT 38


RESULT 218
AZ339890/c
LOCUS       AZ339890                 39 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0071L05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0071L05 R, genomic survey sequence.
ACCESSION   AZ339890
VERSION     AZ339890.1  GI:10414608
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0071  row: L  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
```

```
                     /clone="UUGC1M0071L05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 39;
  Best Local Similarity   81.6%;  Pred. No. 1.8e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2148 TGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              || ||| ||||||| |  |||| ||||||| |||||||
Db         38 TGGTTGGTTTTTTTGTTTTTTGTTTTTTGTTTTTTT 1


RESULT 219
AL638703
LOCUS       AL638703                 40 bp    mRNA    linear   EST 07-NOV-2001
DEFINITION  AL638703 XGC-egg Silurana tropicalis cDNA clone L1E5g04 5', mRNA
            sequence.
ACCESSION   AL638703
VERSION     AL638703.1  GI:16790682
KEYWORDS    EST.
SOURCE      Silurana tropicalis (western clawed frog)
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (10_2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Huckle E
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: L1E5g04.sp6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Silurana tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="L1E5g04"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 40;
  Best Local Similarity   81.6%;  Pred. No. 2e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  |||||||||||||| ||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTGTTTTTTTTTTT 38


RESULT 220
CF332442/c
LOCUS       CF332442                 40 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-P05.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-P05, mRNA sequence.
ACCESSION   CF332442
VERSION     CF332442.1  GI:33813100
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-P05"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 40;
  Best Local Similarity   81.6%;  Pred. No. 2e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||    ||||||
Db         38 TTTTTTTTTTTTTTTTTTTTTTTTTTTCGAAAACTTT 1


RESULT 221
AZ326980
LOCUS       AZ326980                 40 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0050A12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0050A12 F, genomic survey sequence.
ACCESSION   AZ326980
VERSION     AZ326980.1  GI:10385271
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
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            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0050  row: A  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 40.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0050A12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 40;
  Best Local Similarity   81.6%;  Pred. No. 2e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||| ||||| |||||||| ||||||| ||||    ||||
Db          3 TTTGTTCTCTTTTTTTTTGTTTTTTGTTTTTTTTTTG 40


RESULT 222
AZ824309
LOCUS       AZ824309                 37 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0098O17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0098O17 R, genomic survey sequence.
ACCESSION   AZ824309
VERSION     AZ824309.1  GI:12994217
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0098  row: O  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 37.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0098O17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 26.6;  DB 1;  Length 37;
  Best Local Similarity   87.9%;  Pred. No. 1.6e+02;
  Matches   29;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2186
              |||||||| |  |||||||||| ||||||||||
Db          2 ATTTTTTTTTTTTTTTTTTTTCTTTTTTTTTT 34


RESULT 223
CF291979
LOCUS       CF291979                 39 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-K03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-K03, mRNA sequence.
ACCESSION   CF291979
VERSION     CF291979.1  GI:33661012
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
```

```
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-K03"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.9%;  Score 26.6;  DB 1;  Length 39;
  Best Local Similarity   87.9%;  Pred. No. 2e+02;
  Matches   29;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTA 2187
              ||||||| |  |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTATA 33


RESULT 224
BX564796
LOCUS       BX564796                 40 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX564796 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse73g04_p1c, mRNA sequence.
ACCESSION   BX564796
VERSION     BX564796.1  GI:33431939
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse73g04_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.9%;  Score 26.6;  DB 1;  Length 40;
  Best Local Similarity   87.9%;  Pred. No. 2.1e+02;
  Matches   29;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | |||||| |  ||||||||||||||||||||
Db          8 AGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 40


RESULT 225
TA105A11P/c
LOCUS       TA105A11P                40 bp    DNA     linear   GSS 16-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 105a11, forward sequence,
            genomic survey sequence.
ACCESSION   AL464696
VERSION     AL464696.1  GI:11877799
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v+i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="105a11"

  Query Match             0.9%;  Score 26.6;  DB 1;  Length 40;
  Best Local Similarity   87.9%;  Pred. No. 2.1e+02;
  Matches   29;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              ||  |||||||  ||||||||||||||||||||
Db         33 TTTTTTTTTTAACCTTTTTTTTTTTTTTTTT 1


RESULT 226
AL048768/c
LOCUS       AL048768                 37 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp566M083_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566M083, mRNA sequence.
ACCESSION   AL048768
VERSION     AL048768.1  GI:4727839
KEYWORDS    EST.
```

```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp566M083"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

  Query Match             0.9%;  Score 26.4;  DB 1;  Length 37;
  Best Local Similarity   83.3%;  Pred. No. 1.8e+02;
  Matches   30;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                ||  |||||||  |  |||| ||||||||||||||||
Db         37 TTTTTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTT 2


RESULT 227
BX550894
LOCUS       BX550894                 39 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX550894 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse115d09_p1c, mRNA sequence.
ACCESSION   BX550894
VERSION     BX550894.1  GI:33374625
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse115d09_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.9%;  Score 26.4;  DB 1;  Length 39;
  Best Local Similarity   83.3%;  Pred. No. 2.2e+02;
  Matches   30;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                | |||  |||| |  ||||||||||||||||||||
Db          4 TAGATAGTTTTTTTTTTTTTTTTTTTTTTTTTTTT 39


RESULT 228
CF280292/c
LOCUS       CF280292                 39 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--06-O11.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--06-O11, mRNA sequence.
ACCESSION   CF280292
VERSION     CF280292.1  GI:33657678
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--06-O11"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice etiolated leaf plasmid cDNA library
                     (14ETL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.9%;  Score 26.4;  DB 1;  Length 39;
  Best Local Similarity   83.3%;  Pred. No. 2.2e+02;
  Matches   30;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                ||  ||||||||  ||   ||||||||||||||||
Db         37 TTATTTTTTTTCCCCCCCTTTTTTTTTTTTTTTTT 2


RESULT 229
BQ591342
LOCUS       BQ591342                 40 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012713-024-017-G20-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-017-G20 3-PRIME, mRNA sequence.
ACCESSION   BQ591342
VERSION     BQ591342.1  GI:26120925
KEYWORDS    EST.
```

```
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 40   Std Error: 0.00
            Plate: 17  row: G  column: 20
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:188777"
                     /db_xref="taxon:161934"
                     /clone="024-017-G20"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             0.9%;  Score 26.4;  DB 1;  Length 40;
  Best Local Similarity   83.3%;  Pred. No. 2.4e+02;
  Matches   30;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||| ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTATTTCTTTTTTTTTTTTTTTT 36


RESULT 230
BX569502
LOCUS       BX569502                 31 bp    mRNA    linear   EST 14-OCT-2003
DEFINITION  BX569502 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse9a03_p1c, mRNA sequence.
ACCESSION   BX569502
VERSION     BX569502.1  GI:33437420
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse9a03_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 31;
  Best Local Similarity   90.3%;  Pred. No. 1e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 31


RESULT 231
CF278807/c
LOCUS       CF278807                 31 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--04-N15.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--04-N15, mRNA sequence.
ACCESSION   CF278807
VERSION     CF278807.1  GI:33656193
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ETL--04-N15"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
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/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 26.2; DB 1; Length 31;
Best Local Similarity 90.3%; Pred. No. 1e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db         31 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1
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RESULT 232
CF300345
LOCUS CF300345 31 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-L08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--04-L08, mRNA sequence.
ACCESSION CF300345
VERSION CF300345.1 GI:33672106
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 31)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .31
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-L08"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 26.2; DB 1; Length 31;
Best Local Similarity 90.3%; Pred. No. 1e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 31
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RESULT 233
AZ333315
LOCUS AZ333315 31 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0062A21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0062A21 F, genomic survey sequence.
ACCESSION AZ333315
VERSION AZ333315.1 GI:10397811
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: A column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 31.
FEATURES Location/Qualifiers
source 1. .31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0062A21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 26.2; DB 1; Length 31;
Best Local Similarity 90.3%; Pred. No. 1e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 31
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RESULT 234
AZ375973/c
LOCUS AZ375973 31 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0129D08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0129D08 R, genomic survey sequence.
ACCESSION AZ375973
VERSION AZ375973.1 GI:10489673
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0129  row: D  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0129D08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 31;
  Best Local Similarity   90.3%;  Pred. No. 1e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db         31 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 235
AZ510092/c
LOCUS       AZ510092                 31 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0354P14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0354P14 F, genomic survey sequence.
ACCESSION   AZ510092
VERSION     AZ510092.1  GI:10691408
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0354  row: P  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0354P14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 31;
  Best Local Similarity   90.3%;  Pred. No. 1e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db         31 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 236
AZ597046/c
LOCUS       AZ597046                 31 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0410K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0410K08 R, genomic survey sequence.
ACCESSION   AZ597046
VERSION     AZ597046.1  GI:11719236
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0410  row: K  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0410K08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 31;
  Best Local Similarity   90.3%;  Pred. No. 1e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
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Db         31 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 237
AZ623538
LOCUS       AZ623538                 31 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0461G21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0461G21 F, genomic survey sequence.
ACCESSION   AZ623538
VERSION     AZ623538.1  GI:11745728
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0461  row: G  column: 21
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0461G21"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 31;
  Best Local Similarity   90.3%;  Pred. No. 1e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 31


RESULT 238
AZ627692/c
LOCUS       AZ627692                 31 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0469C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0469C09 R, genomic survey sequence.
ACCESSION   AZ627692
VERSION     AZ627692.1  GI:11749882
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
```

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            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0469  row: C  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0469C09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 31;
  Best Local Similarity   90.3%;  Pred. No. 1e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db         31 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 239
AZ778697/c
LOCUS       AZ778697                 31 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0014O02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0014O02 F, genomic survey sequence.
ACCESSION   AZ778697
VERSION     AZ778697.1  GI:12908605
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0014  row: O  column: 02
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0014O02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 31;
  Best Local Similarity   90.3%;  Pred. No. 1e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db         31 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 240
AZ821215/c
LOCUS       AZ821215                 31 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0093F21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0093F21 R, genomic survey sequence.
ACCESSION   AZ821215
VERSION     AZ821215.1  GI:12991123
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0093  row: F  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0093F21"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 31;
  Best Local Similarity   90.3%;  Pred. No. 1e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||
Db         31 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 241
AZ826618/c
LOCUS       AZ826618                  31 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0102C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0102C19 F, genomic survey sequence.
ACCESSION   AZ826618
VERSION     AZ826618.1  GI:12996442
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0102  row: C  column: 19
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0102C19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 31;
  Best Local Similarity   90.3%;  Pred. No. 1e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||
Db         31 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 242
AZ400441/c
LOCUS       AZ400441                  32 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0166C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0166C14 R, genomic survey sequence.
ACCESSION   AZ400441
VERSION     AZ400441.1  GI:10515515
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
```

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            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0166  row: C  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 32.
FEATURES              Location/Qualifiers
     source           1. .32
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0166C14"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 32;
  Best Local Similarity   90.3%;  Pred. No. 1.2e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
                ||||||||  |  ||||||||||||||||||
Db         31 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 243
AU013658
LOCUS       AU013658                33 bp    mRNA    linear   EST 03-AUG-1998
DEFINITION  AU013658 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc08464, mRNA sequence.
ACCESSION   AU013658
VERSION     AU013658.1  GI:3368449
KEYWORDS    EST.
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES              Location/Qualifiers
     source           1. .33
                      /organism="Schizosaccharomyces pombe"
                      /mol_type="mRNA"
                      /strain="972"
                      /db_xref="taxon:4896"
                      /clone="spc08464"
                      /sex="h minus"
                      /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                      /note="Vector: M13mp19; The cDNA library of
                      Schizosaccharomyces pombe was prepared by cloning cDNA
                      into the SmaI site of M13mp19 DNA and the direction of DNA
                      sequences was not always from 5' to 3'. The cDNA data of
                      Schizosaccharomyces pombe are available for searching on
                      the World Wide Web.  (URL, http://www.nirs.go.jp)"

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 33;
  Best Local Similarity   90.3%;  Pred. No. 1.3e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTTTTTTTTTTTTTTAA 2188
                ||||  |  ||||||||||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTAA 31


RESULT 244
BU431802
LOCUS       BU431802                34 bp    mRNA    linear   EST 09-SEP-2002
DEFINITION  601654630R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839742 3',
            mRNA sequence.
ACCESSION   BU431802
VERSION     BU431802.1  GI:22770284
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM528  row: k  column: 07
            High quality sequence stop: 34.
FEATURES              Location/Qualifiers
     source           1. .34
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3839742"
                      /tissue_type="glioblastoma"
                      /lab_host="DH10B (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_57"
                      /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
                      SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                      Double-stranded cDNA was prepared from cell line RNA.  5'
                      and 3' adaptors were used in cloning as follows: 5'
                      adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                      sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                      (where B = A, C, or G and N = A, C,  G, or T).   Average
                      insert size 1.55 kb (range 0.9-4.0 kb).  12/15 colonies
```

contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

Query Match 0.9%; Score 26.2; DB 1; Length 34;
Best Local Similarity 90.3%; Pred. No. 1.5e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTTAAC 2189
              ||| |  ||||||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTAAC 31
```

RESULT 245
BQ590703
LOCUS BQ590703 35 bp mRNA linear EST 06-DEC-2002
DEFINITION S013312-024-018-B02-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-018-B02 3-PRIME, mRNA sequence.
ACCESSION BQ590703
VERSION BQ590703.1 GI:26120286
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 35)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 35 Std Error: 0.00
Plate: 18 row: B column: 02
Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES Location/Qualifiers
source 1. .35
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189418"
/db_xref="taxon:161934"
/clone="024-018-B02"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 26.2; DB 1; Length 35;
Best Local Similarity 90.3%; Pred. No. 1.6e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||  ||||||| ||||||||||||||||||||
Db          5 TTTTTTTTTTTTCCTTTTTTTTTTTTTTT 35
```

RESULT 246
CF298131
LOCUS CF298131 36 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-G07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-G07, mRNA sequence.
ACCESSION CF298131
VERSION CF298131.1 GI:33669892
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 36)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .36
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--01-G07"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 26.2; DB 1; Length 36;
Best Local Similarity 90.3%; Pred. No. 1.8e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 31
```

RESULT 247
T57700
LOCUS T57700 36 bp mRNA linear EST 08-FEB-1995
DEFINITION yc01d11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79413 3' similar to similar to gb:X61970 PROTEASOME ZETA CHAIN (HUMAN), mRNA sequence.
ACCESSION T57700
VERSION T57700.1 GI:659561
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 36)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.

```
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
   PUBMED   8889549
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence starts: 1
            High qality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -21m13
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:483030"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:79413"
                     /sex="male"
                     /dev_stage="72 years"
                     /lab_host="SOLR cells (kanamycin resistant)"
                     /clone_lib="Stratagene lung (#937210)"
                     /note="Organ: lung; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                     Oligo dT. normal lung.  Average insert size: 1.0 kb;
                     Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                     3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 36;
  Best Local Similarity   84.8%;  Pred. No. 1.8e+02;
  Matches   28;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTA 2187
              ||||| |    ||||||||||||||||||||||
Db          1 TTTTTGTNGNTTTTTTTTTTTTTTTTTTTTA 33


RESULT 248
AW245247
LOCUS       AW245247                37 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820028.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820028 3',
            mRNA sequence.
ACCESSION   AW245247
VERSION     AW245247.1  GI:6588240
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820028.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washingtion Genome Center. Vector
            Trimming: cross_match from University of Washingtion Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washingtion Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 37 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM3  row: C  column: 5.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820028"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 37;
  Best Local Similarity   90.3%;  Pred. No. 2e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||||| || |||||||||| ||||||||||
Db          2 TTTTTTTTCATTTTTTTTCTTTTTTTTT 32


RESULT 249
AW248768
LOCUS       AW248768                39 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2820919.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820919 3',
            mRNA sequence.
ACCESSION   AW248768
VERSION     AW248768.1  GI:6591761
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2820919.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washingtion Genome Center. Vector
            Trimming: cross_match from University of Washingtion Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washingtion Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 7 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 39 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: LLCM5  row: H  column: 8
            High quality sequence stop: 7.
FEATURES             Location/Qualifiers
```

```
     source          1. .39
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820919"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 39;
  Best Local Similarity   90.3%;  Pred. No. 2.4e+02;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTATTTTTTTTTTTTTTTTTTT 31


RESULT 250
BJ049570/c
LOCUS       BJ049570                39 bp    mRNA    linear   EST 29-SEP-2003
DEFINITION  BJ049570 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL026j12 3', mRNA sequence.
ACCESSION   BJ049570
VERSION     BJ049570.1  GI:17378969
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="XL026j12"
                     /tissue_type="whole embryo"
                     /dev_stage="stage 15"
                     /clone_lib="NIBB Mochii normalized Xenopus neurula
                     library"

  Query Match             0.9%;  Score 26.2;  DB 1;  Length 39;
  Best Local Similarity   84.8%;  Pred. No. 2.4e+02;
  Matches   28;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGT 2198
              ||||||||||||||||||  || ||  |||||
Db         36 TTTTTTTTTTTTTTTTTTTGNAAGTTANAAAGT 4


RESULT 251
TA115E07P/c
LOCUS       TA115E07P               37 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 115e07, forward sequence,
            genomic survey sequence.
ACCESSION   AL462838
VERSION     AL462838.1  GI:11832519
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="115e07"

  Query Match             0.9%;  Score 26;  DB 1;  Length 37;
  Best Local Similarity   82.9%;  Pred. No. 2.2e+02;
  Matches   29;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||  |||||||| ||   ||||||||||||||||||
Db         35 TTTTTTTTTTTCCCCCNCTTTTTTTTTTTTTTTT 1


RESULT 252
CF328529
LOCUS       CF328529                39 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--03-H18.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--03-H18, mRNA sequence.
ACCESSION   CF328529
VERSION     CF328529.1  GI:33805303
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
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           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--03-H18"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.9%;  Score 26;  DB 1;  Length 39;
  Best Local Similarity   85.3%;  Pred. No. 2.6e+02;
  Matches   29;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAA 2188
              ||||||| |  ||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTCGAA 34


RESULT 253
AA852205
LOCUS       AA852205                 40 bp    mRNA    linear   EST 20-JUN-2002
DEFINITION  NHTBCae11a12r1 Normal Human Trabecular Bone Cells Homo sapiens cDNA
            clone NHTBCae11a12, mRNA sequence.
ACCESSION   AA852205
VERSION     AA852205.1  GI:2940798
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
            Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang,L.M.,
            Robey,P.G., Hotchkiss,R.N. and Francomano,C.A.
  TITLE     SGAP: The Skeletal Genome Anatomy Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Libin Jia
            Medical Genetics Branch
            National Human Genome Research Institute
            10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
            Tel: 301-402-4877
            Fax: 301-496-7157
            Email: libin@helix.nih.gov
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="NHTBCae11a12"
                     /sex="Female"
                     /tissue_type="Bone"
                     /cell_type="Trabecular Bone Cells"
                     /lab_host="SURE"
                     /clone_lib="Normal Human Trabecular Bone Cells"
                     /note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI;
                     Library constructed by Dr. Marian Young and Dr. Pamela
                     Gehron Robey (NIDCR)"

  Query Match             0.9%;  Score 26;  DB 1;  Length 40;
  Best Local Similarity   85.3%;  Pred. No. 2.8e+02;
  Matches   29;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||| |  |||||||||||||||||||||| | |
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTAATTCT 34


RESULT 254
AU267300/c
LOCUS       AU267300                 30 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU267300 VS Dictyostelium discoideum cDNA clone VSH345 5', mRNA
            sequence.
ACCESSION   AU267300
VERSION     AU267300.1  GI:20526098
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSH345"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

  Query Match             0.9%;  Score 25.8;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  |||||||||||||||||||
Db         30 TTTTTTTTTNATTTTTTTTTTTTTTTTTT 1


RESULT 255
AZ627842
LOCUS       AZ627842                 32 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0474G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0474G03 F, genomic survey sequence.
ACCESSION   AZ627842
VERSION     AZ627842.1  GI:11750128
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0474  row: G  column: 03
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 32.
FEATURES              Location/Qualifiers
     source           1. .32
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0474G03"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."

  Query Match             0.9%;  Score 25.8;  DB 1;  Length 32;
  Best Local Similarity   93.1%;  Pred. No. 1.4e+02;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              ||||||| | ||||||||||||||||||||
Db          4 TTTTTTTTTACTTTTTTTTTTTTTTTTT 32


RESULT 256
BJ036312
LOCUS       BJ036312                35 bp    mRNA    linear   EST 26-SEP-2003
DEFINITION  BJ036312 NIBB Mochii normalized Xenopus neurula library Xenopus
            laevis cDNA clone XL035k09 5', mRNA sequence.
ACCESSION   BJ036312
VERSION     BJ036312.1  GI:17396897
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE     Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .35
                      /organism="Xenopus laevis"
                      /mol_type="mRNA"
                      /db_xref="taxon:8355"
                      /clone="XL035k09"
                      /tissue_type="whole embryo"
                      /dev_stage="stage 15"
                      /clone_lib="NIBB Mochii normalized Xenopus neurula
                      library"

  Query Match             0.9%;  Score 25.8;  DB 1;  Length 35;
  Best Local Similarity   93.1%;  Pred. No. 2e+02;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTT 2182
              || ||||| ||||||||||||||||||||
Db          3 ATATTTTTTTCCTTTTTTTTTTTTTTTT 31


RESULT 257
CF321807
LOCUS       CF321807                38 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--13-D01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--13-D01, mRNA sequence.
ACCESSION   CF321807
VERSION     CF321807.1  GI:33693568
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .38
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="HD--13-D01"
                      /tissue_type="callus"
                      /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                      /lab_host="E.coli DH10B"
                      /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                      cDNA library (HD)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                      treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                      reverse transcribed and then used for PCR. mRNA was
                      derived from rice Histone Deacetylase overexpression
                      line."

  Query Match             0.9%;  Score 25.8;  DB 1;  Length 38;
  Best Local Similarity   81.1%;  Pred. No. 2.6e+02;
  Matches   30;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTT 2191
              ||||||| |  |||||||||||| |||||||  | ||
Db          2 TTTTTTTTTTTTTTTTTTTTTTCTTTTTTTGGAATT 38
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```
RESULT 258
CF302459/c
LOCUS       CF302459                32 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--08-A01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--08-A01, mRNA sequence.
ACCESSION   CF302459
VERSION     CF302459.1  GI:33674220
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="7LEAF--08-A01"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.9%;  Score 25.6;  DB 1;  Length 32;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  |||||||||||||||||| ||
Db         32 TTTTTTTTTTTTTTTTTTTTTTTTTTTTGTT 1


RESULT 259
AZ314322
LOCUS       AZ314322                32 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0031N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0031N05 F, genomic survey sequence.
ACCESSION   AZ314322
VERSION     AZ314322.1  GI:10360096
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0031  row: N  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 32.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0031N05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 25.6;  DB 1;  Length 32;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTATTTTTTTTTTTTTT 32


RESULT 260
AZ579652
LOCUS       AZ579652                32 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0367C12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0367C12 R, genomic survey sequence.
ACCESSION   AZ579652
VERSION     AZ579652.1  GI:11694081
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: C column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.

FEATURES Location/Qualifiers
source 1. .32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0367C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25.6; DB 1; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
| ||||| | |||||||||||||||||||
Db 1 TCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 261
CF334899
LOCUS CF334899 33 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--04-F19.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--04-F19, mRNA sequence.
ACCESSION CF334899
VERSION CF334899.1 GI:33818141
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 33)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
source 1. .33
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--04-F19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was pepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."

Query Match 0.9%; Score 25.6; DB 1; Length 33;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
| ||||| | |||||||||||||||||||
Db 2 TTTTTTTTTTTTTTTTTTTTTTTGTTTTTTTT 33

RESULT 262
CF315464
LOCUS CF315464 34 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--04-G09.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--04-G09, mRNA sequence.
ACCESSION CF315464
VERSION CF315464.1 GI:33687225
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 34)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
source 1. .34
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--04-G09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.9%; Score 25.6; DB 1; Length 34;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||| ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTCTTTTTTTTTTTTTT 32


RESULT 263
AZ307192/c
LOCUS       AZ307192                34 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0008B07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0008B07 R, genomic survey sequence.
ACCESSION   AZ307192
VERSION     AZ307192.1  GI:10345947
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0008  row: B  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 34.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0008B07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 25.6;  DB 1;  Length 34;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+02;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  |||||||||| ||||||||||
Db         34 TTTTTTTTTTTTTTTTTTTTCTTTTTTTTTT 3


RESULT 264
DR41A4T/c
LOCUS       DR41A4T                 34 bp    DNA     linear   GSS 22-NOV-2002
DEFINITION  Danio rerio genomic clone DKEY-41A4, genomic survey sequence.
ACCESSION   AL980969
VERSION     AL980969.1  GI:25182658
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Humphray,S.J., Huckle,E. and Hunt,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 41A4. 41A4 is
            part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene.
            Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-41A4"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"

  Query Match             0.9%;  Score 25.6;  DB 1;  Length 34;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+02;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  |||||||||| ||||||||||
Db         34 TTTTTTTTTTTTTTTTTTTTTGTTTTTTTTT 3


RESULT 265
AL587823
LOCUS       AL587823                37 bp    mRNA    linear   EST 02-MAR-2001
DEFINITION  AL587823 BP Chicken Brain Library Gallus gallus cDNA clone
            ROS064A03, mRNA sequence.
ACCESSION   AL587823
VERSION     AL587823.1  GI:13192857
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Murray,F.
  TITLE     BP Chicken Brain Library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
            (*6854-
            Seq primer: M13F.
FEATURES             Location/Qualifiers
```

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    source          1. .37
                    /organism="Gallus gallus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9031"
                    /clone="ROS064A03"
                    /tissue_type="Brain"
                    /dev_stage="Unknown"
                    /lab_host="DH10B"
                    /clone_lib="BP Chicken Brain Library"
                    /note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; Cloned
                    unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
                    5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                    GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
                    Clonetech (*6854-1)"

  Query Match             0.9%;  Score 25.6;  DB 1;  Length 37;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+02;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTT 2182
              || |||||||| |  ||||||||||||||||
Db          3 TTCATTTTTTTTTTTTTTTTTTTTTTTTTT 34


RESULT 266
CF319784/c
LOCUS       CF319784                34 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--10-G18.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-G18, mRNA sequence.
ACCESSION   CF319784
VERSION     CF319784.1  GI:33691545
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--10-G18"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.9%;  Score 25.4;  DB 1;  Length 34;
  Best Local Similarity   96.3%;  Pred. No. 2.1e+02;
  Matches   26;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTT 2180
              |||||||||| ||||||||||||||||
Db         27 ATTTTTTTCTTCTTTTTTTTTTTTT 1


RESULT 267
CF332027
LOCUS       CF332027                37 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--08-F24.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--08-F24, mRNA sequence.
ACCESSION   CF332027
VERSION     CF332027.1  GI:33812274
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--08-F24"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.9%;  Score 25.4;  DB 1;  Length 37;
  Best Local Similarity   82.9%;  Pred. No. 2.9e+02;
  Matches   29;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              |||| |  ||||||||||||||||||||  |||| |
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTCAAACTCT 35


RESULT 268
BX556487
LOCUS       BX556487                38 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX556487 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse27e01_p1c, mRNA sequence.
ACCESSION   BX556487
VERSION     BX556487.1  GI:33427748
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
```

```
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse27e01_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.9%;  Score 25.4;  DB 1;  Length 38;
  Best Local Similarity   82.9%;  Pred. No. 3.1e+02;
  Matches   29;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              | |||  |||| |  ||||||||||||||||||||
Db          4 TAGATAGTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 269
BX555173
LOCUS       BX555173                 39 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX555173 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse19h11_p1c, mRNA sequence.
ACCESSION   BX555173
VERSION     BX555173.1  GI:33379189
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse19h11_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             0.9%;  Score 25.4;  DB 1;  Length 39;
  Best Local Similarity   82.9%;  Pred. No. 3.4e+02;
  Matches   29;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              | |||  |||| |  ||||||||||||||||||||
Db          4 TAGATAGTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 270
CF642215/c
LOCUS       CF642215                 39 bp    mRNA    linear   EST 02-OCT-2003
DEFINITION  D49_A04 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
            sequence.
ACCESSION   CF642215
VERSION     CF642215.1  GI:37409389
KEYWORDS    EST.
SOURCE      Ustilago maydis
  ORGANISM  Ustilago maydis
            Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
            Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Nugent,K.G., Choffe,K. and Saville,B.J.
  TITLE     Gene Expression during Ustilago maydis Diploid Filamentous Growth:
            EST Library Creation and Analyses
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Barry J. Saville
            Saville Lab
            University of Toronto
            3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
            Tel: 905 569 4702
            Fax: 905 828 3792
            Email: bsaville@utm.utoronto.ca
            Plate: UTM-UM-D126/7-049-UTM  row: 04  column: A
            Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGGG 3')
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Ustilago maydis"
                     /mol_type="mRNA"
                     /strain="FBD12"
                     /db_xref="taxon:5270"
                     /cell_type="Mycelia"
                     /dev_stage="Filamentous diploid"
                     /clone_lib="Filamentous Forced Diploid"
                     /note="Vector: pSport; mRNA was extracted from diploid
                     mycelia. A cDNA library was constructed and
                     unidirectionally cloned into pSPORT plasmid, with the use
                     of the Superscript II cDNA Library Construction Kit."

  Query Match             0.9%;  Score 25.4;  DB 1;  Length 39;
  Best Local Similarity   80.6%;  Pred. No. 3.4e+02;
  Matches   29;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2148 TGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              | ||    |||||||||  ||||||||||||||||
Db         36 TTATNTTCTTTTTTCTCTCTTTTTTTTTTTTTTTT 1


RESULT 271
AZ346794
LOCUS       AZ346794                 39 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0082N08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0082N08 F, genomic survey sequence.
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ACCESSION   AZ346794
VERSION     AZ346794.1  GI:10426031
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0082  row: N  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 39.
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0082N08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 25.4;  DB 1;  Length 39;
  Best Local Similarity   82.9%;  Pred. No. 3.4e+02;
  Matches   29;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTTA 2200
              ||||||||| |||||||||||  || ||| |  |||
Db          4 TTTTTTTTTCTTTTTTTTTTTTACGTTGCATCTTA 38


RESULT 272
BG666435/c
LOCUS       BG666435                 30 bp    mRNA    linear   EST 30-APR-2001
DEFINITION  DRACRC02 Rat DRG Library Rattus norvegicus cDNA clone DRACRC02 5',
            mRNA sequence.
ACCESSION   BG666435
VERSION     BG666435.1  GI:13888357
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
            Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
            Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
  TITLE     Identification of gene expression profile of dorsal root ganglion
            in the rat peripheral axotomy model of neuropathic pain
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
  MEDLINE   22056133
   PUBMED   12060780
COMMENT     Contact: Zhang Xu
            Laboratory of Sensory System
            Institute of Neuroscience
            320 Yue Yang Road, Shanghai 200031, P.R.China
            Tel: 86-21-64748700-121
            Fax: 86-21-64713446
            Email: xu.zhang@ion.ac.cn
            This clone is also available at Chinese National Human Genome
            Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
            Pudong New Area, P.R.China. Please contact with Zhang Xu
            (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
            PCR PRimers
            FORWARD: T3
            BACKWARD: T7
            Seq primer: T3
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="DRACRC02"
                     /sex="male"
                     /tissue_type="dorsal root ganglion"
                     /dev_stage="adult"
                     /clone_lib="Rat DRG Library"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 273
CF280699
LOCUS       CF280699                 30 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ETL--07-H15.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--07-H15, mRNA sequence.
ACCESSION   CF280699
VERSION     CF280699.1  GI:33658085
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
```

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            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="14ETL--07-H15"
                      /tissue_type="leaf"
                      /dev_stage="14 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice etiolated leaf plasmid cDNA library
                      (14ETL)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 274
CF292086/c
LOCUS       CF292086                30 bp    mRNA    linear   EST 14-AUG-2003
DEFINITION  14ROOT--02-M10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
            sativa cDNA clone 14ROOT--02-M10, mRNA sequence.
ACCESSION   CF292086
VERSION     CF292086.1  GI:33661119
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="14ROOT--02-M10"
                      /tissue_type="root"
                      /dev_stage="14 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 275
CF299555
LOCUS       CF299555                30 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  7LEAF--03-K01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--03-K01, mRNA sequence.
ACCESSION   CF299555
VERSION     CF299555.1  GI:33671316
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="Oryza sativa"
                      /mol_type="mRNA"
                      /cultivar="Nackdong"
                      /db_xref="taxon:4530"
                      /clone="7LEAF--03-K01"
                      /tissue_type="leaf"
                      /dev_stage="7 days after germination"
                      /lab_host="E.coli DH10B"
                      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 276
CF312417
LOCUS       CF312417                30 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  ABF--08-C19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--08-C19, mRNA sequence.
ACCESSION   CF312417
VERSION     CF312417.1  GI:33684178
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
```

```
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
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                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 277
CF322226
LOCUS       CF322226                30 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--13-M02.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--13-M02, mRNA sequence.
ACCESSION   CF322226
VERSION     CF322226.1  GI:33693987
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /db_xref="taxon:4530"
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                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
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Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 278
CF327835/c
LOCUS       CF327835                30 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--02-H17.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--02-H17, mRNA sequence.
ACCESSION   CF327835
VERSION     CF327835.1  GI:33803920
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
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                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
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Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 279
CF336555
LOCUS       CF336555                30 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--06-K13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-K13, mRNA sequence.
ACCESSION   CF336555
VERSION     CF336555.1  GI:33821487
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa"
                     /mol_type="mRNA"
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                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
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Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 280
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LOCUS       AZ357603                30 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0099H17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0099H17 F, genomic survey sequence.
ACCESSION   AZ357603
VERSION     AZ357603.1  GI:10471303
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0099  row: H  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0099H17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 281
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LOCUS       AZ455741                30 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0258D16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0258D16 F, genomic survey sequence.
ACCESSION   AZ455741
VERSION     AZ455741.1  GI:10613866
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0258  row: D  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
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                    /sex="Male"
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                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained  from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high  molar excess. The
                    adaptored DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptored mouse DNA was annealed to
                    adaptored vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
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Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 282
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LOCUS       AZ481739                 30 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0306N12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0306N12 F, genomic survey sequence.
ACCESSION   AZ481739
VERSION     AZ481739.1  GI:10642804
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0306  row: N  column: 12
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            Class: plasmid ends
            High quality sequence stop: 30.
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                     /clone="UUGC1M0306N12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
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Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 283
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LOCUS       AZ582114                 30 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0374J17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0374J17 F, genomic survey sequence.
ACCESSION   AZ582114
VERSION     AZ582114.1  GI:11700674
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0374  row: J  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Mus musculus"
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Access DB# _____

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner # : _____ Date:
Art Unit: _____ Phone Number 30_____ Serial Number: _____
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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#)_____	STN _____
Searcher Phone #: _____	AA Sequence (#)_____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis_____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify)_____

PTO-1590 (8-01)

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Db          1 GGTTTTTTTTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTGAAA 44


RESULT 16
CF316377/c
LOCUS       CF316377                 44 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--05-K08.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--05-K08, mRNA sequence.
ACCESSION   CF316377
VERSION     CF316377.1  GI:33688138
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
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                     /cultivar="Nackdong"
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                     /clone="HD--05-K08"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.1%;  Score 30.8;  DB 1;  Length 44;
  Best Local Similarity   83.3%;  Pred. No. 41;
  Matches   35;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              || ||||||| |  |||||||||||||||||||| | |||
Db         43 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTTT 2


RESULT 17
BF582680/c
LOCUS       BF582680                 45 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602094085F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208373 5',
            mRNA sequence.
ACCESSION   BF582680
VERSION     BF582680.1  GI:11656398
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9772  row: j  column: 22
            High quality sequence stop: 45.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4208373"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Co24"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."

  Query Match             1.1%;  Score 30.8;  DB 1;  Length 45;
  Best Local Similarity   83.3%;  Pred. No. 45;
  Matches   35;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              || ||||||| |  |||||||||||||||||||| ||||
Db         44 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTT 3


RESULT 18
AW250836
LOCUS       AW250836                 47 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821228.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821228 3',
            mRNA sequence.
ACCESSION   AW250836
VERSION     AW250836.1  GI:6593829
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821228.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 40
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                     /clone="Tse47c06_p1c"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

  Query Match             1.1%;  Score 31.6;  DB 1;  Length 46;
  Best Local Similarity   80.4%;  Pred. No. 33;
  Matches   37;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              ||  ||||||| |  ||||||||||||||||||||||    || ||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGAAA 46


RESULT 13
CF329281
LOCUS       CF329281                 48 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--04-I20.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--04-I20, mRNA sequence.
ACCESSION   CF329281
VERSION     CF329281.1  GI:33806798
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--04-I20"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.1%;  Score 31.6;  DB 1;  Length 48;
  Best Local Similarity   80.4%;  Pred. No. 38;
  Matches   37;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              ||  ||||||| |  |||||||||||||||||||| | || | ||
Db          2 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGTTGGGAA 47


RESULT 14
CF321018
LOCUS       CF321018                 45 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--12-C01.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--12-C01, mRNA sequence.
ACCESSION   CF321018
VERSION     CF321018.1  GI:33692779
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--12-C01"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.1%;  Score 31.4;  DB 1;  Length 45;
  Best Local Similarity   85.4%;  Pred. No. 33;
  Matches   35;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAA 2195
              ||||||| |  ||||||||||||||||||||    ||||||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAA 44


RESULT 15
AV950753
LOCUS       AV950753                 48 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV950753 Nori Satoh unpublished cDNA library, cleavage stage embryo
            Ciona intestinalis cDNA clone cicl03n20 5', mRNA sequence.
ACCESSION   AV950753
VERSION     AV950753.1  GI:19439052
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cicl03n20"
```

```
RESULT 10
AI350847
LOCUS       AI350847                 49 bp    mRNA    linear   EST 30-DEC-1998
DEFINITION  qt11e08.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1947302 3'
            similar to gb:J05021 EZRIN (HUMAN);, mRNA sequence.
ACCESSION   AI350847
VERSION     AI350847.1  GI:4088053
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1947302"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GC4"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "

  Query Match             1.2%;  Score 32.4;  DB 1;  Length 49;
  Best Local Similarity   85.7%;  Pred. No. 28;
  Matches   36;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              ||||||| |  ||||||||||||||||||||  ||||| ||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCCTTTGCAA 42


RESULT 11
CF330635
LOCUS       CF330635                 48 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  NACL--06-G22.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--06-G22, mRNA sequence.
ACCESSION   CF330635
VERSION     CF330635.1  GI:33809506
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-G22"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

  Query Match             1.1%;  Score 32.2;  DB 1;  Length 48;
  Best Local Similarity   82.2%;  Pred. No. 29;
  Matches   37;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAA 2195
              ||  ||||||| |  ||||||||||||||||||||||||  || |
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAACAATGGA 48


RESULT 12
BX560004
LOCUS       BX560004                 46 bp    mRNA    linear   EST 10-OCT-2003
DEFINITION  BX560004 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse47c06_p1c, mRNA sequence.
ACCESSION   BX560004
VERSION     BX560004.1  GI:33367992
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
  ORGANISM  Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidea; Glossinidae; Glossina.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
  JOURNAL   Genome Biol. 4 (10), R63 (2003)
  MEDLINE   22881942
   PUBMED   14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
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          Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189777"
                     /db_xref="taxon:161934"
                     /clone="024-019-E11"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             1.2%;  Score 32.4;  DB 1;  Length 46;
  Best Local Similarity   85.7%;  Pred. No. 22;
  Matches   36;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |||||||||||||||||||||||||   |||
Db          5 TTTTTTTTTTTTCCTTTTTTTTTTTTTTTTTTTTTTTTTTT 46


RESULT 8
CF317896
LOCUS       CF317896                 47 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--07-M03.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--07-M03, mRNA sequence.
ACCESSION   CF317896
VERSION     CF317896.1  GI:33689657
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HD--07-M03"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             1.2%;  Score 32.4;  DB 1;  Length 47;
  Best Local Similarity   85.7%;  Pred. No. 24;
  Matches   36;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              |||||||  |  ||||||||||||||||||||    |||||||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAAA 45


RESULT 9
BQ590523
LOCUS       BQ590523                 48 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012843-024-019-I03-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-I03 3-PRIME, mRNA sequence.
ACCESSION   BQ590523
VERSION     BQ590523.1  GI:26120106
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 48   Std Error: 0.00
            Plate: 19  row: I  column: 03
            Seq primer: T7; GTAATACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:189595"
                     /db_xref="taxon:161934"
                     /clone="024-019-I03"
                     /tissue_type="storage root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-storage root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"

  Query Match             1.2%;  Score 32.4;  DB 1;  Length 48;
  Best Local Similarity   85.7%;  Pred. No. 26;
  Matches   36;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |||||||||||||||||||||||||   |||
Db          7 TTTTTTTTTTTTCCTTTTTTTTTTTTTTTTTTTTTTTTTTT 48
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Oligo dT. Gastrulating embryos were collected at 7.5dpc from C57BL6 x DBA matings, excluding embryos that had developed head folds and all extraembryonic tissues. Average insert size: 1.3 kb (range: 0.5 - 3.0 kb). Referenced in Development 121, 2479-2489 (1995)"

Query Match 1.2%; Score 33; DB 1; Length 49;
Best Local Similarity 79.6%; Pred. No. 21;
Matches 39; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGTT 2199
              ||  |||||||  |  ||||||||||||||||||||||    ||| |||| |
Db         49 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGAT 1
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RESULT 5
CF321820
LOCUS CF321820 46 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--13-D08.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--13-D08, mRNA sequence.
ACCESSION CF321820
VERSION CF321820.1 GI:33693581
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 46)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .46
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--13-D08"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.2%; Score 32.8; DB 1; Length 46;
Best Local Similarity 84.1%; Pred. No. 18;
Matches 37; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGT 2198
              |||||||  |  ||||||||||||||||||||  |||||||  | |
Db          2 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAACTTTGTTACT 45
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RESULT 6
CF332233
LOCUS CF332233 45 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--08-K14.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-K14, mRNA sequence.
ACCESSION CF332233
VERSION CF332233.1 GI:33812694
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 45)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .45
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--08-K14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.2%; Score 32.4; DB 1; Length 45;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              |||||||  |  ||||||||||||||||||||  || | |||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATCTATAAAA 45
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RESULT 7
BQ590334
LOCUS BQ590334 46 bp mRNA linear EST 06-DEC-2002
DEFINITION E012843-024-019-E11-T7 MPIZ-ADIS-024-storage root Beta vulgaris cDNA clone 024-019-E11 3-PRIME, mRNA sequence.
ACCESSION BQ590334
VERSION BQ590334.1 GI:26119917
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 46)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 46 Std Error: 0.00
Plate: 19 row: E column: 11

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AA966391/c
LOCUS       AA966391                 50 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  w4f01a1.r1 Aspergillus nidulans 24hr asexual developmental and
            vegetative cDNA lambda zap library Emericella nidulans cDNA clone
            w4f01a1 5', mRNA sequence.
ACCESSION   AA966391
VERSION     AA966391.1  GI:3140473
KEYWORDS    EST.
SOURCE      Emericella nidulans (anamorph: Aspergillus nidulans)
  ORGANISM  Emericella nidulans
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; Emericella.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
            Prade,R. and Roe,B.
  TITLE     An Aspergillus nidulans EST Database
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Emericella nidulans"
                     /mol_type="mRNA"
                     /strain="FGSC A26"
                     /db_xref="taxon:162425"
                     /clone="w4f01a1"
                     /tissue_type="vegetative mycelia, asexual structures"
                     /clone_lib="Aspergillus nidulans 24hr asexual
                     developmental and vegetative cDNA lambda zap library"
                     /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
                     XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
                     3' end of cDNA cloned into XhoI site of pBluescript"

  Query Match             1.2%;  Score 33.8;  DB 1;  Length 50;
  Best Local Similarity   84.4%;  Pred. No. 15;
  Matches   38;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTGAA 2195
              ||  ||||||| |  ||||||||||||||||||||||||  |||
Db         45 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAACTCCGAA 1


RESULT 3
CF332589
LOCUS       CF332589                 50 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  JMT--01-C13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--01-C13, mRNA sequence.
ACCESSION   CF332589
VERSION     CF332589.1  GI:33813402
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="JMT--01-C13"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                     cDNA library (JMT)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                     was reverse transcribed and then used for PCR. mRNA was
                     pepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."

  Query Match             1.2%;  Score 33.6;  DB 1;  Length 50;
  Best Local Similarity   81.2%;  Pred. No. 17;
  Matches   39;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGT 2198
              ||  ||||||| |  ||||||||||||||||||||||    ||| |||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAGT 48


RESULT 4
AA116935/c
LOCUS       AA116935                 49 bp    mRNA    linear   EST 15-NOV-1996
DEFINITION  mn22g01.r1 Beddington mouse embryonic region Mus musculus cDNA
            clone IMAGE:538704 5', mRNA sequence.
ACCESSION   AA116935
VERSION     AA116935.1  GI:1671951
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:325640
            Seq primer: -40m13 ET.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6 x DBA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:538704"
                     /sex="pooled"
                     /tissue_type="embryo"
                     /dev_stage="7.5dpc"
                     /lab_host="DH12S"
                     /clone_lib="Beddington mouse embryonic region"
                     /note="Organ: whole embryo; Vector: pCMV-SPORT; Site_1:
                     SalI; Site_2: NotI; Cloned unidirectionally.  Primer:
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c3612	12	0.4	12	1	CF332993	ACCESSION:CF332993
3613	12	0.4	12	1	CF333992	ACCESSION:CF333992
c3614	12	0.4	12	1	CF333992	ACCESSION:CF333992
3615	12	0.4	14	1	BQ591949	ACCESSION:BQ591949
c3616	12	0.4	14	1	BQ591949	ACCESSION:BQ591949
3617	12	0.4	14	1	CF291593	ACCESSION:CF291593
3618	12	0.4	14	1	CF330198	ACCESSION:CF330198
c3619	12	0.4	14	1	CF330198	ACCESSION:CF330198
c3620	12	0.4	15	1	AW249689	ACCESSION:AW249689
c3621	12	0.4	15	1	AW250976	ACCESSION:AW250976
3622	12	0.4	16	1	AW248540	ACCESSION:AW248540
c3623	12	0.4	17	1	AW246518	ACCESSION:AW246518
c3624	12	0.4	18	1	AW249853	ACCESSION:AW249853
3625	12	0.4	18	1	AW249970	ACCESSION:AW249970
c3626	12	0.4	18	1	AW249970	ACCESSION:AW249970
3627	12	0.4	18	1	AW251048	ACCESSION:AW251048
c3628	12	0.4	20	1	AZ772074	ACCESSION:AZ772074
c3629	12	0.4	20	1	CF322590	ACCESSION:CF322590
3630	12	0.4	20	1	AZ427740	ACCESSION:AZ427740
3631	12	0.4	21	1	AZ967472	ACCESSION:AZ967472
c3632	12	0.4	21	1	AW248826	ACCESSION:AW248826
c3633	12	0.4	24	1	AZ665864	ACCESSION:AZ665864
3634	11.8	0.4	15	1	CF330669	ACCESSION:CF330669
c3635	11.8	0.4	15	1	AW246494	ACCESSION:AW246494
3636	11.8	0.4	15	1	CF299603	ACCESSION:CF299603
3637	11.8	0.4	15	1	BM658732	ACCESSION:BM658732
c3638	11.8	0.4	15	1	BM658732	ACCESSION:BM658732
3639	11.8	0.4	15	1	CF332179	ACCESSION:CF332179
c3640	11.8	0.4	15	1	CF332179	ACCESSION:CF332179
3641	11.8	0.4	16	1	AW245338	ACCESSION:AW245338
3642	11.8	0.4	16	1	AI798250	ACCESSION:AI798250
c3643	11.8	0.4	16	1	AI798250	ACCESSION:AI798250
c3644	11.8	0.4	18	1	AW250449	ACCESSION:AW250449
c3645	11.8	0.4	19	1	AZ323986	ACCESSION:AZ323986
c3646	11.8	0.4	19	1	AZ810717	ACCESSION:AZ810717
c3647	11.8	0.4	20	1	AZ786781	ACCESSION:AZ786781
3648	11.8	0.4	23	1	AZ810709	ACCESSION:AZ810709
c3649	11.6	0.4	19	1	AI364573	ACCESSION:AI364573
3650	11.6	0.4	19	1	AW248167	ACCESSION:AW248167
3651	11.6	0.4	19	1	AW249918	ACCESSION:AW249918
c3652	11.6	0.4	19	1	AZ447864	ACCESSION:AZ447864
3653	11.6	0.4	19	1	AZ345537	ACCESSION:AZ345537
c3654	11.6	0.4	19	1	AZ493581	ACCESSION:AZ493581
c3655	11.6	0.4	19	1	AZ369369	ACCESSION:AZ369369
3656	11.6	0.4	22	1	AA888191	ACCESSION:AA888191
c3657	11.4	0.4	14	1	CF291593	ACCESSION:CF291593
c3658	11.4	0.4	15	1	AW246551	ACCESSION:AW246551
3659	11.4	0.4	15	1	AW249689	ACCESSION:AW249689
3660	11.4	0.4	16	1	AW246490	ACCESSION:AW246490
c3661	11.4	0.4	16	1	AW248540	ACCESSION:AW248540
c3662	11.4	0.4	17	1	AW251033	ACCESSION:AW251033
c3663	11.4	0.4	17	1	AW246528	ACCESSION:AW246528
3664	11.4	0.4	17	1	AW246518	ACCESSION:AW246518
3665	11.4	0.4	18	1	AW249853	ACCESSION:AW249853
c3666	11.4	0.4	18	1	AW251048	ACCESSION:AW251048
c3667	11.4	0.4	19	1	AZ995149	ACCESSION:AZ995149
3668	11.4	0.4	19	1	AZ514586	ACCESSION:AZ514586
3669	11.4	0.4	20	1	AZ308410	ACCESSION:AZ308410
c3670	11.4	0.4	20	1	AZ469472	ACCESSION:AZ469472
3671	11.4	0.4	20	1	AZ303903	ACCESSION:AZ303903
3672	11.2	0.4	16	1	BQ583458	ACCESSION:BQ583458
c3673	11.2	0.4	19	1	AZ440413	ACCESSION:AZ440413
c3674	11.2	0.4	20	1	AZ957966	ACCESSION:AZ957966
3675	11.2	0.4	22	1	D20705	ACCESSION:D20705
c3676	11.2	0.4	24	1	CF291636	ACCESSION:CF291636
3677	11	0.4	15	1	AW250976	ACCESSION:AW250976
3678	11	0.4	18	1	AW246520	ACCESSION:AW246520
c3679	11	0.4	19	1	AZ328922	ACCESSION:AZ328922
c3680	11	0.4	19	1	AW248934	ACCESSION:AW248934
c3681	11	0.4	20	1	CF317946	ACCESSION:CF317946
c3682	11	0.4	20	1	AZ512414	ACCESSION:AZ512414
c3683	11	0.4	21	1	AZ331046	ACCESSION:AZ331046
3684	11	0.4	22	1	TA181E11P	ACCESSION:AL474328
c3685	10.8	0.4	16	1	AW251049	ACCESSION:AW251049
3686	10.8	0.4	16	1	BQ588093	ACCESSION:BQ588093
c3687	10.8	0.4	18	1	AW246451	ACCESSION:AW246451
c3688	10.8	0.4	19	1	AZ803756	ACCESSION:AZ803756
3689	10.8	0.4	19	1	AZ786308	ACCESSION:AZ786308
3690	10.8	0.4	19	1	AZ595570	ACCESSION:AZ595570
c3691	10.8	0.4	20	1	AU257221	ACCESSION:AU257221
3692	10.8	0.4	20	1	AZ789280	ACCESSION:AZ789280
c3693	10.8	0.4	21	1	AZ629111	ACCESSION:AZ629111
3694	10.8	0.4	25	1	BH791022	ACCESSION:BH791022
3695	10.6	0.4	19	1	AA878744	ACCESSION:AA878744
c3696	10.6	0.4	19	1	AZ782026	ACCESSION:AZ782026
3697	10.6	0.4	20	1	AZ828826	ACCESSION:AZ828826
3698	10.6	0.4	20	1	AZ387816	ACCESSION:AZ387816
c3699	10.4	0.4	16	1	BQ591425	ACCESSION:BQ591425

ALIGNMENTS

RESULT 1
AI270095
LOCUS AI270095 49 bp mRNA linear EST 17-NOV-1998
DEFINITION qt63c08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959950 3', mRNA sequence.
ACCESSION AI270095
VERSION AI270095.1 GI:3889262
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
FEATURES Location/Qualifiers
source 1. .49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1959950"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Eso2"
/note="Organ: esophagus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Life Technologies catalog #: 11502-010"

Query Match 1.3%; Score 35.2; DB 1; Length 49;
Best Local Similarity 83.3%; Pred. No. 7.3;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGT 2198
Db 2 TTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGT 49

RESULT 2

c3465	12.6	0.4	19	1	AZ595570	ACCESSION:AZ595570
3466	12.6	0.4	19	1	AZ760597	ACCESSION:AZ760597
3467	12.6	0.4	19	1	AZ761834	ACCESSION:AZ761834
c3468	12.6	0.4	19	1	AZ775865	ACCESSION:AZ775865
3469	12.6	0.4	19	1	AZ779094	ACCESSION:AZ779094
3470	12.6	0.4	19	1	AZ782026	ACCESSION:AZ782026
3471	12.6	0.4	19	1	AZ789674	ACCESSION:AZ789674
c3472	12.6	0.4	19	1	AZ789674	ACCESSION:AZ789674
3473	12.6	0.4	19	1	AZ807440	ACCESSION:AZ807440
3474	12.6	0.4	19	1	AZ962769	ACCESSION:AZ962769
c3475	12.6	0.4	20	1	AL587630	ACCESSION:AL587630
3476	12.6	0.4	20	1	AU264645	ACCESSION:AU264645
3477	12.6	0.4	20	1	AU267884	ACCESSION:AU267884
3478	12.4	0.4	14	1	CF301021	ACCESSION:CF301021
c3479	12.4	0.4	14	1	CF301021	ACCESSION:CF301021
3480	12.4	0.4	15	1	CF543203	ACCESSION:CF543203
3481	12.4	0.4	15	1	AW245585	ACCESSION:AW245585
c3482	12.4	0.4	15	1	AW245585	ACCESSION:AW245585
3483	12.4	0.4	15	1	AW246494	ACCESSION:AW246494
3484	12.4	0.4	15	1	AW246551	ACCESSION:AW246551
c3485	12.4	0.4	15	1	CF299603	ACCESSION:CF299603
3486	12.4	0.4	16	1	CF319827	ACCESSION:CF319827
c3487	12.4	0.4	16	1	AI564678	ACCESSION:AI564678
c3488	12.4	0.4	16	1	AW246490	ACCESSION:AW246490
c3489	12.4	0.4	16	1	BQ588093	ACCESSION:BQ588093
c3490	12.4	0.4	17	1	AW245664	ACCESSION:AW245664
c3491	12.4	0.4	18	1	BM398017	ACCESSION:BM398017
3492	12.4	0.4	19	1	AZ774536	ACCESSION:AZ774536
c3493	12.4	0.4	19	1	AI648553	ACCESSION:AI648553
3494	12.4	0.4	19	1	AZ369369	ACCESSION:AZ369369
3495	12.4	0.4	19	1	AZ510143	ACCESSION:AZ510143
c3496	12.4	0.4	19	1	AZ514586	ACCESSION:AZ514586
3497	12.4	0.4	19	1	AZ827164	ACCESSION:AZ827164
c3498	12.4	0.4	20	1	CF302637	ACCESSION:CF302637
c3499	12.4	0.4	20	1	AZ772040	ACCESSION:AZ772040
3500	12.4	0.4	22	1	AZ355624	ACCESSION:AZ355624
c3501	12.4	0.4	25	1	BH856226	ACCESSION:BH856226
c3502	12.2	0.4	17	1	AW246446	ACCESSION:AW246446
3503	12.2	0.4	17	1	AW248779	ACCESSION:AW248779
3504	12.2	0.4	17	1	AW246528	ACCESSION:AW246528
3505	12.2	0.4	18	1	AZ924200	ACCESSION:AZ924200
c3506	12.2	0.4	18	1	AW246520	ACCESSION:AW246520
3507	12.2	0.4	19	1	AI476315	ACCESSION:AI476315
3508	12.2	0.4	19	1	AI357421	ACCESSION:AI357421
c3509	12.2	0.4	19	1	AZ608537	ACCESSION:AZ608537
3510	12.2	0.4	25	1	AZ404619	ACCESSION:AZ404619
3511	12	0.4	12	1	BG668943	ACCESSION:BG668943
c3512	12	0.4	12	1	BG668943	ACCESSION:BG668943
3513	12	0.4	12	1	BQ582536	ACCESSION:BQ582536
c3514	12	0.4	12	1	BQ582536	ACCESSION:BQ582536
3515	12	0.4	12	1	BQ588719	ACCESSION:BQ588719
c3516	12	0.4	12	1	BQ588719	ACCESSION:BQ588719
3517	12	0.4	12	1	BQ594698	ACCESSION:BQ594698
c3518	12	0.4	12	1	BQ594698	ACCESSION:BQ594698
3519	12	0.4	12	1	CF279278	ACCESSION:CF279278
c3520	12	0.4	12	1	CF279278	ACCESSION:CF279278
3521	12	0.4	12	1	CF291428	ACCESSION:CF291428
c3522	12	0.4	12	1	CF291428	ACCESSION:CF291428
3523	12	0.4	12	1	CF291800	ACCESSION:CF291800
c3524	12	0.4	12	1	CF291800	ACCESSION:CF291800
3525	12	0.4	12	1	CF291801	ACCESSION:CF291801
c3526	12	0.4	12	1	CF291801	ACCESSION:CF291801
3527	12	0.4	12	1	CF291885	ACCESSION:CF291885
c3528	12	0.4	12	1	CF291885	ACCESSION:CF291885
3529	12	0.4	12	1	CF291886	ACCESSION:CF291886
c3530	12	0.4	12	1	CF291886	ACCESSION:CF291886
3531	12	0.4	12	1	CF292107	ACCESSION:CF292107
c3532	12	0.4	12	1	CF292107	ACCESSION:CF292107
3533	12	0.4	12	1	CF295593	ACCESSION:CF295593
c3534	12	0.4	12	1	CF295593	ACCESSION:CF295593
3535	12	0.4	12	1	CF298686	ACCESSION:CF298686
c3536	12	0.4	12	1	CF298686	ACCESSION:CF298686
3537	12	0.4	12	1	CF298872	ACCESSION:CF298872
c3538	12	0.4	12	1	CF298872	ACCESSION:CF298872
3539	12	0.4	12	1	CF299343	ACCESSION:CF299343
c3540	12	0.4	12	1	CF299343	ACCESSION:CF299343
3541	12	0.4	12	1	CF299514	ACCESSION:CF299514
c3542	12	0.4	12	1	CF299514	ACCESSION:CF299514
3543	12	0.4	12	1	CF300272	ACCESSION:CF300272
c3544	12	0.4	12	1	CF300272	ACCESSION:CF300272
3545	12	0.4	12	1	CF300420	ACCESSION:CF300420
c3546	12	0.4	12	1	CF300420	ACCESSION:CF300420
3547	12	0.4	12	1	CF300558	ACCESSION:CF300558
c3548	12	0.4	12	1	CF300558	ACCESSION:CF300558
3549	12	0.4	12	1	CF300881	ACCESSION:CF300881
c3550	12	0.4	12	1	CF300881	ACCESSION:CF300881
3551	12	0.4	12	1	CF301006	ACCESSION:CF301006
c3552	12	0.4	12	1	CF301006	ACCESSION:CF301006
3553	12	0.4	12	1	CF301075	ACCESSION:CF301075
c3554	12	0.4	12	1	CF301075	ACCESSION:CF301075
3555	12	0.4	12	1	CF301489	ACCESSION:CF301489
c3556	12	0.4	12	1	CF301489	ACCESSION:CF301489
3557	12	0.4	12	1	CF301940	ACCESSION:CF301940
c3558	12	0.4	12	1	CF301940	ACCESSION:CF301940
3559	12	0.4	12	1	CF302029	ACCESSION:CF302029
c3560	12	0.4	12	1	CF302029	ACCESSION:CF302029
3561	12	0.4	12	1	CF302122	ACCESSION:CF302122
c3562	12	0.4	12	1	CF302122	ACCESSION:CF302122
3563	12	0.4	12	1	CF302289	ACCESSION:CF302289
c3564	12	0.4	12	1	CF302289	ACCESSION:CF302289
3565	12	0.4	12	1	CF302486	ACCESSION:CF302486
c3566	12	0.4	12	1	CF302486	ACCESSION:CF302486
3567	12	0.4	12	1	CF308112	ACCESSION:CF308112
c3568	12	0.4	12	1	CF308112	ACCESSION:CF308112
3569	12	0.4	12	1	CF311835	ACCESSION:CF311835
c3570	12	0.4	12	1	CF311835	ACCESSION:CF311835
3571	12	0.4	12	1	CF311836	ACCESSION:CF311836
c3572	12	0.4	12	1	CF311836	ACCESSION:CF311836
3573	12	0.4	12	1	CF313356	ACCESSION:CF313356
c3574	12	0.4	12	1	CF313356	ACCESSION:CF313356
3575	12	0.4	12	1	CF315565	ACCESSION:CF315565
c3576	12	0.4	12	1	CF315565	ACCESSION:CF315565
3577	12	0.4	12	1	CF317551	ACCESSION:CF317551
c3578	12	0.4	12	1	CF317551	ACCESSION:CF317551
3579	12	0.4	12	1	CF317798	ACCESSION:CF317798
c3580	12	0.4	12	1	CF317798	ACCESSION:CF317798
3581	12	0.4	12	1	CF320426	ACCESSION:CF320426
c3582	12	0.4	12	1	CF320426	ACCESSION:CF320426
3583	12	0.4	12	1	CF324793	ACCESSION:CF324793
c3584	12	0.4	12	1	CF324793	ACCESSION:CF324793
3585	12	0.4	12	1	CF326913	ACCESSION:CF326913
c3586	12	0.4	12	1	CF326913	ACCESSION:CF326913
3587	12	0.4	12	1	CF327376	ACCESSION:CF327376
c3588	12	0.4	12	1	CF327376	ACCESSION:CF327376
3589	12	0.4	12	1	CF327962	ACCESSION:CF327962
c3590	12	0.4	12	1	CF327962	ACCESSION:CF327962
3591	12	0.4	12	1	CF328229	ACCESSION:CF328229
c3592	12	0.4	12	1	CF328229	ACCESSION:CF328229
3593	12	0.4	12	1	CF329141	ACCESSION:CF329141
c3594	12	0.4	12	1	CF329141	ACCESSION:CF329141
3595	12	0.4	12	1	CF329142	ACCESSION:CF329142
c3596	12	0.4	12	1	CF329142	ACCESSION:CF329142
3597	12	0.4	12	1	CF329346	ACCESSION:CF329346
c3598	12	0.4	12	1	CF329346	ACCESSION:CF329346
3599	12	0.4	12	1	CF329872	ACCESSION:CF329872
c3600	12	0.4	12	1	CF329872	ACCESSION:CF329872
3601	12	0.4	12	1	CF329929	ACCESSION:CF329929
c3602	12	0.4	12	1	CF329929	ACCESSION:CF329929
3603	12	0.4	12	1	CF331241	ACCESSION:CF331241
c3604	12	0.4	12	1	CF331241	ACCESSION:CF331241
3605	12	0.4	12	1	CF331858	ACCESSION:CF331858
c3606	12	0.4	12	1	CF331858	ACCESSION:CF331858
3607	12	0.4	12	1	CF331904	ACCESSION:CF331904
c3608	12	0.4	12	1	CF331904	ACCESSION:CF331904
3609	12	0.4	12	1	CF331950	ACCESSION:CF331950
c3610	12	0.4	12	1	CF331950	ACCESSION:CF331950

c3319	13	0.5	13	1	CF316439	ACCESSION:CF316439
3320	13	0.5	13	1	CF316440	ACCESSION:CF316440
c3321	13	0.5	13	1	CF316440	ACCESSION:CF316440
3322	13	0.5	13	1	CF316637	ACCESSION:CF316637
c3323	13	0.5	13	1	CF316637	ACCESSION:CF316637
3324	13	0.5	13	1	CF318290	ACCESSION:CF318290
c3325	13	0.5	13	1	CF318290	ACCESSION:CF318290
3326	13	0.5	13	1	CF319066	ACCESSION:CF319066
c3327	13	0.5	13	1	CF319066	ACCESSION:CF319066
3328	13	0.5	13	1	CF319531	ACCESSION:CF319531
c3329	13	0.5	13	1	CF319531	ACCESSION:CF319531
3330	13	0.5	13	1	CF319532	ACCESSION:CF319532
c3331	13	0.5	13	1	CF319532	ACCESSION:CF319532
3332	13	0.5	13	1	CF319919	ACCESSION:CF319919
c3333	13	0.5	13	1	CF319919	ACCESSION:CF319919
3334	13	0.5	13	1	CF320017	ACCESSION:CF320017
c3335	13	0.5	13	1	CF320017	ACCESSION:CF320017
3336	13	0.5	13	1	CF320018	ACCESSION:CF320018
c3337	13	0.5	13	1	CF320018	ACCESSION:CF320018
3338	13	0.5	13	1	CF320143	ACCESSION:CF320143
c3339	13	0.5	13	1	CF320143	ACCESSION:CF320143
3340	13	0.5	13	1	CF320938	ACCESSION:CF320938
c3341	13	0.5	13	1	CF320938	ACCESSION:CF320938
3342	13	0.5	13	1	CF326844	ACCESSION:CF326844
c3343	13	0.5	13	1	CF326844	ACCESSION:CF326844
3344	13	0.5	13	1	CF327070	ACCESSION:CF327070
c3345	13	0.5	13	1	CF327070	ACCESSION:CF327070
3346	13	0.5	13	1	CF327339	ACCESSION:CF327339
c3347	13	0.5	13	1	CF327339	ACCESSION:CF327339
3348	13	0.5	13	1	CF327340	ACCESSION:CF327340
c3349	13	0.5	13	1	CF327340	ACCESSION:CF327340
3350	13	0.5	13	1	CF327576	ACCESSION:CF327576
c3351	13	0.5	13	1	CF327576	ACCESSION:CF327576
3352	13	0.5	13	1	CF327888	ACCESSION:CF327888
c3353	13	0.5	13	1	CF327888	ACCESSION:CF327888
3354	13	0.5	13	1	CF327939	ACCESSION:CF327939
c3355	13	0.5	13	1	CF327939	ACCESSION:CF327939
3356	13	0.5	13	1	CF328153	ACCESSION:CF328153
c3357	13	0.5	13	1	CF328153	ACCESSION:CF328153
3358	13	0.5	13	1	CF328228	ACCESSION:CF328228
c3359	13	0.5	13	1	CF328228	ACCESSION:CF328228
3360	13	0.5	13	1	CF328807	ACCESSION:CF328807
c3361	13	0.5	13	1	CF328807	ACCESSION:CF328807
3362	13	0.5	13	1	CF329075	ACCESSION:CF329075
c3363	13	0.5	13	1	CF329075	ACCESSION:CF329075
3364	13	0.5	13	1	CF329076	ACCESSION:CF329076
c3365	13	0.5	13	1	CF329076	ACCESSION:CF329076
3366	13	0.5	13	1	CF329417	ACCESSION:CF329417
c3367	13	0.5	13	1	CF329417	ACCESSION:CF329417
3368	13	0.5	13	1	CF329460	ACCESSION:CF329460
c3369	13	0.5	13	1	CF329460	ACCESSION:CF329460
3370	13	0.5	13	1	CF329729	ACCESSION:CF329729
c3371	13	0.5	13	1	CF329729	ACCESSION:CF329729
3372	13	0.5	13	1	CF329800	ACCESSION:CF329800
c3373	13	0.5	13	1	CF329800	ACCESSION:CF329800
3374	13	0.5	13	1	CF329801	ACCESSION:CF329801
c3375	13	0.5	13	1	CF329801	ACCESSION:CF329801
3376	13	0.5	13	1	CF329869	ACCESSION:CF329869
c3377	13	0.5	13	1	CF329869	ACCESSION:CF329869
3378	13	0.5	13	1	CF329946	ACCESSION:CF329946
c3379	13	0.5	13	1	CF329946	ACCESSION:CF329946
3380	13	0.5	13	1	CF329988	ACCESSION:CF329988
c3381	13	0.5	13	1	CF329988	ACCESSION:CF329988
3382	13	0.5	13	1	CF330023	ACCESSION:CF330023
c3383	13	0.5	13	1	CF330023	ACCESSION:CF330023
3384	13	0.5	13	1	CF330725	ACCESSION:CF330725
c3385	13	0.5	13	1	CF330725	ACCESSION:CF330725
3386	13	0.5	13	1	CF331041	ACCESSION:CF331041
c3387	13	0.5	13	1	CF331041	ACCESSION:CF331041
3388	13	0.5	13	1	CF331266	ACCESSION:CF331266
c3389	13	0.5	13	1	CF331266	ACCESSION:CF331266
3390	13	0.5	13	1	CF331273	ACCESSION:CF331273
c3391	13	0.5	13	1	CF331273	ACCESSION:CF331273
3392	13	0.5	13	1	CF331903	ACCESSION:CF331903
c3393	13	0.5	13	1	CF331903	ACCESSION:CF331903
3394	13	0.5	13	1	CF332079	ACCESSION:CF332079
c3395	13	0.5	13	1	CF332079	ACCESSION:CF332079
3396	13	0.5	13	1	CF332695	ACCESSION:CF332695
c3397	13	0.5	13	1	CF332695	ACCESSION:CF332695
3398	13	0.5	13	1	CF332696	ACCESSION:CF332696
c3399	13	0.5	13	1	CF332696	ACCESSION:CF332696
3400	13	0.5	13	1	CF333486	ACCESSION:CF333486
c3401	13	0.5	13	1	CF333486	ACCESSION:CF333486
3402	13	0.5	13	1	CF333972	ACCESSION:CF333972
c3403	13	0.5	13	1	CF333972	ACCESSION:CF333972
3404	13	0.5	13	1	CF333973	ACCESSION:CF333973
c3405	13	0.5	13	1	CF333973	ACCESSION:CF333973
3406	13	0.5	13	1	CF334347	ACCESSION:CF334347
c3407	13	0.5	13	1	CF334347	ACCESSION:CF334347
3408	13	0.5	13	1	CF337022	ACCESSION:CF337022
c3409	13	0.5	13	1	CF337022	ACCESSION:CF337022
3410	13	0.5	14	1	CF327203	ACCESSION:CF327203
c3411	13	0.5	14	1	CF327203	ACCESSION:CF327203
3412	13	0.5	16	1	AW251049	ACCESSION:AW251049
3413	13	0.5	17	1	AW251033	ACCESSION:AW251033
3414	13	0.5	18	1	AW246451	ACCESSION:AW246451
3415	13	0.5	19	1	AZ764511	ACCESSION:AZ764511
c3416	13	0.5	19	1	AZ764511	ACCESSION:AZ764511
3417	13	0.5	19	1	AZ995149	ACCESSION:AZ995149
c3418	13	0.5	20	1	AZ479732	ACCESSION:AZ479732
c3419	13	0.5	20	1	AZ427740	ACCESSION:AZ427740
3420	13	0.5	20	1	AZ506216	ACCESSION:AZ506216
c3421	13	0.5	20	1	AZ506216	ACCESSION:AZ506216
3422	13	0.5	20	1	AZ764514	ACCESSION:AZ764514
c3423	13	0.5	20	1	AZ764514	ACCESSION:AZ764514
3424	13	0.5	20	1	AZ772040	ACCESSION:AZ772040
3425	13	0.5	20	1	AZ773905	ACCESSION:AZ773905
c3426	13	0.5	20	1	AZ773905	ACCESSION:AZ773905
c3427	13	0.5	20	1	AZ834769	ACCESSION:AZ834769
c3428	13	0.5	21	1	AZ589400	ACCESSION:AZ589400
3429	13	0.5	21	1	AZ346714	ACCESSION:AZ346714
3430	13	0.5	23	1	CB305256	ACCESSION:CB305256
c3431	13	0.5	23	1	AZ615086	ACCESSION:AZ615086
3432	13	0.5	23	1	AZ819376	ACCESSION:AZ819376
3433	12.8	0.5	16	1	AA937877	ACCESSION:AA937877
c3434	12.8	0.5	16	1	AA937877	ACCESSION:AA937877
c3435	12.8	0.5	16	1	AW245338	ACCESSION:AW245338
3436	12.8	0.5	16	1	BQ591425	ACCESSION:BQ591425
c3437	12.8	0.5	17	1	AW247976	ACCESSION:AW247976
3438	12.8	0.5	18	1	CF312453	ACCESSION:CF312453
c3439	12.8	0.5	18	1	CF312453	ACCESSION:CF312453
3440	12.8	0.5	19	1	AI149192	ACCESSION:AI149192
c3441	12.8	0.5	19	1	AI357421	ACCESSION:AI357421
3442	12.8	0.5	19	1	AZ608537	ACCESSION:AZ608537
c3443	12.8	0.5	19	1	AZ786308	ACCESSION:AZ786308
3444	12.8	0.5	19	1	AZ830469	ACCESSION:AZ830469
3445	12.8	0.5	22	1	AZ326642	ACCESSION:AZ326642
c3446	12.8	0.5	25	1	BG929133	ACCESSION:BG929133
3447	12.8	0.5	25	1	AI745099	ACCESSION:AI745099
c3448	12.8	0.5	28	1	AZ785005	ACCESSION:AZ785005
c3449	12.6	0.4	19	1	AI371092	ACCESSION:AI371092
3450	12.6	0.4	19	1	AZ408157	ACCESSION:AZ408157
c3451	12.6	0.4	19	1	AZ850833	ACCESSION:AZ850833
3452	12.6	0.4	19	1	AW246477	ACCESSION:AW246477
c3453	12.6	0.4	19	1	AW246477	ACCESSION:AW246477
3454	12.6	0.4	19	1	AW246513	ACCESSION:AW246513
c3455	12.6	0.4	19	1	AW246513	ACCESSION:AW246513
3456	12.6	0.4	19	1	AW248820	ACCESSION:AW248820
c3457	12.6	0.4	19	1	AW248820	ACCESSION:AW248820
c3458	12.6	0.4	19	1	BQ593604	ACCESSION:BQ593604
c3459	12.6	0.4	19	1	AZ345537	ACCESSION:AZ345537
c3460	12.6	0.4	19	1	AZ345792	ACCESSION:AZ345792
3461	12.6	0.4	19	1	AZ424216	ACCESSION:AZ424216
c3462	12.6	0.4	19	1	AZ424216	ACCESSION:AZ424216
3463	12.6	0.4	19	1	AZ440413	ACCESSION:AZ440413
3464	12.6	0.4	19	1	AZ493581	ACCESSION:AZ493581

3173	13.4	0.5	19	1	AZ803756	ACCESSION:AZ803756
3174	13.4	0.5	19	1	AZ810717	ACCESSION:AZ810717
c3175	13.4	0.5	20	1	AZ387816	ACCESSION:AZ387816
3176	13.4	0.5	20	1	AZ772074	ACCESSION:AZ772074
3177	13.4	0.5	20	1	AZ836069	ACCESSION:AZ836069
3178	13.4	0.5	20	1	AZ957966	ACCESSION:AZ957966
c3179	13.4	0.5	22	1	BX563723	ACCESSION:BX563723
3180	13.4	0.5	25	1	AU008929	ACCESSION:AU008929
3181	13.4	0.5	32	1	AZ445446	ACCESSION:AZ445446
3182	13.2	0.5	18	1	AW247875	ACCESSION:AW247875
3183	13.2	0.5	18	1	CF314887	ACCESSION:CF314887
c3184	13.2	0.5	18	1	CF314887	ACCESSION:CF314887
3185	13.2	0.5	19	1	CF332005	ACCESSION:CF332005
c3186	13.2	0.5	19	1	AA878744	ACCESSION:AA878744
c3187	13.2	0.5	19	1	AI476315	ACCESSION:AI476315
3188	13.2	0.5	19	1	AW247975	ACCESSION:AW247975
c3189	13.2	0.5	19	1	AW248167	ACCESSION:AW248167
3190	13.2	0.5	19	1	AW248934	ACCESSION:AW248934
c3191	13.2	0.5	19	1	AW249918	ACCESSION:AW249918
3192	13.2	0.5	19	1	AW250451	ACCESSION:AW250451
3193	13.2	0.5	19	1	BQ588375	ACCESSION:BQ588375
c3194	13.2	0.5	19	1	BQ588375	ACCESSION:BQ588375
3195	13.2	0.5	19	1	AZ447864	ACCESSION:AZ447864
3196	13.2	0.5	19	1	AZ514792	ACCESSION:AZ514792
c3197	13.2	0.5	19	1	AZ514792	ACCESSION:AZ514792
c3198	13.2	0.5	19	1	AZ579133	ACCESSION:AZ579133
3199	13.2	0.5	19	1	AZ648404	ACCESSION:AZ648404
c3200	13.2	0.5	19	1	AZ841555	ACCESSION:AZ841555
3201	13.2	0.5	19	1	AZ850833	ACCESSION:AZ850833
3202	13.2	0.5	20	1	AZ345646	ACCESSION:AZ345646
3203	13.2	0.5	20	1	AZ346143	ACCESSION:AZ346143
3204	13.2	0.5	20	1	AZ387841	ACCESSION:AZ387841
c3205	13.2	0.5	20	1	AU264645	ACCESSION:AU264645
c3206	13.2	0.5	20	1	AU267884	ACCESSION:AU267884
3207	13.2	0.5	20	1	AW249928	ACCESSION:AW249928
c3208	13.2	0.5	20	1	C53693	ACCESSION:C53693
3209	13.2	0.5	20	1	CF302574	ACCESSION:CF302574
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3211	13.2	0.5	20	1	CF302637	ACCESSION:CF302637
3212	13.2	0.5	20	1	CF322590	ACCESSION:CF322590
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3216	13.2	0.5	21	1	AZ483617	ACCESSION:AZ483617
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3222	13	0.5	13	1	BQ589180	ACCESSION:BQ589180
c3223	13	0.5	13	1	BQ589180	ACCESSION:BQ589180
3224	13	0.5	13	1	BQ590337	ACCESSION:BQ590337
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3232	13	0.5	13	1	CF280757	ACCESSION:CF280757
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3236	13	0.5	13	1	CF290970	ACCESSION:CF290970
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3240	13	0.5	13	1	CF291011	ACCESSION:CF291011
c3241	13	0.5	13	1	CF291011	ACCESSION:CF291011
3242	13	0.5	13	1	CF291060	ACCESSION:CF291060
c3243	13	0.5	13	1	CF291060	ACCESSION:CF291060
3244	13	0.5	13	1	CF291061	ACCESSION:CF291061
c3245	13	0.5	13	1	CF291061	ACCESSION:CF291061
3246	13	0.5	13	1	CF291167	ACCESSION:CF291167
c3247	13	0.5	13	1	CF291167	ACCESSION:CF291167
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c3249	13	0.5	13	1	CF291214	ACCESSION:CF291214
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c3251	13	0.5	13	1	CF291427	ACCESSION:CF291427
3252	13	0.5	13	1	CF291469	ACCESSION:CF291469
c3253	13	0.5	13	1	CF291469	ACCESSION:CF291469
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3098	14	0.5	14	1	CF335781
c3099	14	0.5	14	1	CF335781

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c3116	14	0.5	17	1	BG673623
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3123	14	0.5	21	1	AZ785791
3124	14	0.5	22	1	AZ375417
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3130	14	0.5	25	1	AU012885
3131	14	0.5	25	1	AZ510128
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3138	13.8	0.5	17	1	BQ797972
3139	13.8	0.5	18	1	AW249856
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3146	13.8	0.5	20	1	AZ304038
3147	13.8	0.5	20	1	AZ469472
3148	13.8	0.5	20	1	AZ512414
3149	13.8	0.5	21	1	AZ331619
c3150	13.8	0.5	21	1	AZ788269
c3151	13.8	0.5	21	1	AZ386904
c3152	13.8	0.5	23	1	AW249550
3153	13.8	0.5	25	1	AI560179
3154	13.6	0.5	20	1	AZ426873
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3157	13.6	0.5	20	1	AZ479732
3158	13.6	0.5	20	1	AZ645269
3159	13.6	0.5	20	1	AZ786781
c3160	13.6	0.5	23	1	AU267211
c3161	13.6	0.5	23	1	CK277017
3162	13.4	0.5	15	1	CF290849
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3164	13.4	0.5	15	1	CF291030
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3166	13.4	0.5	15	1	CF301470
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c3168	13.4	0.5	15	1	CF330669
c3169	13.4	0.5	15	1	CF543203
c3170	13.4	0.5	16	1	BQ583458
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3172	13.4	0.5	17	1	BG673623

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2888	15	0.5	21	1	AZ963501
c2889	15	0.5	21	1	AZ963501
c2890	15	0.5	22	1	AZ317017
c2891	15	0.5	23	1	CF308058
2892	15	0.5	23	1	AZ390689
c2893	15	0.5	23	1	AZ654389
2894	15	0.5	23	1	AZ771221
c2895	15	0.5	23	1	AZ771221
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2897	15	0.5	23	1	TA120E05P
2898	15	0.5	24	1	TA155F12Q
c2899	15	0.5	26	1	TA319G03Q
c2900	15	0.5	27	1	AW246455
2901	15	0.5	29	1	TA224C08P
2902	15	0.5	33	1	AZ504854
c2903	14.8	0.5	18	1	CF329020
2904	14.8	0.5	18	1	AW246505
c2905	14.8	0.5	18	1	AW246505
c2906	14.8	0.5	18	1	AW247875
2907	14.8	0.5	19	1	CF309858
2908	14.8	0.5	19	1	AZ475079
2909	14.8	0.5	19	1	AZ789309
c2910	14.8	0.5	19	1	AZ789309
c2911	14.8	0.5	19	1	AZ962226
c2912	14.8	0.5	20	1	CF297010
c2913	14.8	0.5	20	1	CF313751
2914	14.8	0.5	20	1	CF313752
c2915	14.8	0.5	20	1	AZ828826
2916	14.8	0.5	21	1	AZ625662
c2917	14.8	0.5	21	1	AU254546
c2918	14.8	0.5	21	1	AZ331619
c2919	14.8	0.5	23	1	AZ984045
c2920	14.8	0.5	24	1	AZ349008
c2921	14.8	0.5	24	1	AZ782507
c2922	14.8	0.5	27	1	AU264164
c2923	14.6	0.5	21	1	AZ346714
c2924	14.6	0.5	21	1	AZ483617
c2925	14.6	0.5	21	1	AZ787674
2926	14.6	0.5	21	1	AZ788269
c2927	14.6	0.5	22	1	AZ845735
2928	14.6	0.5	22	1	AZ470212
c2929	14.6	0.5	22	1	AA888191
c2930	14.6	0.5	22	1	AI184101
c2931	14.6	0.5	22	1	BQ595200
2932	14.6	0.5	22	1	BX563723
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c2934	14.6	0.5	22	1	AZ854229
c2935	14.6	0.5	23	1	AU267170
c2936	14.6	0.5	23	1	AW332764
2937	14.6	0.5	23	1	CF292525
c2938	14.6	0.5	23	1	AZ390689
c2939	14.4	0.5	16	1	CF312586
2940	14.4	0.5	16	1	CF317778
c2941	14.4	0.5	16	1	CF317778
2942	14.4	0.5	17	1	AW247165
c2943	14.4	0.5	17	1	AW247165
c2944	14.4	0.5	19	1	AZ774536
2945	14.4	0.5	22	1	CF196152
c2946	14.4	0.5	23	1	TA120E05P
c2947	14.4	0.5	25	1	BZ767540
2948	14.4	0.5	27	1	AZ785639
2949	14.2	0.5	19	1	AZ766990
2950	14.2	0.5	19	1	AZ962226
2951	14.2	0.5	19	1	AI364573
2952	14.2	0.5	19	1	AI371092
c2953	14.2	0.5	19	1	CF337608

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2959	14.2	0.5	20	1	CF297010
2960	14.2	0.5	20	1	AL587630
2961	14.2	0.5	20	1	AU257221
2962	14.2	0.5	20	1	CF339443
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2971	14.2	0.5	21	1	AW248826
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2973	14.2	0.5	21	1	AZ629111
2974	14.2	0.5	22	1	AZ471736
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2978	14.2	0.5	26	1	AU265714
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2980	14	0.5	14	1	BQ586422
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3004	14	0.5	14	1	CF278001
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c3023	14	0.5	14	1	CF297969
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2737	15.4	0.5	21	1	AZ589400
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2747	15.4	0.5	23	1	AZ615086
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2749	15.4	0.5	25	1	AZ343444
c2750	15.4	0.5	25	1	AZ329925
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2752	15.2	0.5	20	1	CF282165
2753	15.2	0.5	20	1	CF336815
c2754	15.2	0.5	20	1	AZ316368
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2763	15.2	0.5	23	1	CK277017
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2791	15	0.5	15	1	CF290920
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2795	15	0.5	15	1	CF291103
c2796	15	0.5	15	1	CF291103
2797	15	0.5	15	1	CF291717
c2798	15	0.5	15	1	CF291717
2799	15	0.5	15	1	CF291798
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c2802	15	0.5	15	1	CF292458
2803	15	0.5	15	1	CF292461
c2804	15	0.5	15	1	CF292461
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c2807	15	0.5	15	1	CF298148

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2861	15	0.5	16	1	BQ590207
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2863	15	0.5	16	1	CF291803
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2876	15	0.5	19	1	AZ950028
2877	15	0.5	20	1	CF301222
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2879	15	0.5	20	1	CF331733
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c2589	16.2	0.6	25	1	AV740046
c2590	16.2	0.6	27	1	AV739265
2591	16	0.6	16	1	BQ590166
c2592	16	0.6	16	1	BQ590166
2593	16	0.6	16	1	BQ590507
2594	16	0.6	16	1	BQ592600
c2595	16	0.6	16	1	BQ592600
2596	16	0.6	16	1	BQ592965
c2597	16	0.6	16	1	BQ592965
2598	16	0.6	16	1	BQ595369
2599	16	0.6	16	1	BQ595717
c2600	16	0.6	16	1	BQ595717
2601	16	0.6	16	1	CF279325
c2602	16	0.6	16	1	CF279325
2603	16	0.6	16	1	CF296130
2604	16	0.6	16	1	CF311057
c2605	16	0.6	16	1	CF311057
2606	16	0.6	16	1	CF314013
2607	16	0.6	16	1	CF314377
c2608	16	0.6	16	1	CF314377
2609	16	0.6	16	1	CF315789
c2610	16	0.6	16	1	CF315789
2611	16	0.6	16	1	CF316056
c2612	16	0.6	16	1	CF316056
2613	16	0.6	16	1	CF317718
c2614	16	0.6	16	1	CF317718
2615	16	0.6	16	1	CF320356
c2616	16	0.6	16	1	CF320356
2617	16	0.6	16	1	CF327722
c2618	16	0.6	16	1	CF327722
2619	16	0.6	16	1	CF329320
2620	16	0.6	16	1	CF333386
c2621	16	0.6	16	1	CF333386
c2622	16	0.6	17	1	BQ590128
c2623	16	0.6	17	1	CF294668
c2624	16	0.6	17	1	CF295988
2625	16	0.6	17	1	CF302447
2626	16	0.6	17	1	CF313013
c2627	16	0.6	17	1	CF336950
2628	16	0.6	17	1	BQ591181
2629	16	0.6	17	1	CF295807
c2630	16	0.6	17	1	CF295807
2631	16	0.6	17	1	CF299639
c2632	16	0.6	17	1	CF299639
c2633	16	0.6	17	1	CF299997
2634	16	0.6	17	1	CF311499
2635	16	0.6	17	1	CF319075
c2636	16	0.6	18	1	CF302409
c2637	16	0.6	18	1	CF301359
2638	16	0.6	19	1	CF308042
2639	16	0.6	19	1	CF298134
2640	16	0.6	19	1	CF311668
c2641	16	0.6	19	1	CF311668
2642	16	0.6	19	1	CF327587
c2643	16	0.6	19	1	CF327587
2644	16	0.6	19	1	AZ764517
c2645	16	0.6	19	1	AZ764517
2646	16	0.6	21	1	AZ316019
2647	16	0.6	21	1	CF309614
c2648	16	0.6	22	1	CF310806
2649	16	0.6	22	1	AZ316361
2650	16	0.6	22	1	AZ307559
2651	16	0.6	22	1	AZ310057
c2652	16	0.6	22	1	AZ310057
c2653	16	0.6	22	1	AZ375417
2654	16	0.6	22	1	TA367G08P
c2655	16	0.6	23	1	CF290997
c2656	16	0.6	23	1	CF280704
2657	16	0.6	23	1	TA367D08P
c2658	16	0.6	24	1	AZ768927
c2659	16	0.6	25	1	AW249476
2660	16	0.6	25	1	AZ442170
c2661	16	0.6	25	1	AZ476141

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ACCESSION:AZ442170
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c2662	16	0.6	25	1	AW247153
2663	16	0.6	25	1	TA324F07P
c2664	16	0.6	26	1	AZ437459
2665	16	0.6	26	1	AU265818
2666	16	0.6	26	1	AU268466
c2667	16	0.6	26	1	BX552372
c2668	16	0.6	26	1	BX553653
c2669	16	0.6	26	1	BX553888
c2670	16	0.6	26	1	BX557791
c2671	16	0.6	26	1	BX566514
c2672	16	0.6	26	1	BX567795
2673	16	0.6	27	1	AU267251
2674	15.8	0.6	19	1	CF329137
c2675	15.8	0.6	19	1	AZ345499
c2676	15.8	0.6	19	1	AZ447251
c2677	15.8	0.6	19	1	AZ786336
c2678	15.8	0.6	19	1	CF298472
c2679	15.8	0.6	19	1	CF298134
2680	15.8	0.6	19	1	CF300236
c2681	15.8	0.6	19	1	CF300236
c2682	15.8	0.6	19	1	CF309858
2683	15.8	0.6	19	1	AZ509929
c2684	15.8	0.6	19	1	AZ509929
2685	15.8	0.6	19	1	AZ611602
c2686	15.8	0.6	19	1	AZ611602
c2687	15.8	0.6	20	1	AW333777
2688	15.8	0.6	20	1	CF330490
2689	15.8	0.6	20	1	AZ633741
2690	15.8	0.6	20	1	AZ368518
c2691	15.8	0.6	20	1	CF336815
2692	15.8	0.6	20	1	CF340627
c2693	15.8	0.6	21	1	AW248782
c2694	15.8	0.6	21	1	AZ597932
c2695	15.8	0.6	21	1	AZ647578
c2696	15.8	0.6	22	1	AZ442146
c2697	15.8	0.6	22	1	AZ345485
c2698	15.8	0.6	22	1	AZ355624
2699	15.8	0.6	23	1	AZ447220
c2700	15.8	0.6	23	1	BX560037
c2701	15.8	0.6	24	1	AZ514388
c2702	15.8	0.6	24	1	AZ814559
c2703	15.8	0.6	24	1	AZ827015
c2704	15.8	0.6	24	1	CF300715
2705	15.6	0.6	22	1	CF300339
c2706	15.6	0.6	22	1	CF300339
2707	15.6	0.6	22	1	BH906256
2708	15.6	0.6	23	1	AW332764
2709	15.6	0.6	23	1	AZ632757
c2710	15.6	0.6	24	1	AW247816
2711	15.6	0.6	24	1	CNS00HLD
2712	15.6	0.6	25	1	AU268810
2713	15.6	0.6	33	1	AZ346849
c2714	15.4	0.5	17	1	BQ591181
2715	15.4	0.5	17	1	CF299997
c2716	15.4	0.5	17	1	CF311499
c2717	15.4	0.5	17	1	CF319075
2718	15.4	0.5	17	1	AW245664
2719	15.4	0.5	17	1	AW248574
c2720	15.4	0.5	17	1	AW248574
2721	15.4	0.5	17	1	BQ591588
c2722	15.4	0.5	17	1	BQ591588
2723	15.4	0.5	17	1	CF276637
c2724	15.4	0.5	17	1	CF276637
2725	15.4	0.5	17	1	CF291802
c2726	15.4	0.5	17	1	CF291802
2727	15.4	0.5	17	1	CF297251
c2728	15.4	0.5	17	1	CF297251
c2729	15.4	0.5	17	1	CF298341
2730	15.4	0.5	17	1	CF299675
c2731	15.4	0.5	17	1	CF299675
c2732	15.4	0.5	18	1	CF309376
c2733	15.4	0.5	18	1	CF329484
2734	15.4	0.5	18	1	CF329485

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c2443	17	0.6	27	1	BX555567
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c2445	17	0.6	27	1	BX555829
c2446	17	0.6	27	1	BX555864
c2447	17	0.6	27	1	BX555901
c2448	17	0.6	27	1	BX555930
c2449	17	0.6	27	1	BX556112
c2450	17	0.6	27	1	BX556156
c2451	17	0.6	27	1	BX556515
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c2458	17	0.6	27	1	BX560210
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c2460	17	0.6	27	1	BX562177
c2461	17	0.6	27	1	BX564083
c2462	17	0.6	28	1	AL587605
c2463	17	0.6	31	1	AI207866
c2464	17	0.6	32	1	AZ451251
c2465	17	0.6	35	1	BJ036312
2466	17	0.6	35	1	AZ351309
2467	17	0.6	37	1	TA115E07P
c2468	16.8	0.6	20	1	CF299570
2469	16.8	0.6	20	1	CF301101
2470	16.8	0.6	20	1	AZ343730
2471	16.8	0.6	20	1	AW333777
c2472	16.8	0.6	20	1	CF282165
2473	16.8	0.6	20	1	CF298018
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2475	16.8	0.6	20	1	CF300961
c2476	16.8	0.6	20	1	CF300961
c2477	16.8	0.6	20	1	CF330490
c2478	16.8	0.6	20	1	AZ633741
c2479	16.8	0.6	21	1	CF293087
2480	16.8	0.6	22	1	AW246884
c2481	16.8	0.6	22	1	AW246884
2482	16.8	0.6	22	1	AZ845735
c2483	16.8	0.6	22	1	TA330H07Q
2484	16.8	0.6	23	1	AL048695
2485	16.8	0.6	23	1	CF302134
2486	16.8	0.6	23	1	AZ382429
2487	16.8	0.6	23	1	CF334146
2488	16.8	0.6	23	1	CF290997
2489	16.8	0.6	23	1	CF308058
2490	16.8	0.6	24	1	CF302406
2491	16.8	0.6	24	1	AZ827015
c2492	16.8	0.6	25	1	BZ765670
c2493	16.8	0.6	25	1	AZ404619
c2494	16.8	0.6	27	1	CF300303
2495	16.8	0.6	28	1	AI971979
c2496	16.8	0.6	30	1	AL953605
2497	16.8	0.6	34	1	AU265130
2498	16.8	0.6	35	1	BF239380
2499	16.6	0.6	23	1	CF290998
2500	16.6	0.6	23	1	AW249550
2501	16.6	0.6	23	1	AZ330773
c2502	16.6	0.6	24	1	CF292725
2503	16.6	0.6	24	1	CF291636
2504	16.6	0.6	24	1	AZ399663
2505	16.6	0.6	24	1	AZ782507
2506	16.6	0.6	25	1	CF296608
c2507	16.6	0.6	25	1	AI682835
c2508	16.6	0.6	25	1	AI745099
c2509	16.6	0.6	25	1	AZ510128
2510	16.6	0.6	25	1	BH856226
c2511	16.6	0.6	27	1	AZ495352
c2512	16.6	0.6	27	1	BQ591183
c2513	16.6	0.6	33	1	CF335736
c2514	16.4	0.6	18	1	CF298591
2515	16.4	0.6	18	1	CF300456

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2517	16.4	0.6	18	1	AL048754
c2518	16.4	0.6	18	1	AL048754
2519	16.4	0.6	18	1	BM658677
c2520	16.4	0.6	18	1	BM658677
2521	16.4	0.6	18	1	CF309376
2522	16.4	0.6	18	1	CF329285
c2523	16.4	0.6	18	1	CF329285
2524	16.4	0.6	18	1	CF329484
c2525	16.4	0.6	18	1	CF329485
2526	16.4	0.6	19	1	CF309636
c2527	16.4	0.6	19	1	CF334610
c2528	16.4	0.6	19	1	AZ360314
c2529	16.4	0.6	19	1	CF278272
2530	16.4	0.6	19	1	CF295672
2531	16.4	0.6	19	1	CF298472
c2532	16.4	0.6	19	1	CF308042
2533	16.4	0.6	19	1	CF319596
c2534	16.4	0.6	19	1	CF319596
2535	16.4	0.6	19	1	CF326845
c2536	16.4	0.6	19	1	CF326845
2537	16.4	0.6	19	1	AZ465954
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c2539	16.4	0.6	20	1	CF319428
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c2541	16.4	0.6	20	1	AZ368518
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2543	16.4	0.6	21	1	CF293087
c2544	16.4	0.6	21	1	CF319122
2545	16.4	0.6	22	1	CF318882
c2546	16.4	0.6	22	1	AZ307896
c2547	16.4	0.6	22	1	BQ591193
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2553	16.4	0.6	23	1	AZ984045
c2554	16.4	0.6	24	1	CF302406
c2555	16.4	0.6	24	1	AZ399663
2556	16.4	0.6	24	1	CF295238
2557	16.4	0.6	24	1	AZ665864
2558	16.4	0.6	25	1	AZ329925
2559	16.4	0.6	25	1	AZ515233
c2560	16.4	0.6	25	1	AZ997733
c2561	16.4	0.6	26	1	BM658913
c2562	16.4	0.6	26	1	AU265518
c2563	16.4	0.6	26	1	BX563414
2564	16.4	0.6	27	1	AU265398
2565	16.4	0.6	27	1	CF318113
2566	16.4	0.6	27	1	AW250467
c2567	16.4	0.6	29	1	AZ827060
2568	16.4	0.6	29	1	AU269375
2569	16.4	0.6	31	1	AU264794
c2570	16.4	0.6	32	1	BX556940
c2571	16.4	0.6	33	1	R38731
2572	16.4	0.6	34	1	CF319784
2573	16.4	0.6	39	1	AZ339890
c2574	16.4	0.6	40	1	AZ326980
c2575	16.2	0.6	21	1	CF330439
2576	16.2	0.6	21	1	CF319122
c2577	16.2	0.6	21	1	AZ316019
2578	16.2	0.6	21	1	AZ345540
2579	16.2	0.6	21	1	AZ346717
c2580	16.2	0.6	21	1	AZ625662
c2581	16.2	0.6	22	1	AZ316361
2582	16.2	0.6	23	1	AU267170
2583	16.2	0.6	23	1	AZ468097
c2584	16.2	0.6	24	1	CF337747
2585	16.2	0.6	24	1	CF328535
2586	16.2	0.6	24	1	AZ308225
2587	16.2	0.6	25	1	AI445764
c2588	16.2	0.6	25	1	CF308158

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2298	17.4	0.6	20	1	CF333052
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c2300	17.4	0.6	20	1	AZ343730
2301	17.4	0.6	21	1	AL048772
c2302	17.4	0.6	21	1	BX548564
c2303	17.4	0.6	21	1	CF296213
c2304	17.4	0.6	21	1	AZ308846
c2305	17.4	0.6	21	1	AZ317208
c2306	17.4	0.6	21	1	AZ486776
2307	17.4	0.6	21	1	AZ822825
2308	17.4	0.6	21	1	AZ853429
c2309	17.4	0.6	21	1	AZ627840
c2310	17.4	0.6	21	1	CF319625
c2311	17.4	0.6	21	1	AZ341108
2312	17.4	0.6	22	1	TA303G05P
c2313	17.4	0.6	22	1	CF318882
2314	17.4	0.6	22	1	AZ307896
2315	17.4	0.6	22	1	AZ317017
c2316	17.4	0.6	23	1	AZ486853
c2317	17.4	0.6	23	1	AZ645254
2318	17.4	0.6	23	1	AZ382013
c2319	17.4	0.6	23	1	AZ627841
2320	17.4	0.6	23	1	TA55C06P
2321	17.4	0.6	23	1	AW335179
c2322	17.4	0.6	23	1	CF334146
2323	17.4	0.6	24	1	AZ627850
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c2325	17.4	0.6	24	1	CF331868
2326	17.4	0.6	24	1	CF327904
c2327	17.4	0.6	24	1	CF327904
c2328	17.4	0.6	24	1	TA155F12Q
2329	17.4	0.6	25	1	TA388E06P
2330	17.4	0.6	25	1	AV737092
c2331	17.4	0.6	25	1	AU012885
c2332	17.4	0.6	26	1	BX554728
c2333	17.4	0.6	26	1	BQ585188
2334	17.4	0.6	26	1	TA319G03Q
2335	17.4	0.6	29	1	BX568027
2336	17.4	0.6	31	1	AU268044
2337	17.4	0.6	31	1	AZ579477
c2338	17.4	0.6	32	1	AL941390
2339	17.4	0.6	37	1	TA369C05P
2340	17.4	0.6	39	1	CF642215
2341	17.2	0.6	22	1	AZ345485
c2342	17.2	0.6	22	1	AZ471736
c2343	17.2	0.6	23	1	CF311534
2344	17.2	0.6	23	1	AU267617
c2345	17.2	0.6	23	1	CF290998
2346	17.2	0.6	24	1	BI094838
2347	17.2	0.6	24	1	CF328136
c2348	17.2	0.6	24	1	CF328136
2349	17.2	0.6	24	1	AZ349008
2350	17.2	0.6	25	1	AV740046
2351	17.2	0.6	25	1	AW247153
c2352	17.2	0.6	25	1	CF296608
c2353	17.2	0.6	26	1	BZ593276
2354	17	0.6	17	1	BQ590128
2355	17	0.6	17	1	BQ590687
c2356	17	0.6	17	1	BQ590687
2357	17	0.6	17	1	BQ591177
c2358	17	0.6	17	1	BQ591177
2359	17	0.6	17	1	CF290854
c2360	17	0.6	17	1	CF290854
2361	17	0.6	17	1	CF294668
2362	17	0.6	17	1	CF295988
2363	17	0.6	17	1	CF298589
c2364	17	0.6	17	1	CF298589
c2365	17	0.6	17	1	CF302447
2366	17	0.6	17	1	CF310219
c2367	17	0.6	17	1	CF310219
c2368	17	0.6	17	1	CF313013
2369	17	0.6	17	1	CF334566

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2371	17	0.6	17	1	CF336950
2372	17	0.6	18	1	CF301057
c2373	17	0.6	18	1	CF301151
c2374	17	0.6	18	1	CF320418
2375	17	0.6	18	1	CF298591
c2376	17	0.6	18	1	CF300456
2377	17	0.6	18	1	CF302409
2378	17	0.6	18	1	CF320046
2379	17	0.6	19	1	AZ450180
c2380	17	0.6	19	1	AZ853220
2381	17	0.6	19	1	CF278272
2382	17	0.6	20	1	CF298207
c2383	17	0.6	20	1	AZ818055
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c2385	17	0.6	21	1	AZ943299
c2386	17	0.6	21	1	CF333393
2387	17	0.6	22	1	BQ591193
c2388	17	0.6	22	1	CF297521
2389	17	0.6	22	1	TA211D06P
c2390	17	0.6	22	1	TA211D06P
2391	17	0.6	23	1	CF291486
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2393	17	0.6	23	1	AZ435597
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2397	17	0.6	24	1	CF292725
c2398	17	0.6	25	1	CF315032
c2399	17	0.6	25	1	T57657
c2400	17	0.6	25	1	CF319953
c2401	17	0.6	25	1	AI560179
2402	17	0.6	25	1	BG929133
c2403	17	0.6	25	1	AZ343444
2404	17	0.6	25	1	AZ658622
2405	17	0.6	25	1	BZ767540
c2406	17	0.6	25	1	TA324F07P
2407	17	0.6	26	1	BX552372
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2413	17	0.6	26	1	BX566514
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2415	17	0.6	26	1	AZ818035
c2416	17	0.6	26	1	AZ818035
c2417	17	0.6	27	1	BX555323
2418	17	0.6	27	1	BI094728
c2419	17	0.6	27	1	BX550767
c2420	17	0.6	27	1	BX550946
c2421	17	0.6	27	1	BX551145
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c2423	17	0.6	27	1	BX551505
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c2430	17	0.6	27	1	BX552041
c2431	17	0.6	27	1	BX553159
c2432	17	0.6	27	1	BX553354
c2433	17	0.6	27	1	BX553476
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c2435	17	0.6	27	1	BX553766
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c2439	17	0.6	27	1	BX555155
c2440	17	0.6	27	1	BX555158
c2441	17	0.6	27	1	BX555385
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2151	18	0.6	27	1	BX555829	ACCESSION:BX555829
2152	18	0.6	27	1	BX555864	ACCESSION:BX555864
2153	18	0.6	27	1	BX555901	ACCESSION:BX555901
2154	18	0.6	27	1	BX555930	ACCESSION:BX555930
2155	18	0.6	27	1	BX556112	ACCESSION:BX556112
2156	18	0.6	27	1	BX556156	ACCESSION:BX556156
2157	18	0.6	27	1	BX556515	ACCESSION:BX556515
2158	18	0.6	27	1	BX556518	ACCESSION:BX556518
c2159	18	0.6	27	1	BX556518	ACCESSION:BX556518
2160	18	0.6	27	1	BX557271	ACCESSION:BX557271
2161	18	0.6	27	1	BX557363	ACCESSION:BX557363
2162	18	0.6	27	1	BX557794	ACCESSION:BX557794
2163	18	0.6	27	1	BX558430	ACCESSION:BX558430
2164	18	0.6	27	1	BX559230	ACCESSION:BX559230
2165	18	0.6	27	1	BX559542	ACCESSION:BX559542
2166	18	0.6	27	1	BX560210	ACCESSION:BX560210
2167	18	0.6	27	1	BX560901	ACCESSION:BX560901
2168	18	0.6	27	1	BX562177	ACCESSION:BX562177
2169	18	0.6	27	1	BX564083	ACCESSION:BX564083
c2170	18	0.6	27	1	AZ785639	ACCESSION:AZ785639
2171	18	0.6	27	1	TA386G03Q	ACCESSION:AL498287
c2172	18	0.6	27	1	TA386G03Q	ACCESSION:AL498287
c2173	18	0.6	28	1	AZ836072	ACCESSION:AZ836072
c2174	18	0.6	28	1	TA29A09P	ACCESSION:AL453073
c2175	18	0.6	28	1	CF307749	ACCESSION:CF307749
c2176	18	0.6	28	1	AZ654007	ACCESSION:AZ654007
c2177	18	0.6	28	1	BX554747	ACCESSION:BX554747
c2178	18	0.6	28	1	CF277114	ACCESSION:CF277114
c2179	18	0.6	28	1	BX555317	ACCESSION:BX555317
c2180	18	0.6	28	1	BX564177	ACCESSION:BX564177
c2181	18	0.6	28	1	BX556035	ACCESSION:BX556035
c2182	18	0.6	28	1	TA338C09P	ACCESSION:AL493148
c2183	18	0.6	29	1	BX551653	ACCESSION:BX551653
c2184	18	0.6	29	1	BX552148	ACCESSION:BX552148
c2185	18	0.6	29	1	BX553633	ACCESSION:BX553633
c2186	18	0.6	29	1	BX554047	ACCESSION:BX554047
2187	18	0.6	29	1	BX554140	ACCESSION:BX554140
c2188	18	0.6	29	1	BX555929	ACCESSION:BX555929
2189	18	0.6	29	1	BX556509	ACCESSION:BX556509
2190	18	0.6	29	1	BX556531	ACCESSION:BX556531
2191	18	0.6	29	1	BX557480	ACCESSION:BX557480
2192	18	0.6	29	1	BX558487	ACCESSION:BX558487
c2193	18	0.6	29	1	BX560399	ACCESSION:BX560399
c2194	18	0.6	29	1	BX561329	ACCESSION:BX561329
c2195	18	0.6	31	1	AW249485	ACCESSION:AW249485
c2196	18	0.6	31	1	AZ486763	ACCESSION:AZ486763
c2197	18	0.6	32	1	AZ627842	ACCESSION:AZ627842
c2198	18	0.6	32	1	AZ314322	ACCESSION:AZ314322
2199	18	0.6	32	1	AZ326012	ACCESSION:AZ326012
2200	18	0.6	33	1	DR85L9T	ACCESSION:AL983097
c2201	18	0.6	33	1	AU252805	ACCESSION:AU252805
c2202	18	0.6	33	1	AV859963	ACCESSION:AV859963
c2203	18	0.6	39	1	AW247125	ACCESSION:AW247125
2204	17.8	0.6	21	1	AW248782	ACCESSION:AW248782
2205	17.8	0.6	21	1	CF333393	ACCESSION:CF333393
2206	17.8	0.6	21	1	AZ597932	ACCESSION:AZ597932
2207	17.8	0.6	21	1	AZ627840	ACCESSION:AZ627840
2208	17.8	0.6	21	1	AZ647578	ACCESSION:AZ647578
c2209	17.8	0.6	22	1	CF298427	ACCESSION:CF298427
c2210	17.8	0.6	22	1	CF302435	ACCESSION:CF302435
2211	17.8	0.6	22	1	AZ442146	ACCESSION:AZ442146
c2212	17.8	0.6	23	1	CF313297	ACCESSION:CF313297
2213	17.8	0.6	23	1	CF297907	ACCESSION:CF297907
c2214	17.8	0.6	23	1	AL048695	ACCESSION:AL048695
2215	17.8	0.6	23	1	CF300172	ACCESSION:CF300172
c2216	17.8	0.6	23	1	CF300172	ACCESSION:CF300172
c2217	17.8	0.6	23	1	CF302134	ACCESSION:CF302134
c2218	17.8	0.6	23	1	AZ382429	ACCESSION:AZ382429
c2219	17.8	0.6	23	1	AZ447220	ACCESSION:AZ447220
c2220	17.8	0.6	24	1	BI094838	ACCESSION:BI094838
c2221	17.8	0.6	25	1	CC883604	ACCESSION:CC883604
c2222	17.8	0.6	25	1	AZ442170	ACCESSION:AZ442170
2223	17.8	0.6	25	1	AZ476141	ACCESSION:AZ476141
2224	17.8	0.6	25	1	BZ765670	ACCESSION:BZ765670
2225	17.8	0.6	26	1	CF302323	ACCESSION:CF302323
2226	17.8	0.6	26	1	BZ593276	ACCESSION:BZ593276
2227	17.8	0.6	27	1	CF328811	ACCESSION:CF328811
2228	17.8	0.6	28	1	BI094792	ACCESSION:BI094792
c2229	17.8	0.6	28	1	AW335064	ACCESSION:AW335064
2230	17.8	0.6	32	1	BI693086	ACCESSION:BI693086
c2231	17.8	0.6	39	1	AZ346794	ACCESSION:AZ346794
c2232	17.6	0.6	24	1	AZ626101	ACCESSION:AZ626101
c2233	17.6	0.6	24	1	AW247159	ACCESSION:AW247159
c2234	17.6	0.6	24	1	CF281313	ACCESSION:CF281313
c2235	17.6	0.6	24	1	AZ458112	ACCESSION:AZ458112
c2236	17.6	0.6	24	1	AZ621257	ACCESSION:AZ621257
c2237	17.6	0.6	24	1	CF331867	ACCESSION:CF331867
2238	17.6	0.6	24	1	CF331868	ACCESSION:CF331868
2239	17.6	0.6	24	1	CF337747	ACCESSION:CF337747
2240	17.6	0.6	25	1	AZ404078	ACCESSION:AZ404078
c2241	17.6	0.6	25	1	AZ427752	ACCESSION:AZ427752
2242	17.6	0.6	25	1	CF296242	ACCESSION:CF296242
2243	17.6	0.6	25	1	CF300334	ACCESSION:CF300334
2244	17.6	0.6	25	1	CF308158	ACCESSION:CF308158
2245	17.6	0.6	25	1	CF319953	ACCESSION:CF319953
c2246	17.6	0.6	25	1	BH791022	ACCESSION:BH791022
2247	17.6	0.6	26	1	AZ316353	ACCESSION:AZ316353
2248	17.6	0.6	26	1	AU267694	ACCESSION:AU267694
2249	17.6	0.6	27	1	AV739265	ACCESSION:AV739265
2250	17.6	0.6	27	1	AV741507	ACCESSION:AV741507
c2251	17.6	0.6	27	1	AW250467	ACCESSION:AW250467
2252	17.6	0.6	28	1	T81587	ACCESSION:T81587
c2253	17.6	0.6	29	1	BQ583967	ACCESSION:BQ583967
c2254	17.6	0.6	29	1	AZ492630	ACCESSION:AZ492630
2255	17.6	0.6	29	1	BQ586486	ACCESSION:BQ586486
c2256	17.6	0.6	30	1	CF331804	ACCESSION:CF331804
c2257	17.6	0.6	33	1	AU266959	ACCESSION:AU266959
2258	17.4	0.6	19	1	AZ345795	ACCESSION:AZ345795
2259	17.4	0.6	19	1	AZ650575	ACCESSION:AZ650575
2260	17.4	0.6	19	1	AW248747	ACCESSION:AW248747
c2261	17.4	0.6	19	1	AW248747	ACCESSION:AW248747
2262	17.4	0.6	19	1	CF291665	ACCESSION:CF291665
c2263	17.4	0.6	19	1	CF291665	ACCESSION:CF291665
2264	17.4	0.6	19	1	CF291899	ACCESSION:CF291899
c2265	17.4	0.6	19	1	CF291899	ACCESSION:CF291899
2266	17.4	0.6	19	1	CF292072	ACCESSION:CF292072
c2267	17.4	0.6	19	1	CF292072	ACCESSION:CF292072
2268	17.4	0.6	19	1	CF292144	ACCESSION:CF292144
c2269	17.4	0.6	19	1	CF292144	ACCESSION:CF292144
c2270	17.4	0.6	19	1	CF309636	ACCESSION:CF309636
2271	17.4	0.6	19	1	CF310688	ACCESSION:CF310688
c2272	17.4	0.6	19	1	CF310688	ACCESSION:CF310688
2273	17.4	0.6	19	1	CF329136	ACCESSION:CF329136
c2274	17.4	0.6	19	1	CF329136	ACCESSION:CF329136
c2275	17.4	0.6	19	1	CF329137	ACCESSION:CF329137
2276	17.4	0.6	19	1	CF334610	ACCESSION:CF334610
2277	17.4	0.6	19	1	AZ345499	ACCESSION:AZ345499
2278	17.4	0.6	19	1	AZ360314	ACCESSION:AZ360314
2279	17.4	0.6	19	1	AZ363907	ACCESSION:AZ363907
c2280	17.4	0.6	19	1	AZ363907	ACCESSION:AZ363907
2281	17.4	0.6	19	1	AZ447251	ACCESSION:AZ447251
2282	17.4	0.6	19	1	AZ513919	ACCESSION:AZ513919
c2283	17.4	0.6	19	1	AZ513919	ACCESSION:AZ513919
2284	17.4	0.6	19	1	AZ645841	ACCESSION:AZ645841
c2285	17.4	0.6	19	1	AZ645841	ACCESSION:AZ645841
2286	17.4	0.6	19	1	AZ650252	ACCESSION:AZ650252
c2287	17.4	0.6	19	1	AZ650252	ACCESSION:AZ650252
2288	17.4	0.6	19	1	AZ654747	ACCESSION:AZ654747
c2289	17.4	0.6	19	1	AZ654747	ACCESSION:AZ654747
2290	17.4	0.6	19	1	AZ786336	ACCESSION:AZ786336
c2291	17.4	0.6	20	1	CF308984	ACCESSION:CF308984
2292	17.4	0.6	20	1	AZ375620	ACCESSION:AZ375620
c2293	17.4	0.6	20	1	AZ486787	ACCESSION:AZ486787
2294	17.4	0.6	20	1	AZ579122	ACCESSION:AZ579122
2295	17.4	0.6	20	1	AZ949997	ACCESSION:AZ949997
2296	17.4	0.6	20	1	CF299570	ACCESSION:CF299570

2005	18.4	0.7	27	1	BX555323
2006	18.4	0.7	28	1	AW335064
2007	18.4	0.7	28	1	AZ785005
2008	18.4	0.7	28	1	TA338C09P
c2009	18.4	0.7	29	1	CF328988
2010	18.4	0.7	29	1	T67079
c2011	18.4	0.7	30	1	N31821
c2012	18.4	0.7	30	1	CF333289
c2013	18.4	0.7	30	1	AU269441
c2014	18.4	0.7	30	1	BX554139
c2015	18.4	0.7	30	1	BX555094
c2016	18.4	0.7	30	1	BX556477
c2017	18.4	0.7	30	1	BX565681
c2018	18.4	0.7	30	1	BX566679
c2019	18.4	0.7	32	1	CF334956
c2020	18.4	0.7	33	1	AU269499
2021	18.4	0.7	34	1	C21199
c2022	18.4	0.7	34	1	CF319950
2023	18.2	0.6	23	1	AW334124
c2024	18.2	0.6	23	1	CB305256
c2025	18.2	0.6	23	1	CF297907
2026	18.2	0.6	23	1	CF318266
c2027	18.2	0.6	23	1	CF318266
2028	18.2	0.6	24	1	AZ814559
2029	18.2	0.6	25	1	AW245275
c2030	18.2	0.6	25	1	AU268810
c2031	18.2	0.6	25	1	CF296242
c2032	18.2	0.6	25	1	CF300334
2033	18.2	0.6	26	1	CF328135
c2034	18.2	0.6	26	1	CF328135
c2035	18.2	0.6	27	1	AZ785554
2036	18.2	0.6	29	1	CF334023
c2037	18.2	0.6	31	1	AW245279
c2038	18.2	0.6	34	1	CF315464
c2039	18.2	0.6	36	1	AZ945733
2040	18	0.6	18	1	BQ582676
c2041	18	0.6	18	1	BQ582676
2042	18	0.6	18	1	BQ590027
c2043	18	0.6	18	1	BQ590027
2044	18	0.6	18	1	CF277873
c2045	18	0.6	18	1	CF277873
2046	18	0.6	18	1	CF297446
c2047	18	0.6	18	1	CF297446
2048	18	0.6	18	1	CF299027
c2049	18	0.6	18	1	CF299027
2050	18	0.6	18	1	CF299674
c2051	18	0.6	18	1	CF299674
c2052	18	0.6	18	1	CF301057
2053	18	0.6	18	1	CF301151
2054	18	0.6	18	1	CF301325
c2055	18	0.6	18	1	CF301325
2056	18	0.6	18	1	CF301760
c2057	18	0.6	18	1	CF301760
2058	18	0.6	18	1	CF320418
2059	18	0.6	19	1	CF293167
c2060	18	0.6	19	1	CF293167
2061	18	0.6	19	1	CF298396
c2062	18	0.6	19	1	CF298396
2063	18	0.6	19	1	CF302456
c2064	18	0.6	19	1	CF302456
2065	18	0.6	19	1	CF309821
c2066	18	0.6	19	1	CF309821
2067	18	0.6	19	1	CF311778
c2068	18	0.6	19	1	CF311778
2069	18	0.6	19	1	CF331361
c2070	18	0.6	19	1	CF331361
2071	18	0.6	19	1	CF335293
c2072	18	0.6	19	1	CF335293
c2073	18	0.6	19	1	AZ450180
2074	18	0.6	19	1	AZ853220
c2075	18	0.6	20	1	AL587759
c2076	18	0.6	20	1	AZ345856
2077	18	0.6	20	1	AZ370699

ACCESSION:BX555323
ACCESSION:AW335064
ACCESSION:AZ785005
ACCESSION:AL493148
ACCESSION:CF328988
ACCESSION:T67079
ACCESSION:N31821
ACCESSION:CF333289
ACCESSION:AU269441
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ACCESSION:BX556477
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ACCESSION:BX566679
ACCESSION:CF334956
ACCESSION:AU269499
ACCESSION:C21199
ACCESSION:CF319950
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ACCESSION:CF297907
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ACCESSION:CF318266
ACCESSION:AZ814559
ACCESSION:AW245275
ACCESSION:AU268810
ACCESSION:CF296242
ACCESSION:CF300334
ACCESSION:CF328135
ACCESSION:CF328135
ACCESSION:AZ785554
ACCESSION:CF334023
ACCESSION:AW245279
ACCESSION:CF315464
ACCESSION:AZ945733
ACCESSION:BQ582676
ACCESSION:BQ582676
ACCESSION:BQ590027
ACCESSION:BQ590027
ACCESSION:CF277873
ACCESSION:CF277873
ACCESSION:CF297446
ACCESSION:CF297446
ACCESSION:CF299027
ACCESSION:CF299027
ACCESSION:CF299674
ACCESSION:CF299674
ACCESSION:CF301057
ACCESSION:CF301151
ACCESSION:CF301325
ACCESSION:CF301325
ACCESSION:CF301760
ACCESSION:CF301760
ACCESSION:CF320418
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ACCESSION:CF302456
ACCESSION:CF302456
ACCESSION:CF309821
ACCESSION:CF309821
ACCESSION:CF311778
ACCESSION:CF311778
ACCESSION:CF331361
ACCESSION:CF331361
ACCESSION:CF335293
ACCESSION:CF335293
ACCESSION:AZ450180
ACCESSION:AZ853220
ACCESSION:AL587759
ACCESSION:AZ345856
ACCESSION:AZ370699

2078	18	0.6	20	1	AL587572
c2079	18	0.6	20	1	AL587572
2080	18	0.6	20	1	AL587727
c2081	18	0.6	20	1	AL587727
2082	18	0.6	20	1	CA853586
c2083	18	0.6	20	1	CA853586
2084	18	0.6	20	1	CF282002
c2085	18	0.6	20	1	CF282002
2086	18	0.6	20	1	CF316662
c2087	18	0.6	20	1	CF316662
2088	18	0.6	20	1	CF320843
c2089	18	0.6	20	1	CF320843
2090	18	0.6	20	1	AZ821905
c2091	18	0.6	20	1	AZ821905
c2092	18	0.6	21	1	AL587702
c2093	18	0.6	21	1	BX558161
2094	18	0.6	21	1	CF276747
c2095	18	0.6	21	1	CF276747
2096	18	0.6	22	1	TA231E08Q
c2097	18	0.6	22	1	BX556059
2098	18	0.6	22	1	TA386H07Q
2099	18	0.6	22	1	CF328832
2100	18	0.6	22	1	AZ843648
c2101	18	0.6	22	1	AZ843648
c2102	18	0.6	23	1	AL587621
c2103	18	0.6	23	1	CF314322
c2104	18	0.6	23	1	CF293321
c2105	18	0.6	23	1	AW334124
2106	18	0.6	24	1	AZ764519
c2107	18	0.6	24	1	AZ764519
2108	18	0.6	25	1	AZ867155
2109	18	0.6	25	1	T57657
c2110	18	0.6	26	1	CF337311
2111	18	0.6	26	1	AZ355083
c2112	18	0.6	26	1	AZ623156
c2113	18	0.6	26	1	AZ635695
c2114	18	0.6	26	1	CF336199
2115	18	0.6	26	1	BX563414
2116	18	0.6	26	1	CF300335
c2117	18	0.6	26	1	CF300335
2118	18	0.6	26	1	TA236D08P
c2119	18	0.6	26	1	TA236D08P
2120	18	0.6	27	1	AZ434285
2121	18	0.6	27	1	AZ458228
c2122	18	0.6	27	1	T52979
c2123	18	0.6	27	1	CF298133
c2124	18	0.6	27	1	BI094728
2125	18	0.6	27	1	BX550767
2126	18	0.6	27	1	BX550946
2127	18	0.6	27	1	BX551145
2128	18	0.6	27	1	BX551153
2129	18	0.6	27	1	BX551505
2130	18	0.6	27	1	BX551552
2131	18	0.6	27	1	BX551708
2132	18	0.6	27	1	BX551731
2133	18	0.6	27	1	BX551875
2134	18	0.6	27	1	BX551974
2135	18	0.6	27	1	BX552003
2136	18	0.6	27	1	BX552041
2137	18	0.6	27	1	BX553159
2138	18	0.6	27	1	BX553354
2139	18	0.6	27	1	BX553476
2140	18	0.6	27	1	BX553666
2141	18	0.6	27	1	BX553766
2142	18	0.6	27	1	BX554327
2143	18	0.6	27	1	BX554598
2144	18	0.6	27	1	BX555101
2145	18	0.6	27	1	BX555155
2146	18	0.6	27	1	BX555158
2147	18	0.6	27	1	BX555385
2148	18	0.6	27	1	BX555500
2149	18	0.6	27	1	BX555567
2150	18	0.6	27	1	BX555594

ACCESSION:AL587572
ACCESSION:AL587572
ACCESSION:AL587727
ACCESSION:AL587727
ACCESSION:CA853586
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ACCESSION:CF282002
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ACCESSION:CF320843
ACCESSION:CF320843
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ACCESSION:AZ821905
ACCESSION:AL587702
ACCESSION:BX558161
ACCESSION:CF276747
ACCESSION:CF276747
ACCESSION:AL480935
ACCESSION:BX556059
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ACCESSION:CF328832
ACCESSION:AZ843648
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ACCESSION:AL587621
ACCESSION:CF314322
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ACCESSION:AZ764519
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ACCESSION:T57657
ACCESSION:CF337311
ACCESSION:AZ355083
ACCESSION:AZ623156
ACCESSION:AZ635695
ACCESSION:CF336199
ACCESSION:BX563414
ACCESSION:CF300335
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ACCESSION:AL482943
ACCESSION:AL482943
ACCESSION:AZ434285
ACCESSION:AZ458228
ACCESSION:T52979
ACCESSION:CF298133
ACCESSION:BI094728
ACCESSION:BX550767
ACCESSION:BX550946
ACCESSION:BX551145
ACCESSION:BX551153
ACCESSION:BX551505
ACCESSION:BX551552
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ACCESSION:BX555101
ACCESSION:BX555155
ACCESSION:BX555158
ACCESSION:BX555385
ACCESSION:BX555500
ACCESSION:BX555567
ACCESSION:BX555594

c1859	19	0.7	29	1	BX554610	ACCESSION:BX554610
1860	19	0.7	29	1	BX555411	ACCESSION:BX555411
c1861	19	0.7	29	1	BX555411	ACCESSION:BX555411
1862	19	0.7	29	1	BX555799	ACCESSION:BX555799
c1863	19	0.7	29	1	BX555799	ACCESSION:BX555799
1864	19	0.7	29	1	BX555929	ACCESSION:BX555929
1865	19	0.7	29	1	BX555944	ACCESSION:BX555944
c1866	19	0.7	29	1	BX555944	ACCESSION:BX555944
1867	19	0.7	29	1	BX556323	ACCESSION:BX556323
c1868	19	0.7	29	1	BX556323	ACCESSION:BX556323
1869	19	0.7	29	1	BX556342	ACCESSION:BX556342
c1870	19	0.7	29	1	BX556342	ACCESSION:BX556342
1871	19	0.7	29	1	BX556455	ACCESSION:BX556455
c1872	19	0.7	29	1	BX556455	ACCESSION:BX556455
1873	19	0.7	29	1	BX556494	ACCESSION:BX556494
c1874	19	0.7	29	1	BX556494	ACCESSION:BX556494
c1875	19	0.7	29	1	BX556509	ACCESSION:BX556509
1876	19	0.7	29	1	BX556517	ACCESSION:BX556517
c1877	19	0.7	29	1	BX556517	ACCESSION:BX556517
c1878	19	0.7	29	1	BX556531	ACCESSION:BX556531
1879	19	0.7	29	1	BX556670	ACCESSION:BX556670
c1880	19	0.7	29	1	BX556670	ACCESSION:BX556670
1881	19	0.7	29	1	BX557474	ACCESSION:BX557474
c1882	19	0.7	29	1	BX557474	ACCESSION:BX557474
c1883	19	0.7	29	1	BX557480	ACCESSION:BX557480
1884	19	0.7	29	1	BX557715	ACCESSION:BX557715
c1885	19	0.7	29	1	BX557715	ACCESSION:BX557715
1886	19	0.7	29	1	BX557718	ACCESSION:BX557718
c1887	19	0.7	29	1	BX557718	ACCESSION:BX557718
1888	19	0.7	29	1	BX557758	ACCESSION:BX557758
c1889	19	0.7	29	1	BX557758	ACCESSION:BX557758
1890	19	0.7	29	1	BX557952	ACCESSION:BX557952
c1891	19	0.7	29	1	BX557952	ACCESSION:BX557952
c1892	19	0.7	29	1	BX558487	ACCESSION:BX558487
1893	19	0.7	29	1	BX558583	ACCESSION:BX558583
c1894	19	0.7	29	1	BX558583	ACCESSION:BX558583
1895	19	0.7	29	1	BX560399	ACCESSION:BX560399
1896	19	0.7	29	1	BX561329	ACCESSION:BX561329
1897	19	0.7	29	1	BX562299	ACCESSION:BX562299
c1898	19	0.7	29	1	BX562299	ACCESSION:BX562299
1899	19	0.7	29	1	BX563480	ACCESSION:BX563480
c1900	19	0.7	29	1	BX563480	ACCESSION:BX563480
1901	19	0.7	29	1	CF306409	ACCESSION:CF306409
c1902	19	0.7	29	1	CF306409	ACCESSION:CF306409
1903	19	0.7	30	1	AU267300	ACCESSION:AU267300
c1904	19	0.7	30	1	BX554779	ACCESSION:BX554779
c1905	19	0.7	30	1	TA247F06P	ACCESSION:AL483252
c1906	19	0.7	30	1	BX548619	ACCESSION:BX548619
c1907	19	0.7	30	1	BX549675	ACCESSION:BX549675
c1908	19	0.7	30	1	BX551003	ACCESSION:BX551003
c1909	19	0.7	30	1	BX552051	ACCESSION:BX552051
c1910	19	0.7	30	1	BX554304	ACCESSION:BX554304
c1911	19	0.7	30	1	BX555710	ACCESSION:BX555710
c1912	19	0.7	30	1	BX558083	ACCESSION:BX558083
c1913	19	0.7	30	1	BX558827	ACCESSION:BX558827
c1914	19	0.7	30	1	BX559425	ACCESSION:BX559425
c1915	19	0.7	30	1	BX563547	ACCESSION:BX563547
c1916	19	0.7	30	1	BX565972	ACCESSION:BX565972
1917	19	0.7	30	1	TA226G05P	ACCESSION:AL480085
c1918	19	0.7	31	1	AZ785111	ACCESSION:AZ785111
c1919	19	0.7	31	1	AV966771	ACCESSION:AV966771
c1920	19	0.7	31	1	BX554068	ACCESSION:BX554068
c1921	19	0.7	31	1	BX557470	ACCESSION:BX557470
c1922	19	0.7	31	1	BX558479	ACCESSION:BX558479
c1923	19	0.7	31	1	BX559254	ACCESSION:BX559254
c1924	19	0.7	31	1	AV947772	ACCESSION:AV947772
c1925	19	0.7	31	1	AV959965	ACCESSION:AV959965
c1926	19	0.7	32	1	AW250841	ACCESSION:AW250841
1927	19	0.7	32	1	AL036826	ACCESSION:AL036826
c1928	19	0.7	32	1	AL588429	ACCESSION:AL588429
c1929	19	0.7	32	1	BX551100	ACCESSION:BX551100
c1930	19	0.7	32	1	BX551460	ACCESSION:BX551460
c1931	19	0.7	32	1	BX558102	ACCESSION:BX558102
c1932	19	0.7	32	1	BX560723	ACCESSION:BX560723
c1933	19	0.7	32	1	BX564047	ACCESSION:BX564047
c1934	19	0.7	33	1	AZ310096	ACCESSION:AZ310096
1935	19	0.7	33	1	AL048719	ACCESSION:AL048719
1936	19	0.7	33	1	AL048733	ACCESSION:AL048733
1937	19	0.7	35	1	AZ475373	ACCESSION:AZ475373
c1938	19	0.7	37	1	AW245247	ACCESSION:AW245247
c1939	19	0.7	38	1	AZ773771	ACCESSION:AZ773771
c1940	19	0.7	39	1	CNS004NT	ACCESSION:AL054298
1941	19	0.7	39	1	CF280292	ACCESSION:CF280292
c1942	19	0.7	40	1	BQ591342	ACCESSION:BQ591342
1943	18.8	0.7	22	1	CF302435	ACCESSION:CF302435
c1944	18.8	0.7	22	1	CF328832	ACCESSION:CF328832
c1945	18.8	0.7	23	1	CF333801	ACCESSION:CF333801
c1946	18.8	0.7	23	1	BX568055	ACCESSION:BX568055
1947	18.8	0.7	23	1	CF311534	ACCESSION:CF311534
c1948	18.8	0.7	25	1	CF317378	ACCESSION:CF317378
c1949	18.8	0.7	25	1	AW245275	ACCESSION:AW245275
c1950	18.8	0.7	25	1	CF319499	ACCESSION:CF319499
c1951	18.8	0.7	26	1	AW333508	ACCESSION:AW333508
1952	18.8	0.7	26	1	AU265518	ACCESSION:AU265518
c1953	18.8	0.7	26	1	CF302323	ACCESSION:CF302323
c1954	18.8	0.7	27	1	CF300765	ACCESSION:CF300765
1955	18.8	0.7	27	1	CF315308	ACCESSION:CF315308
1956	18.8	0.7	27	1	BQ591183	ACCESSION:BQ591183
1957	18.8	0.7	27	1	CF279147	ACCESSION:CF279147
1958	18.8	0.7	27	1	AZ785554	ACCESSION:AZ785554
c1959	18.8	0.7	28	1	T81587	ACCESSION:T81587
c1960	18.8	0.7	29	1	AU267990	ACCESSION:AU267990
c1961	18.8	0.7	31	1	AV960178	ACCESSION:AV960178
c1962	18.8	0.7	32	1	BX557478	ACCESSION:BX557478
1963	18.6	0.7	25	1	AW249476	ACCESSION:AW249476
1964	18.6	0.7	25	1	AZ427752	ACCESSION:AZ427752
c1965	18.6	0.7	26	1	AU265818	ACCESSION:AU265818
c1966	18.6	0.7	26	1	AU268466	ACCESSION:AU268466
1967	18.6	0.7	27	1	TA257B07P	ACCESSION:AL483278
1968	18.6	0.7	27	1	AU264164	ACCESSION:AU264164
c1969	18.6	0.7	27	1	AU267251	ACCESSION:AU267251
1970	18.6	0.7	27	1	AW246455	ACCESSION:AW246455
1971	18.6	0.7	27	1	AZ953355	ACCESSION:AZ953355
c1972	18.6	0.7	28	1	AI623404	ACCESSION:AI623404
c1973	18.6	0.7	28	1	AI971979	ACCESSION:AI971979
c1974	18.6	0.7	28	1	BI094792	ACCESSION:BI094792
1975	18.6	0.7	28	1	BX556035	ACCESSION:BX556035
1976	18.6	0.7	33	1	AV743346	ACCESSION:AV743346
1977	18.6	0.7	34	1	BG612023	ACCESSION:BG612023
1978	18.6	0.7	40	1	TA105A11P	ACCESSION:AL464696
1979	18.4	0.7	20	1	AZ849506	ACCESSION:AZ849506
1980	18.4	0.7	20	1	AZ645312	ACCESSION:AZ645312
1981	18.4	0.7	20	1	CF308984	ACCESSION:CF308984
c1982	18.4	0.7	20	1	AZ375620	ACCESSION:AZ375620
1983	18.4	0.7	20	1	AZ486787	ACCESSION:AZ486787
c1984	18.4	0.7	20	1	AZ579122	ACCESSION:AZ579122
1985	18.4	0.7	20	1	AZ818055	ACCESSION:AZ818055
c1986	18.4	0.7	20	1	AZ949997	ACCESSION:AZ949997
1987	18.4	0.7	21	1	BX564412	ACCESSION:BX564412
c1988	18.4	0.7	21	1	AZ610868	ACCESSION:AZ610868
1989	18.4	0.7	21	1	AZ764492	ACCESSION:AZ764492
1990	18.4	0.7	21	1	BX558161	ACCESSION:BX558161
1991	18.4	0.7	21	1	CF330439	ACCESSION:CF330439
1992	18.4	0.7	22	1	AL048750	ACCESSION:AL048750
1993	18.4	0.7	22	1	CF310806	ACCESSION:CF310806
c1994	18.4	0.7	23	1	BX550903	ACCESSION:BX550903
1995	18.4	0.7	23	1	AL587602	ACCESSION:AL587602
1996	18.4	0.7	23	1	BQ590647	ACCESSION:BQ590647
c1997	18.4	0.7	23	1	BQ590647	ACCESSION:BQ590647
1998	18.4	0.7	24	1	AZ448207	ACCESSION:AZ448207
c1999	18.4	0.7	25	1	AU265663	ACCESSION:AU265663
2000	18.4	0.7	25	1	TA12F02Q	ACCESSION:AL451366
2001	18.4	0.7	25	1	CF319499	ACCESSION:CF319499
c2002	18.4	0.7	25	1	AV737092	ACCESSION:AV737092
2003	18.4	0.7	26	1	CF336199	ACCESSION:CF336199
c2004	18.4	0.7	27	1	CF279147	ACCESSION:CF279147

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1714	19	0.7	22	1	AZ304806
c1715	19	0.7	22	1	AZ310066
1716	19	0.7	22	1	AZ351527
1717	19	0.7	22	1	AZ357630
1718	19	0.7	22	1	AZ388103
c1719	19	0.7	22	1	AZ401908
c1720	19	0.7	22	1	AZ424307
c1721	19	0.7	22	1	AZ428818
c1722	19	0.7	22	1	AZ459654
c1723	19	0.7	22	1	AZ463503
c1724	19	0.7	22	1	AZ463652
1725	19	0.7	22	1	AZ505769
1726	19	0.7	22	1	AZ582403
1727	19	0.7	22	1	AZ607658
1728	19	0.7	22	1	AZ654691
1729	19	0.7	22	1	AZ760533
c1730	19	0.7	22	1	AZ779844
c1731	19	0.7	22	1	AZ785019
c1732	19	0.7	22	1	AZ787098
c1733	19	0.7	22	1	AZ787606
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c1735	19	0.7	22	1	AZ810674
c1736	19	0.7	22	1	AZ820439
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1739	19	0.7	22	1	AZ946102
1740	19	0.7	22	1	BH000233
1741	19	0.7	22	1	TA131B09P
1742	19	0.7	22	1	TA329F10P
c1743	19	0.7	22	1	TA35C12Q
1744	19	0.7	22	1	TA380A07P
1745	19	0.7	22	1	AZ309907
c1746	19	0.7	22	1	TA386H07Q
c1747	19	0.7	23	1	CF279238
c1748	19	0.7	23	1	CF297943
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c1768	19	0.7	23	1	AZ647637
1769	19	0.7	23	1	AZ654903
1770	19	0.7	23	1	AZ778751
1771	19	0.7	23	1	AZ787184
c1772	19	0.7	23	1	AZ792751
1773	19	0.7	23	1	AZ859570
1774	19	0.7	23	1	AZ939608
c1775	19	0.7	23	1	BH000534
1776	19	0.7	23	1	TA151C02Q
c1777	19	0.7	23	1	TA274B03P
1778	19	0.7	23	1	TA353A10P
c1779	19	0.7	23	1	BX559898
1780	19	0.7	23	1	AZ315640
1781	19	0.7	23	1	AZ621676
1782	19	0.7	23	1	AZ817623
c1783	19	0.7	23	1	AW335179
1784	19	0.7	23	1	BX550903
1785	19	0.7	23	1	CF293321

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c1786	19	0.7	24	1	CA853764
c1787	19	0.7	24	1	CF312319
1788	19	0.7	24	1	AZ438069
1789	19	0.7	24	1	AZ786257
1790	19	0.7	24	1	CF326993
c1791	19	0.7	24	1	AZ448207
1792	19	0.7	24	1	AZ764496
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1794	19	0.7	24	1	AZ764513
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1796	19	0.7	25	1	AZ386891
c1797	19	0.7	25	1	CG726337
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c1799	19	0.7	25	1	CF310471
1800	19	0.7	25	1	AL048782
c1801	19	0.7	25	1	CF326989
1802	19	0.7	25	1	AL587718
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1804	19	0.7	25	1	AZ774476
c1805	19	0.7	25	1	AZ774476
c1806	19	0.7	25	1	TA12F02Q
1807	19	0.7	26	1	TA321G11P
c1808	19	0.7	26	1	CF280688
1809	19	0.7	26	1	AZ485624
c1810	19	0.7	26	1	CF318508
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1814	19	0.7	26	1	AZ764502
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c1820	19	0.7	27	1	AU265398
1821	19	0.7	27	1	CF300303
c1822	19	0.7	27	1	CF318113
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c1824	19	0.7	28	1	AU257468
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c1827	19	0.7	28	1	AL587582
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1570	19	0.7	20	1	CF310604
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1605	19	0.7	20	1	AZ650271
1606	19	0.7	20	1	AZ760838
1607	19	0.7	20	1	AZ764504
c1608	19	0.7	20	1	AZ765211
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1629	19	0.7	20	1	AZ858052
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c1632	19	0.7	20	1	AZ949180
c1633	19	0.7	20	1	AZ963973
1634	19	0.7	20	1	AL587759
c1635	19	0.7	20	1	CF298207
1636	19	0.7	20	1	CF318278
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1638	19	0.7	20	1	AZ341237
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c1644	19	0.7	20	1	AZ645312
1645	19	0.7	21	1	AL048777
1646	19	0.7	21	1	CF282216
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1656	19	0.7	21	1	CF327391
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1660	19	0.7	21	1	AZ348593
1661	19	0.7	21	1	AZ350611
1662	19	0.7	21	1	AZ386711
1663	19	0.7	21	1	AZ386794
1664	19	0.7	21	1	AZ389287
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c1667	19	0.7	21	1	AZ412739
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1684	19	0.7	21	1	AZ832198
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1686	19	0.7	21	1	AZ960063
1687	19	0.7	21	1	BH000837
c1688	19	0.7	21	1	BX556006
c1689	19	0.7	21	1	CF311914
1690	19	0.7	21	1	AZ461824
1691	19	0.7	21	1	AZ493766
c1692	19	0.7	21	1	CF302218
c1693	19	0.7	21	1	CF314260
c1694	19	0.7	21	1	AZ792613
1695	19	0.7	21	1	AL587702
1696	19	0.7	21	1	AZ610868
c1697	19	0.7	21	1	AZ764492
1698	19	0.7	22	1	AZ823875
c1699	19	0.7	22	1	AW332181
c1700	19	0.7	22	1	AW332399
c1701	19	0.7	22	1	CF282024
c1702	19	0.7	22	1	CF299342
c1703	19	0.7	22	1	CF300133
c1704	19	0.7	22	1	CF310366
c1705	19	0.7	22	1	CF311269
1706	19	0.7	22	1	CF311713
1707	19	0.7	22	1	CF312498
c1708	19	0.7	22	1	CF330679
c1709	19	0.7	22	1	CF333430
c1710	19	0.7	22	1	CF334781
c1711	19	0.7	22	1	CF336250
1712	19	0.7	22	1	CF337580

ACCESSION:AZ345856
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ACCESSION:AZ579178
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ACCESSION:AZ645312
ACCESSION:AL048777
ACCESSION:CF282216
ACCESSION:CF292703
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ACCESSION:AZ960063
ACCESSION:BH000837
ACCESSION:BX556006
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ACCESSION:CF312498
ACCESSION:CF330679
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ACCESSION:CF334781
ACCESSION:CF336250
ACCESSION:CF337580

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c1422	19	0.7	19	1	CF309801	ACCESSION:CF309801
1423	19	0.7	19	1	CF309943	ACCESSION:CF309943
c1424	19	0.7	19	1	CF309943	ACCESSION:CF309943
1425	19	0.7	19	1	CF311496	ACCESSION:CF311496
c1426	19	0.7	19	1	CF311496	ACCESSION:CF311496
1427	19	0.7	19	1	CF311513	ACCESSION:CF311513
c1428	19	0.7	19	1	CF311513	ACCESSION:CF311513
1429	19	0.7	19	1	CF312403	ACCESSION:CF312403
c1430	19	0.7	19	1	CF312403	ACCESSION:CF312403
1431	19	0.7	19	1	CF315299	ACCESSION:CF315299
c1432	19	0.7	19	1	CF315299	ACCESSION:CF315299
1433	19	0.7	19	1	CF316480	ACCESSION:CF316480
c1434	19	0.7	19	1	CF316480	ACCESSION:CF316480
1435	19	0.7	19	1	CF318788	ACCESSION:CF318788
c1436	19	0.7	19	1	CF318788	ACCESSION:CF318788
1437	19	0.7	19	1	CF329986	ACCESSION:CF329986
c1438	19	0.7	19	1	CF329986	ACCESSION:CF329986
1439	19	0.7	19	1	CF332063	ACCESSION:CF332063
c1440	19	0.7	19	1	CF332063	ACCESSION:CF332063
1441	19	0.7	19	1	CF333507	ACCESSION:CF333507
c1442	19	0.7	19	1	CF333507	ACCESSION:CF333507
1443	19	0.7	19	1	CF333753	ACCESSION:CF333753
c1444	19	0.7	19	1	CF333753	ACCESSION:CF333753
1445	19	0.7	19	1	CF334014	ACCESSION:CF334014
c1446	19	0.7	19	1	CF334014	ACCESSION:CF334014
1447	19	0.7	19	1	AZ307313	ACCESSION:AZ307313
c1448	19	0.7	19	1	AZ307313	ACCESSION:AZ307313
1449	19	0.7	19	1	AZ310079	ACCESSION:AZ310079
c1450	19	0.7	19	1	AZ310079	ACCESSION:AZ310079
1451	19	0.7	19	1	AZ310105	ACCESSION:AZ310105
c1452	19	0.7	19	1	AZ310105	ACCESSION:AZ310105
1453	19	0.7	19	1	AZ317743	ACCESSION:AZ317743
c1454	19	0.7	19	1	AZ317743	ACCESSION:AZ317743
1455	19	0.7	19	1	AZ340311	ACCESSION:AZ340311
c1456	19	0.7	19	1	AZ340311	ACCESSION:AZ340311
c1457	19	0.7	19	1	AZ345795	ACCESSION:AZ345795
1458	19	0.7	19	1	AZ350519	ACCESSION:AZ350519
c1459	19	0.7	19	1	AZ350519	ACCESSION:AZ350519
1460	19	0.7	19	1	AZ364226	ACCESSION:AZ364226
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1462	19	0.7	19	1	AZ365696	ACCESSION:AZ365696
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1466	19	0.7	19	1	AZ374619	ACCESSION:AZ374619
c1467	19	0.7	19	1	AZ374619	ACCESSION:AZ374619
1468	19	0.7	19	1	AZ385952	ACCESSION:AZ385952
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1470	19	0.7	19	1	AZ391509	ACCESSION:AZ391509
c1471	19	0.7	19	1	AZ391509	ACCESSION:AZ391509
1472	19	0.7	19	1	AZ410050	ACCESSION:AZ410050
c1473	19	0.7	19	1	AZ410050	ACCESSION:AZ410050
1474	19	0.7	19	1	AZ414413	ACCESSION:AZ414413
c1475	19	0.7	19	1	AZ414413	ACCESSION:AZ414413
1476	19	0.7	19	1	AZ422604	ACCESSION:AZ422604
c1477	19	0.7	19	1	AZ422604	ACCESSION:AZ422604
1478	19	0.7	19	1	AZ424716	ACCESSION:AZ424716
c1479	19	0.7	19	1	AZ424716	ACCESSION:AZ424716
1480	19	0.7	19	1	AZ441329	ACCESSION:AZ441329
c1481	19	0.7	19	1	AZ441329	ACCESSION:AZ441329
1482	19	0.7	19	1	AZ442365	ACCESSION:AZ442365
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1484	19	0.7	19	1	AZ453930	ACCESSION:AZ453930
c1485	19	0.7	19	1	AZ453930	ACCESSION:AZ453930
1486	19	0.7	19	1	AZ460906	ACCESSION:AZ460906
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1488	19	0.7	19	1	AZ471494	ACCESSION:AZ471494
c1489	19	0.7	19	1	AZ471494	ACCESSION:AZ471494
1490	19	0.7	19	1	AZ476576	ACCESSION:AZ476576
c1491	19	0.7	19	1	AZ476576	ACCESSION:AZ476576
1492	19	0.7	19	1	AZ486786	ACCESSION:AZ486786
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1494	19	0.7	19	1	AZ490652	ACCESSION:AZ490652
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1496	19	0.7	19	1	AZ508040	ACCESSION:AZ508040
c1497	19	0.7	19	1	AZ508040	ACCESSION:AZ508040
1498	19	0.7	19	1	AZ579119	ACCESSION:AZ579119
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c1501	19	0.7	19	1	AZ583970	ACCESSION:AZ583970
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1510	19	0.7	19	1	AZ631701	ACCESSION:AZ631701
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1512	19	0.7	19	1	AZ633821	ACCESSION:AZ633821
c1513	19	0.7	19	1	AZ633821	ACCESSION:AZ633821
1514	19	0.7	19	1	AZ643659	ACCESSION:AZ643659
c1515	19	0.7	19	1	AZ643659	ACCESSION:AZ643659
1516	19	0.7	19	1	AZ644698	ACCESSION:AZ644698
c1517	19	0.7	19	1	AZ644698	ACCESSION:AZ644698
1518	19	0.7	19	1	AZ648335	ACCESSION:AZ648335
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1520	19	0.7	19	1	AZ649888	ACCESSION:AZ649888
c1521	19	0.7	19	1	AZ649888	ACCESSION:AZ649888
c1522	19	0.7	19	1	AZ650575	ACCESSION:AZ650575
1523	19	0.7	19	1	AZ764497	ACCESSION:AZ764497
c1524	19	0.7	19	1	AZ764497	ACCESSION:AZ764497
1525	19	0.7	19	1	AZ764522	ACCESSION:AZ764522
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1527	19	0.7	19	1	AZ764534	ACCESSION:AZ764534
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1529	19	0.7	19	1	AZ770387	ACCESSION:AZ770387
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1531	19	0.7	19	1	AZ778858	ACCESSION:AZ778858
c1532	19	0.7	19	1	AZ778858	ACCESSION:AZ778858
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c1534	19	0.7	19	1	AZ779901	ACCESSION:AZ779901
1535	19	0.7	19	1	AZ781876	ACCESSION:AZ781876
c1536	19	0.7	19	1	AZ781876	ACCESSION:AZ781876
1537	19	0.7	19	1	AZ787634	ACCESSION:AZ787634
c1538	19	0.7	19	1	AZ787634	ACCESSION:AZ787634
1539	19	0.7	19	1	AZ788058	ACCESSION:AZ788058
c1540	19	0.7	19	1	AZ788058	ACCESSION:AZ788058
1541	19	0.7	19	1	AZ789590	ACCESSION:AZ789590
c1542	19	0.7	19	1	AZ789590	ACCESSION:AZ789590
1543	19	0.7	19	1	AZ792713	ACCESSION:AZ792713
c1544	19	0.7	19	1	AZ792713	ACCESSION:AZ792713
1545	19	0.7	19	1	AZ795403	ACCESSION:AZ795403
c1546	19	0.7	19	1	AZ795403	ACCESSION:AZ795403
1547	19	0.7	19	1	AZ801970	ACCESSION:AZ801970
c1548	19	0.7	19	1	AZ801970	ACCESSION:AZ801970
1549	19	0.7	19	1	AZ822225	ACCESSION:AZ822225
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1553	19	0.7	19	1	AZ841622	ACCESSION:AZ841622
c1554	19	0.7	19	1	AZ841622	ACCESSION:AZ841622
1555	19	0.7	19	1	AZ861896	ACCESSION:AZ861896
c1556	19	0.7	19	1	AZ861896	ACCESSION:AZ861896
1557	19	0.7	19	1	AZ936798	ACCESSION:AZ936798
c1558	19	0.7	19	1	AZ936798	ACCESSION:AZ936798
1559	19	0.7	19	1	AZ985501	ACCESSION:AZ985501
c1560	19	0.7	19	1	AZ985501	ACCESSION:AZ985501
1561	19	0.7	19	1	BH000498	ACCESSION:BH000498
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1564	19	0.7	20	1	CF280913	ACCESSION:CF280913
1565	19	0.7	20	1	CF282035	ACCESSION:CF282035
1566	19	0.7	20	1	CF282414	ACCESSION:CF282414

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1276	19.6	0.7	45	1	BF525658	ACCESSION:BF525658
c1277	19.6	0.7	45	1	CF316064	ACCESSION:CF316064
c1278	19.6	0.7	46	1	BQ589206	ACCESSION:BQ589206
c1279	19.6	0.7	46	1	BQ591313	ACCESSION:BQ591313
1280	19.4	0.7	21	1	BX548564	ACCESSION:BX548564
c1281	19.4	0.7	21	1	BX564412	ACCESSION:BX564412
1282	19.4	0.7	21	1	CF296213	ACCESSION:CF296213
1283	19.4	0.7	21	1	CF302218	ACCESSION:CF302218
1284	19.4	0.7	21	1	CF314260	ACCESSION:CF314260
1285	19.4	0.7	21	1	AZ308846	ACCESSION:AZ308846
1286	19.4	0.7	21	1	AZ317208	ACCESSION:AZ317208
1287	19.4	0.7	21	1	AZ486776	ACCESSION:AZ486776
1288	19.4	0.7	21	1	AZ792613	ACCESSION:AZ792613
c1289	19.4	0.7	21	1	AZ822825	ACCESSION:AZ822825
c1290	19.4	0.7	21	1	AZ853429	ACCESSION:AZ853429
1291	19.4	0.7	21	1	AZ943299	ACCESSION:AZ943299
c1292	19.4	0.7	22	1	AL048750	ACCESSION:AL048750
1293	19.4	0.7	22	1	BX556059	ACCESSION:BX556059
c1294	19.4	0.7	22	1	TA303G05P	ACCESSION:AL497383
c1295	19.4	0.7	23	1	CF332379	ACCESSION:CF332379
1296	19.4	0.7	23	1	AL048776	ACCESSION:AL048776
1297	19.4	0.7	23	1	AL048745	ACCESSION:AL048745
1298	19.4	0.7	23	1	CF279593	ACCESSION:CF279593
1299	19.4	0.7	23	1	BX568055	ACCESSION:BX568055
1300	19.4	0.7	23	1	CF314322	ACCESSION:CF314322
c1301	19.4	0.7	23	1	AZ382013	ACCESSION:AZ382013
1302	19.4	0.7	23	1	AZ627841	ACCESSION:AZ627841
c1303	19.4	0.7	23	1	TA55C06P	ACCESSION:AL455778
1304	19.4	0.7	24	1	AL048765	ACCESSION:AL048765
1305	19.4	0.7	24	1	AZ404871	ACCESSION:AZ404871
1306	19.4	0.7	24	1	AZ309553	ACCESSION:AZ309553
1307	19.4	0.7	24	1	AW247159	ACCESSION:AW247159
1308	19.4	0.7	24	1	CF281313	ACCESSION:CF281313
1309	19.4	0.7	24	1	AZ458112	ACCESSION:AZ458112
1310	19.4	0.7	24	1	AZ514388	ACCESSION:AZ514388
1311	19.4	0.7	24	1	AZ621257	ACCESSION:AZ621257
c1312	19.4	0.7	25	1	N27663	ACCESSION:N27663
c1313	19.4	0.7	25	1	T49097	ACCESSION:T49097
c1314	19.4	0.7	25	1	AU008929	ACCESSION:AU008929
1315	19.4	0.7	25	1	AU265663	ACCESSION:AU265663
c1316	19.4	0.7	25	1	AZ867155	ACCESSION:AZ867155
c1317	19.4	0.7	26	1	BQ583199	ACCESSION:BQ583199
1318	19.4	0.7	26	1	CF318508	ACCESSION:CF318508
1319	19.4	0.7	27	1	CF311022	ACCESSION:CF311022
c1320	19.4	0.7	27	1	N34515	ACCESSION:N34515
c1321	19.4	0.7	27	1	CF315308	ACCESSION:CF315308
c1322	19.4	0.7	27	1	CF328811	ACCESSION:CF328811
1323	19.4	0.7	28	1	AL587605	ACCESSION:AL587605
1324	19.4	0.7	28	1	BX555317	ACCESSION:BX555317
1325	19.4	0.7	29	1	AL048694	ACCESSION:AL048694
c1326	19.4	0.7	29	1	CF312595	ACCESSION:CF312595
c1327	19.4	0.7	29	1	CF334023	ACCESSION:CF334023
1328	19.4	0.7	29	1	CF336137	ACCESSION:CF336137
c1329	19.4	0.7	29	1	TA224C08P	ACCESSION:AL480654
1330	19.4	0.7	30	1	AL048796	ACCESSION:AL048796
1331	19.4	0.7	30	1	AL048729	ACCESSION:AL048729
c1332	19.4	0.7	31	1	CF319504	ACCESSION:CF319504
1333	19.4	0.7	31	1	AU267441	ACCESSION:AU267441
c1334	19.4	0.7	32	1	BX555194	ACCESSION:BX555194
c1335	19.4	0.7	32	1	BX554291	ACCESSION:BX554291
c1336	19.4	0.7	32	1	BX555135	ACCESSION:BX555135
1337	19.4	0.7	32	1	BJ078010	ACCESSION:BJ078010
c1338	19.4	0.7	33	1	BX565664	ACCESSION:BX565664
c1339	19.4	0.7	35	1	T50295	ACCESSION:T50295
1340	19.2	0.7	24	1	BG670391	ACCESSION:BG670391
c1341	19.2	0.7	24	1	BX554611	ACCESSION:BX554611
1342	19.2	0.7	24	1	CF276855	ACCESSION:CF276855
c1343	19.2	0.7	24	1	CF301561	ACCESSION:CF301561
c1344	19.2	0.7	24	1	CF320862	ACCESSION:CF320862
1345	19.2	0.7	24	1	AZ328848	ACCESSION:AZ328848
1346	19.2	0.7	24	1	AZ363562	ACCESSION:AZ363562
1347	19.2	0.7	24	1	AZ386491	ACCESSION:AZ386491
c1348	19.2	0.7	24	1	AZ390642	ACCESSION:AZ390642
c1349	19.2	0.7	24	1	AZ459280	ACCESSION:AZ459280
c1350	19.2	0.7	24	1	AZ644621	ACCESSION:AZ644621
1351	19.2	0.7	24	1	AZ834990	ACCESSION:AZ834990
1352	19.2	0.7	24	1	AZ970038	ACCESSION:AZ970038
1353	19.2	0.7	24	1	AZ984490	ACCESSION:AZ984490
c1354	19.2	0.7	24	1	AZ993423	ACCESSION:AZ993423
c1355	19.2	0.7	24	1	TA169D12P	ACCESSION:AL478922
1356	19.2	0.7	24	1	TA27B08Q	ACCESSION:AL453584
1357	19.2	0.7	24	1	TA354C06P	ACCESSION:AL494439
1358	19.2	0.7	24	1	TA371F11P	ACCESSION:AL495622
1359	19.2	0.7	24	1	TA95B08P	ACCESSION:AL459003
c1360	19.2	0.7	24	1	AZ486788	ACCESSION:AZ486788
c1361	19.2	0.7	24	1	AZ627850	ACCESSION:AZ627850
1362	19.2	0.7	25	1	CF638767	ACCESSION:CF638767
c1363	19.2	0.7	25	1	AL587648	ACCESSION:AL587648
c1364	19.2	0.7	25	1	CF291048	ACCESSION:CF291048
c1365	19.2	0.7	25	1	CF291646	ACCESSION:CF291646
1366	19.2	0.7	25	1	CF299288	ACCESSION:CF299288
c1367	19.2	0.7	25	1	CF300333	ACCESSION:CF300333
c1368	19.2	0.7	25	1	CF316323	ACCESSION:CF316323
c1369	19.2	0.7	25	1	CF317714	ACCESSION:CF317714
c1370	19.2	0.7	25	1	CF319073	ACCESSION:CF319073
c1371	19.2	0.7	25	1	CF330786	ACCESSION:CF330786
c1372	19.2	0.7	25	1	N33150	ACCESSION:N33150
1373	19.2	0.7	25	1	AZ344725	ACCESSION:AZ344725
c1374	19.2	0.7	25	1	AZ350777	ACCESSION:AZ350777
1375	19.2	0.7	25	1	AZ381039	ACCESSION:AZ381039
1376	19.2	0.7	25	1	AZ389458	ACCESSION:AZ389458
c1377	19.2	0.7	25	1	AZ609234	ACCESSION:AZ609234
c1378	19.2	0.7	25	1	AZ623157	ACCESSION:AZ623157
c1379	19.2	0.7	25	1	AZ788646	ACCESSION:AZ788646
1380	19.2	0.7	25	1	AZ949287	ACCESSION:AZ949287
c1381	19.2	0.7	25	1	AZ980407	ACCESSION:AZ980407
c1382	19.2	0.7	25	1	TA324E10P	ACCESSION:AL493396
1383	19.2	0.7	25	1	CF326989	ACCESSION:CF326989
c1384	19.2	0.7	26	1	AL587774	ACCESSION:AL587774
c1385	19.2	0.7	26	1	CF296851	ACCESSION:CF296851
1386	19.2	0.7	26	1	BX554728	ACCESSION:BX554728
c1387	19.2	0.7	27	1	AZ970621	ACCESSION:AZ970621
c1388	19.2	0.7	27	1	CF299084	ACCESSION:CF299084
c1389	19.2	0.7	27	1	N34459	ACCESSION:N34459
c1390	19.2	0.7	28	1	AZ481286	ACCESSION:AZ481286
c1391	19.2	0.7	28	1	AW332443	ACCESSION:AW332443
1392	19.2	0.7	28	1	CF299294	ACCESSION:CF299294
1393	19.2	0.7	28	1	AZ358038	ACCESSION:AZ358038
1394	19.2	0.7	29	1	CF328476	ACCESSION:CF328476
c1395	19.2	0.7	29	1	CF330960	ACCESSION:CF330960
1396	19.2	0.7	30	1	AZ443322	ACCESSION:AZ443322
1397	19.2	0.7	30	1	DR31A15T	ACCESSION:AL987581
c1398	19.2	0.7	31	1	BQ591372	ACCESSION:BQ591372
c1399	19.2	0.7	32	1	CF298526	ACCESSION:CF298526
1400	19.2	0.7	32	1	BG501238	ACCESSION:BG501238
1401	19.2	0.7	33	1	BI152241	ACCESSION:BI152241
c1402	19.2	0.7	34	1	AL047464	ACCESSION:AL047464
c1403	19.2	0.7	35	1	BQ590703	ACCESSION:BQ590703
c1404	19.2	0.7	41	1	CF302032	ACCESSION:CF302032
1405	19	0.7	19	1	BQ588729	ACCESSION:BQ588729
c1406	19	0.7	19	1	BQ588729	ACCESSION:BQ588729
1407	19	0.7	19	1	CB174047	ACCESSION:CB174047
c1408	19	0.7	19	1	CB174047	ACCESSION:CB174047
1409	19	0.7	19	1	CF279008	ACCESSION:CF279008
c1410	19	0.7	19	1	CF279008	ACCESSION:CF279008
1411	19	0.7	19	1	CF291089	ACCESSION:CF291089
c1412	19	0.7	19	1	CF291089	ACCESSION:CF291089
1413	19	0.7	19	1	CF291090	ACCESSION:CF291090
c1414	19	0.7	19	1	CF291090	ACCESSION:CF291090
1415	19	0.7	19	1	CF299598	ACCESSION:CF299598
c1416	19	0.7	19	1	CF299598	ACCESSION:CF299598
1417	19	0.7	19	1	CF302327	ACCESSION:CF302327
c1418	19	0.7	19	1	CF302327	ACCESSION:CF302327
1419	19	0.7	19	1	CF304589	ACCESSION:CF304589
c1420	19	0.7	19	1	CF304589	ACCESSION:CF304589

c1129	19.6	0.7	32	1	AZ459536	ACCESSION:AZ459536
1130	19.6	0.7	32	1	AZ470832	ACCESSION:AZ470832
c1131	19.6	0.7	32	1	AZ611890	ACCESSION:AZ611890
1132	19.6	0.7	32	1	AZ778018	ACCESSION:AZ778018
1133	19.6	0.7	32	1	DR85L21T	ACCESSION:AL986044
1134	19.6	0.7	32	1	AZ400441	ACCESSION:AZ400441
1135	19.6	0.7	32	1	CF302459	ACCESSION:CF302459
c1136	19.6	0.7	32	1	AZ579652	ACCESSION:AZ579652
c1137	19.6	0.7	32	1	DR1F7S	ACCESSION:AL735323
1138	19.6	0.7	32	1	AZ397471	ACCESSION:AZ397471
c1139	19.6	0.7	32	1	CA853459	ACCESSION:CA853459
c1140	19.6	0.7	33	1	AL587609	ACCESSION:AL587609
c1141	19.6	0.7	33	1	CF291613	ACCESSION:CF291613
c1142	19.6	0.7	33	1	CF311229	ACCESSION:CF311229
c1143	19.6	0.7	33	1	CF326967	ACCESSION:CF326967
1144	19.6	0.7	33	1	CF328313	ACCESSION:CF328313
c1145	19.6	0.7	33	1	CF336752	ACCESSION:CF336752
c1146	19.6	0.7	33	1	CF337105	ACCESSION:CF337105
c1147	19.6	0.7	33	1	AZ486795	ACCESSION:AZ486795
c1148	19.6	0.7	33	1	AZ627839	ACCESSION:AZ627839
c1149	19.6	0.7	33	1	CF334899	ACCESSION:CF334899
c1150	19.6	0.7	34	1	AL587876	ACCESSION:AL587876
c1151	19.6	0.7	34	1	CF302250	ACCESSION:CF302250
c1152	19.6	0.7	34	1	AZ465350	ACCESSION:AZ465350
1153	19.6	0.7	34	1	AZ501040	ACCESSION:AZ501040
1154	19.6	0.7	34	1	AZ809643	ACCESSION:AZ809643
1155	19.6	0.7	34	1	DR41A4T	ACCESSION:AL980969
c1156	19.6	0.7	34	1	BQ594010	ACCESSION:BQ594010
1157	19.6	0.7	35	1	BF338797	ACCESSION:BF338797
1158	19.6	0.7	35	1	CF315871	ACCESSION:CF315871
c1159	19.6	0.7	35	1	CF334198	ACCESSION:CF334198
c1160	19.6	0.7	35	1	CF335633	ACCESSION:CF335633
c1161	19.6	0.7	35	1	AZ623128	ACCESSION:AZ623128
c1162	19.6	0.7	35	1	AZ803371	ACCESSION:AZ803371
1163	19.6	0.7	36	1	BE894682	ACCESSION:BE894682
c1164	19.6	0.7	36	1	AL587891	ACCESSION:AL587891
1165	19.6	0.7	36	1	BE876160	ACCESSION:BE876160
c1166	19.6	0.7	36	1	CF317028	ACCESSION:CF317028
c1167	19.6	0.7	36	1	CF331983	ACCESSION:CF331983
c1168	19.6	0.7	36	1	AZ470916	ACCESSION:AZ470916
c1169	19.6	0.7	36	1	AZ628484	ACCESSION:AZ628484
c1170	19.6	0.7	36	1	AZ793484	ACCESSION:AZ793484
c1171	19.6	0.7	36	1	AZ949866	ACCESSION:AZ949866
c1172	19.6	0.7	36	1	AZ957867	ACCESSION:AZ957867
1173	19.6	0.7	36	1	BI761940	ACCESSION:BI761940
c1174	19.6	0.7	36	1	CF279874	ACCESSION:CF279874
c1175	19.6	0.7	36	1	CF331913	ACCESSION:CF331913
c1176	19.6	0.7	36	1	CF333863	ACCESSION:CF333863
c1177	19.6	0.7	36	1	CF298131	ACCESSION:CF298131
1178	19.6	0.7	37	1	CF291807	ACCESSION:CF291807
1179	19.6	0.7	37	1	BG033620	ACCESSION:BG033620
c1180	19.6	0.7	37	1	CF291818	ACCESSION:CF291818
1181	19.6	0.7	37	1	CF300002	ACCESSION:CF300002
1182	19.6	0.7	37	1	CF300328	ACCESSION:CF300328
c1183	19.6	0.7	37	1	CF301864	ACCESSION:CF301864
c1184	19.6	0.7	37	1	CF307971	ACCESSION:CF307971
1185	19.6	0.7	37	1	CF316114	ACCESSION:CF316114
1186	19.6	0.7	37	1	CF321294	ACCESSION:CF321294
c1187	19.6	0.7	37	1	CF326975	ACCESSION:CF326975
c1188	19.6	0.7	37	1	CF333624	ACCESSION:CF333624
c1189	19.6	0.7	37	1	CF336769	ACCESSION:CF336769
1190	19.6	0.7	37	1	AZ321759	ACCESSION:AZ321759
c1191	19.6	0.7	37	1	AZ463801	ACCESSION:AZ463801
1192	19.6	0.7	37	1	AZ831214	ACCESSION:AZ831214
c1193	19.6	0.7	37	1	DR102P24T	ACCESSION:AL977144
1194	19.6	0.7	37	1	DR102P2T	ACCESSION:AL985556
1195	19.6	0.7	37	1	CF301560	ACCESSION:CF301560
c1196	19.6	0.7	37	1	CF299167	ACCESSION:CF299167
c1197	19.6	0.7	37	1	CF278363	ACCESSION:CF278363
c1198	19.6	0.7	37	1	BX556312	ACCESSION:BX556312
c1199	19.6	0.7	37	1	BX562242	ACCESSION:BX562242
1200	19.6	0.7	37	1	BG430173	ACCESSION:BG430173
c1201	19.6	0.7	38	1	AW333985	ACCESSION:AW333985
1202	19.6	0.7	38	1	CF316791	ACCESSION:CF316791
c1203	19.6	0.7	38	1	CF291176	ACCESSION:CF291176
c1204	19.6	0.7	38	1	CF301164	ACCESSION:CF301164
c1205	19.6	0.7	38	1	CF301819	ACCESSION:CF301819
c1206	19.6	0.7	38	1	CF315184	ACCESSION:CF315184
c1207	19.6	0.7	38	1	CF321261	ACCESSION:CF321261
1208	19.6	0.7	38	1	CF328351	ACCESSION:CF328351
c1209	19.6	0.7	38	1	CF329605	ACCESSION:CF329605
1210	19.6	0.7	38	1	CF329690	ACCESSION:CF329690
c1211	19.6	0.7	38	1	CF329730	ACCESSION:CF329730
c1212	19.6	0.7	38	1	AZ785034	ACCESSION:AZ785034
1213	19.6	0.7	38	1	BF526154	ACCESSION:BF526154
1214	19.6	0.7	38	1	BF525501	ACCESSION:BF525501
c1215	19.6	0.7	38	1	BX556487	ACCESSION:BX556487
1216	19.6	0.7	39	1	CF319510	ACCESSION:CF319510
1217	19.6	0.7	39	1	BE891613	ACCESSION:BE891613
1218	19.6	0.7	39	1	BF032623	ACCESSION:BF032623
c1219	19.6	0.7	39	1	CF298508	ACCESSION:CF298508
c1220	19.6	0.7	39	1	CF302356	ACCESSION:CF302356
c1221	19.6	0.7	39	1	CF315736	ACCESSION:CF315736
c1222	19.6	0.7	39	1	CF321323	ACCESSION:CF321323
c1223	19.6	0.7	39	1	CF330732	ACCESSION:CF330732
c1224	19.6	0.7	39	1	AZ639088	ACCESSION:AZ639088
1225	19.6	0.7	39	1	BG287495	ACCESSION:BG287495
1226	19.6	0.7	39	1	BI694035	ACCESSION:BI694035
c1227	19.6	0.7	39	1	BX550894	ACCESSION:BX550894
c1228	19.6	0.7	40	1	AL449576	ACCESSION:AL449576
c1229	19.6	0.7	40	1	CF311814	ACCESSION:CF311814
c1230	19.6	0.7	40	1	CF327027	ACCESSION:CF327027
c1231	19.6	0.7	40	1	CF328199	ACCESSION:CF328199
1232	19.6	0.7	40	1	CF328306	ACCESSION:CF328306
c1233	19.6	0.7	40	1	CF334545	ACCESSION:CF334545
c1234	19.6	0.7	40	1	CF336399	ACCESSION:CF336399
1235	19.6	0.7	40	1	AZ831983	ACCESSION:AZ831983
1236	19.6	0.7	40	1	BG166502	ACCESSION:BG166502
1237	19.6	0.7	40	1	DR85H22T	ACCESSION:AL982088
c1238	19.6	0.7	40	1	BX562248	ACCESSION:BX562248
c1239	19.6	0.7	40	1	BX567930	ACCESSION:BX567930
c1240	19.6	0.7	40	1	AL638703	ACCESSION:AL638703
c1241	19.6	0.7	40	1	BX564796	ACCESSION:BX564796
c1242	19.6	0.7	41	1	CF301837	ACCESSION:CF301837
c1243	19.6	0.7	41	1	CF291539	ACCESSION:CF291539
c1244	19.6	0.7	41	1	CF305364	ACCESSION:CF305364
c1245	19.6	0.7	41	1	CF318677	ACCESSION:CF318677
c1246	19.6	0.7	41	1	CF320203	ACCESSION:CF320203
c1247	19.6	0.7	41	1	CF330464	ACCESSION:CF330464
c1248	19.6	0.7	41	1	CF334638	ACCESSION:CF334638
1249	19.6	0.7	41	1	AZ775066	ACCESSION:AZ775066
1250	19.6	0.7	41	1	AZ827008	ACCESSION:AZ827008
1251	19.6	0.7	41	1	CF328487	ACCESSION:CF328487
1252	19.6	0.7	41	1	AV742106	ACCESSION:AV742106
c1253	19.6	0.7	41	1	CF300448	ACCESSION:CF300448
c1254	19.6	0.7	42	1	AW334133	ACCESSION:AW334133
c1255	19.6	0.7	42	1	CF318962	ACCESSION:CF318962
c1256	19.6	0.7	42	1	CF319867	ACCESSION:CF319867
1257	19.6	0.7	42	1	CF320056	ACCESSION:CF320056
c1258	19.6	0.7	42	1	CF332408	ACCESSION:CF332408
c1259	19.6	0.7	42	1	CF330901	ACCESSION:CF330901
1260	19.6	0.7	42	1	BF343329	ACCESSION:BF343329
1261	19.6	0.7	42	1	BG292448	ACCESSION:BG292448
c1262	19.6	0.7	42	1	CF318540	ACCESSION:CF318540
c1263	19.6	0.7	43	1	BX554654	ACCESSION:BX554654
c1264	19.6	0.7	43	1	CF302691	ACCESSION:CF302691
c1265	19.6	0.7	43	1	AL587884	ACCESSION:AL587884
1266	19.6	0.7	43	1	BG028362	ACCESSION:BG028362
c1267	19.6	0.7	43	1	CF302744	ACCESSION:CF302744
1268	19.6	0.7	43	1	CF334344	ACCESSION:CF334344
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1270	19.6	0.7	43	1	BI908698	ACCESSION:BI908698
c1271	19.6	0.7	44	1	CF298596	ACCESSION:CF298596
1272	19.6	0.7	44	1	CF316388	ACCESSION:CF316388
1273	19.6	0.7	44	1	BG117508	ACCESSION:BG117508
c1274	19.6	0.7	44	1	CF310325	ACCESSION:CF310325

983	20	0.7	30	1	BX566679
984	20	0.7	30	1	AL953605
c 985	20	0.7	30	1	TA226G05P
c 986	20	0.7	32	1	AL587570
c 987	20	0.7	36	1	BI094774
c 988	20	0.7	44	1	CF305383
989	20	0.7	44	1	BQ587867
c 990	20	0.7	44	1	CF313794
c 991	20	0.7	44	1	CF318325
c 992	20	0.7	44	1	CF321724
c 993	20	0.7	44	1	CF330416
c 994	20	0.7	44	1	CF331035
c 995	20	0.7	44	1	CF331425
c 996	20	0.7	44	1	CF332339
c 997	20	0.7	44	1	CF337983
c 998	20	0.7	46	1	BQ590334
c 999	20	0.7	46	1	BX560004
c1000	20	0.7	47	1	CF301565
1001	19.8	0.7	23	1	AZ801003
c1002	19.8	0.7	23	1	CF279593
1003	19.8	0.7	23	1	CF313297
1004	19.8	0.7	23	1	AZ486853
1005	19.8	0.7	23	1	AZ645254
1006	19.8	0.7	24	1	AZ607198
c1007	19.8	0.7	25	1	AL048782
1008	19.8	0.7	25	1	CC883604
1009	19.8	0.7	26	1	AZ437459
1010	19.8	0.7	31	1	N25903
c1011	19.8	0.7	33	1	CF300359
c1012	19.6	0.7	26	1	AW327613
c1013	19.6	0.7	26	1	CF278359
1014	19.6	0.7	26	1	CF282426
1015	19.6	0.7	26	1	CF297087
c1016	19.6	0.7	26	1	CF299701
c1017	19.6	0.7	26	1	CF302874
c1018	19.6	0.7	26	1	CF311369
c1019	19.6	0.7	26	1	CF331439
1020	19.6	0.7	26	1	AZ359871
1021	19.6	0.7	26	1	AZ376664
1022	19.6	0.7	26	1	AZ389765
1023	19.6	0.7	26	1	AZ414673
1024	19.6	0.7	26	1	AZ593300
c1025	19.6	0.7	26	1	AZ612722
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1028	19.6	0.7	26	1	AZ652515
c1029	19.6	0.7	26	1	AZ800453
c1030	19.6	0.7	26	1	AZ963974
1031	19.6	0.7	26	1	TA324D07P
c1032	19.6	0.7	26	1	AU265714
c1033	19.6	0.7	26	1	AZ316353
1034	19.6	0.7	26	1	AZ635695
1035	19.6	0.7	27	1	AW327923
c1036	19.6	0.7	27	1	CF291968
c1037	19.6	0.7	27	1	CF329725
c1038	19.6	0.7	27	1	CF330557
c1039	19.6	0.7	27	1	CF335229
c1040	19.6	0.7	27	1	AZ344642
c1041	19.6	0.7	27	1	AZ401672
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c1043	19.6	0.7	27	1	AZ511894
c1044	19.6	0.7	27	1	AZ580921
c1045	19.6	0.7	27	1	AZ616094
c1046	19.6	0.7	27	1	AZ623186
c1047	19.6	0.7	27	1	AZ627847
1048	19.6	0.7	27	1	AZ809295
1049	19.6	0.7	27	1	TA355B06P
c1050	19.6	0.7	27	1	N52529
1051	19.6	0.7	27	1	CF298133
1052	19.6	0.7	27	1	CF300765
1053	19.6	0.7	28	1	AL048439
c1054	19.6	0.7	28	1	CF282351
c1055	19.6	0.7	28	1	CF321885

ACCESSION:BX566679
ACCESSION:AL953605
ACCESSION:AL480085
ACCESSION:AL587570
ACCESSION:BI094774
ACCESSION:CF305383
ACCESSION:BQ587867
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ACCESSION:CF298133
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c1057	19.6	0.7	28	1	CF330748
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c1059	19.6	0.7	28	1	AZ399637
1060	19.6	0.7	28	1	AZ401766
c1061	19.6	0.7	28	1	AZ471744
1062	19.6	0.7	28	1	AZ493138
c1063	19.6	0.7	28	1	AZ653365
c1064	19.6	0.7	28	1	AZ785035
c1065	19.6	0.7	28	1	AZ824519
1066	19.6	0.7	28	1	AZ833425
c1067	19.6	0.7	28	1	AZ866569
1068	19.6	0.7	28	1	TA291A01Q
c1069	19.6	0.7	28	1	TA379D11P
c1070	19.6	0.7	28	1	T52836
1071	19.6	0.7	28	1	BX554747
1072	19.6	0.7	28	1	BX555569
1073	19.6	0.7	28	1	CF277114
c1074	19.6	0.7	29	1	CF279536
1075	19.6	0.7	29	1	CF299920
1076	19.6	0.7	29	1	CF312601
1077	19.6	0.7	29	1	AZ389566
c1078	19.6	0.7	29	1	AZ414283
c1079	19.6	0.7	29	1	AZ451930
c1080	19.6	0.7	29	1	AZ468402
c1081	19.6	0.7	29	1	AZ486793
c1082	19.6	0.7	29	1	AZ661709
1083	19.6	0.7	29	1	AZ784208
1084	19.6	0.7	29	1	AZ806470
1085	19.6	0.7	29	1	AZ812242
1086	19.6	0.7	29	1	AZ868731
c1087	19.6	0.7	29	1	TA334G09Q
c1088	19.6	0.7	29	1	BQ590537
1089	19.6	0.7	29	1	AZ819924
1090	19.6	0.7	29	1	AZ492630
1091	19.6	0.7	30	1	BG666435
c1092	19.6	0.7	30	1	CF280699
1093	19.6	0.7	30	1	CF292086
c1094	19.6	0.7	30	1	CF299555
c1095	19.6	0.7	30	1	CF312417
c1096	19.6	0.7	30	1	CF322226
1097	19.6	0.7	30	1	CF327835
c1098	19.6	0.7	30	1	CF336555
c1099	19.6	0.7	30	1	AZ357603
1100	19.6	0.7	30	1	AZ455741
c1101	19.6	0.7	30	1	AZ481739
c1102	19.6	0.7	30	1	AZ582114
1103	19.6	0.7	30	1	BG865511
c1104	19.6	0.7	30	1	AZ458127
1105	19.6	0.7	30	1	AZ962183
c1106	19.6	0.7	31	1	BX569502
1107	19.6	0.7	31	1	CF278807
c1108	19.6	0.7	31	1	CF300345
c1109	19.6	0.7	31	1	AZ333315
1110	19.6	0.7	31	1	AZ375973
1111	19.6	0.7	31	1	AZ510092
1112	19.6	0.7	31	1	AZ597046
c1113	19.6	0.7	31	1	AZ623538
1114	19.6	0.7	31	1	AZ627692
1115	19.6	0.7	31	1	AZ778697
1116	19.6	0.7	31	1	AZ821215
1117	19.6	0.7	31	1	AZ826618
1118	19.6	0.7	31	1	BG292912
1119	19.6	0.7	31	1	CF297930
1120	19.6	0.7	32	1	AW327277
c1121	19.6	0.7	32	1	CF291773
c1122	19.6	0.7	32	1	CF299386
1123	19.6	0.7	32	1	CF309233
c1124	19.6	0.7	32	1	CF309345
c1125	19.6	0.7	32	1	CF313717
c1126	19.6	0.7	32	1	CF321046
c1127	19.6	0.7	32	1	CF328471
c1128	19.6	0.7	32	1	CF331270

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c	839	20.2	0.7	31	1	TA244G08P
	840	20.2	0.7	31	1	AV947772
	841	20.2	0.7	31	1	AV959965
c	842	20.2	0.7	33	1	BU431798
c	843	20.2	0.7	34	1	BU431799
c	844	20.2	0.7	34	1	BQ587432
c	845	20.2	0.7	34	1	CF328492
c	846	20.2	0.7	38	1	CF315043
c	847	20.2	0.7	39	1	CF327755
c	848	20.2	0.7	42	1	CF336692
c	849	20.2	0.7	49	1	AI350847
	850	20	0.7	20	1	AW334823
c	851	20	0.7	20	1	CF280913
c	852	20	0.7	20	1	CF282035
c	853	20	0.7	20	1	CF282414
	854	20	0.7	20	1	CF299822
	855	20	0.7	20	1	CF301720
	856	20	0.7	20	1	CF302027
c	857	20	0.7	20	1	CF310604
c	858	20	0.7	20	1	CF313067
	859	20	0.7	20	1	CF313569
	860	20	0.7	20	1	CF319133
	861	20	0.7	20	1	CF321721
c	862	20	0.7	20	1	CF328565
	863	20	0.7	20	1	CF333173
	864	20	0.7	20	1	CF334170
	865	20	0.7	20	1	CF336525
	866	20	0.7	20	1	CF337494
	867	20	0.7	20	1	T50579
	868	20	0.7	20	1	AZ307671
	869	20	0.7	20	1	AZ333980
c	870	20	0.7	20	1	AZ341530
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c	872	20	0.7	20	1	AZ351273
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c	876	20	0.7	20	1	AZ396481
c	877	20	0.7	20	1	AZ442328
	878	20	0.7	20	1	AZ463331
	879	20	0.7	20	1	AZ477734
	880	20	0.7	20	1	AZ479464
	881	20	0.7	20	1	AZ486784
	882	20	0.7	20	1	AZ498625
c	883	20	0.7	20	1	AZ514729
c	884	20	0.7	20	1	AZ581208
c	885	20	0.7	20	1	AZ588011
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	887	20	0.7	20	1	AZ623155
	888	20	0.7	20	1	AZ623214
	889	20	0.7	20	1	AZ638704
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	891	20	0.7	20	1	AZ645829
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c	893	20	0.7	20	1	AZ760838
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	895	20	0.7	20	1	AZ765211
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	897	20	0.7	20	1	AZ779425
c	898	20	0.7	20	1	AZ784041
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	900	20	0.7	20	1	AZ798529
c	901	20	0.7	20	1	AZ805163
c	902	20	0.7	20	1	AZ806521
c	903	20	0.7	20	1	AZ806585
c	904	20	0.7	20	1	AZ809306
c	905	20	0.7	20	1	AZ810986
c	906	20	0.7	20	1	AZ813908
c	907	20	0.7	20	1	AZ817323
c	908	20	0.7	20	1	AZ817414
c	909	20	0.7	20	1	AZ817467

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	911	20	0.7	20	1	AZ818489
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c	913	20	0.7	20	1	AZ837491
c	914	20	0.7	20	1	AZ841342
	915	20	0.7	20	1	AZ841558
c	916	20	0.7	20	1	AZ849506
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c	919	20	0.7	20	1	AZ936914
	920	20	0.7	20	1	AZ949180
	921	20	0.7	20	1	AZ963973
c	922	20	0.7	21	1	AL048772
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	924	20	0.7	21	1	CF276638
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c	927	20	0.7	21	1	AZ461824
c	928	20	0.7	21	1	AZ493766
	929	20	0.7	22	1	AZ374487
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c	938	20	0.7	24	1	CF326993
c	939	20	0.7	24	1	AZ309553
c	940	20	0.7	25	1	CF301712
c	941	20	0.7	25	1	AZ832800
	942	20	0.7	25	1	CF310471
	943	20	0.7	25	1	T49097
	944	20	0.7	26	1	CF639306
	945	20	0.7	26	1	CNS00BGV
	946	20	0.7	26	1	CF280688
c	947	20	0.7	26	1	AZ485624
c	948	20	0.7	27	1	N29432
c	949	20	0.7	27	1	R31539
	950	20	0.7	27	1	CF334654
c	951	20	0.7	27	1	CF334654
	952	20	0.7	27	1	T52979
c	953	20	0.7	28	1	TA327D04P
c	954	20	0.7	28	1	AA852828
	955	20	0.7	28	1	CF334115
c	956	20	0.7	28	1	AZ357605
	957	20	0.7	29	1	BX627582
	958	20	0.7	29	1	AL048741
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c	960	20	0.7	29	1	AU269375
	961	20	0.7	29	1	BX567540
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	963	20	0.7	30	1	AL048684
c	964	20	0.7	30	1	AL048684
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	967	20	0.7	30	1	AU269441
	968	20	0.7	30	1	BX548619
	969	20	0.7	30	1	BX549675
	970	20	0.7	30	1	BX551003
	971	20	0.7	30	1	BX552051
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	979	20	0.7	30	1	BX559425
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	981	20	0.7	30	1	BX565681
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	693	21	0.7	24	1	CA853764
c	694	21	0.7	24	1	CF276855
	695	21	0.7	24	1	CF301561
	696	21	0.7	24	1	CF312319
	697	21	0.7	24	1	CF320862
c	698	21	0.7	24	1	AZ328848
c	699	21	0.7	24	1	AZ363562
c	700	21	0.7	24	1	AZ386491
	701	21	0.7	24	1	AZ390642
c	702	21	0.7	24	1	AZ438069
	703	21	0.7	24	1	AZ459280
	704	21	0.7	24	1	AZ644621
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c	706	21	0.7	24	1	AZ812579
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c	708	21	0.7	24	1	AZ970038
c	709	21	0.7	24	1	AZ984490
	710	21	0.7	24	1	AZ993423
	711	21	0.7	24	1	TA169D12P
c	712	21	0.7	24	1	TA27B08Q
c	713	21	0.7	24	1	TA354C06P
c	714	21	0.7	24	1	TA371F11P
c	715	21	0.7	24	1	TA95B08P
	716	21	0.7	25	1	AL587648
	717	21	0.7	25	1	CF291048
	718	21	0.7	25	1	CF291646
c	719	21	0.7	25	1	CF299288
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	721	21	0.7	25	1	CF301712
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	723	21	0.7	25	1	CF317714
	724	21	0.7	25	1	CF319073
	725	21	0.7	25	1	CF330786
	726	21	0.7	25	1	N33150
c	727	21	0.7	25	1	AZ344725
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	737	21	0.7	25	1	AZ980407
	738	21	0.7	25	1	CG726337
	739	21	0.7	25	1	TA154D03P
	740	21	0.7	25	1	TA324E10P
	741	21	0.7	26	1	CF296851
c	742	21	0.7	26	1	TA321G11P
c	743	21	0.7	27	1	CF310745
	744	21	0.7	27	1	AZ812708
c	745	21	0.7	28	1	AZ358038
c	746	21	0.7	29	1	BX568027
	747	21	0.7	29	1	CF300706
	748	21	0.7	29	1	CF312595
	749	21	0.7	29	1	AZ827060
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	751	21	0.7	30	1	TA247F06P
	752	21	0.7	31	1	AI207866
c	753	21	0.7	31	1	AU264794
	754	21	0.7	31	1	BX554068
	755	21	0.7	31	1	BX557470
	756	21	0.7	31	1	BX558479
	757	21	0.7	31	1	BX559254
	758	21	0.7	31	1	TA244G08P
	759	21	0.7	32	1	AL588429
c	760	21	0.7	32	1	BG501238
c	761	21	0.7	32	1	BJ078010
	762	21	0.7	32	1	BX551100
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	766	21	0.7	32	1	BX564047
	767	21	0.7	36	1	AW059764
c	768	21	0.7	37	1	AL587823
c	769	21	0.7	39	1	CF291979
c	770	21	0.7	40	1	CF309581
	771	21	0.7	45	1	AZ467950
	772	20.8	0.7	24	1	AZ626101
c	773	20.8	0.7	25	1	TA388E06P
c	774	20.8	0.7	26	1	CF639306
c	775	20.8	0.7	27	1	N89936
c	776	20.8	0.7	28	1	AZ514352
	777	20.8	0.7	28	1	R37697
	778	20.8	0.7	28	1	AZ654007
c	779	20.8	0.7	30	1	CF302271
c	780	20.8	0.7	32	1	CF318239
c	781	20.8	0.7	32	1	R16114
	782	20.8	0.7	32	1	BX557478
c	783	20.8	0.7	32	1	AZ445446
	784	20.8	0.7	34	1	BX562266
	785	20.8	0.7	35	1	AV834098
c	786	20.8	0.7	36	1	T57700
c	787	20.8	0.7	37	1	CF292043
c	788	20.8	0.7	45	1	CF321018
c	789	20.8	0.7	48	1	CF329281
c	790	20.6	0.7	26	1	CNS00BGV
c	791	20.6	0.7	27	1	CF310560
c	792	20.6	0.7	27	1	AZ458228
c	793	20.6	0.7	31	1	N25903
c	794	20.6	0.7	37	1	CF329026
c	795	20.6	0.7	39	1	CF300591
	796	20.6	0.7	39	1	BJ081937
c	797	20.6	0.7	39	1	BX555173
c	798	20.6	0.7	42	1	CF292085
c	799	20.6	0.7	44	1	CF331239
c	800	20.6	0.7	44	1	CF332388
	801	20.4	0.7	22	1	CF310486
	802	20.4	0.7	22	1	CF298427
c	803	20.4	0.7	22	1	TA231E08Q
c	804	20.4	0.7	23	1	CF329694
c	805	20.4	0.7	23	1	AL048745
	806	20.4	0.7	23	1	CF333801
c	807	20.4	0.7	24	1	AZ404871
	808	20.4	0.7	24	1	AZ486788
c	809	20.4	0.7	24	1	AZ607198
c	810	20.4	0.7	25	1	CF317007
c	811	20.4	0.7	26	1	R26779
c	812	20.4	0.7	26	1	AZ358846
	813	20.4	0.7	26	1	AW333508
c	814	20.4	0.7	27	1	N51845
c	815	20.4	0.7	27	1	CF333518
	816	20.4	0.7	27	1	CF310560
	817	20.4	0.7	27	1	N34515
c	818	20.4	0.7	28	1	R37697
c	819	20.4	0.7	29	1	CF314795
c	820	20.4	0.7	29	1	CF299155
c	821	20.4	0.7	29	1	TA378G07P
c	822	20.4	0.7	29	1	T67079
	823	20.4	0.7	30	1	CF333289
c	824	20.4	0.7	31	1	AU267441
	825	20.4	0.7	31	1	AV960178
c	826	20.4	0.7	32	1	BF032851
c	827	20.4	0.7	32	1	BX556161
	828	20.4	0.7	34	1	BJ054454
	829	20.4	0.7	34	1	BX553519
c	830	20.4	0.7	36	1	BX565764
c	831	20.2	0.7	25	1	AI445764
	832	20.2	0.7	25	1	CF315032
c	833	20.2	0.7	27	1	AZ862643
c	834	20.2	0.7	28	1	CF334115
	835	20.2	0.7	29	1	CF330960
c	836	20.2	0.7	30	1	CF299716

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ACCESSION:AI445764
ACCESSION:CF315032
ACCESSION:AZ862643
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ACCESSION:CF330960
ACCESSION:CF299716

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	546	21.2	0.8	27	1	N52529
c	547	21.2	0.8	27	1	TA257B07P
c	548	21.2	0.8	28	1	AZ824574
	549	21.2	0.8	28	1	AA852828
c	550	21.2	0.8	28	1	CF299294
	551	21.2	0.8	28	1	T52836
	552	21.2	0.8	30	1	N31821
	553	21.2	0.8	31	1	AV966771
	554	21.2	0.8	34	1	AZ307192
	555	21.2	0.8	34	1	BG531309
c	556	21.2	0.8	37	1	AZ824309
	557	21.2	0.8	37	1	AL048768
c	558	21.2	0.8	38	1	AZ589726
c	559	21.2	0.8	39	1	TA116F09P
c	560	21.2	0.8	42	1	CF330825
	561	21.2	0.8	43	1	AZ374531
	562	21.2	0.8	44	1	CF316377
c	563	21.2	0.8	44	1	CF305473
c	564	21.2	0.8	44	1	CF334384
	565	21.2	0.8	45	1	BF582680
c	566	21.2	0.8	48	1	AV950753
c	567	21	0.7	21	1	AL048777
c	568	21	0.7	21	1	CF282216
	569	21	0.7	21	1	CF292703
	570	21	0.7	21	1	CF295642
c	571	21	0.7	21	1	CF297615
	572	21	0.7	21	1	CF298322
	573	21	0.7	21	1	CF300809
c	574	21	0.7	21	1	CF312715
	575	21	0.7	21	1	CF316073
	576	21	0.7	21	1	CF318152
	577	21	0.7	21	1	CF326952
c	578	21	0.7	21	1	CF327391
	579	21	0.7	21	1	CF332956
c	580	21	0.7	21	1	CF338057
	581	21	0.7	21	1	CF338522
c	582	21	0.7	21	1	AZ348593
c	583	21	0.7	21	1	AZ350611
c	584	21	0.7	21	1	AZ386711
c	585	21	0.7	21	1	AZ386794
c	586	21	0.7	21	1	AZ389287
c	587	21	0.7	21	1	AZ389687
	588	21	0.7	21	1	AZ406936
	589	21	0.7	21	1	AZ412739
	590	21	0.7	21	1	AZ412931
c	591	21	0.7	21	1	AZ415029
	592	21	0.7	21	1	AZ465890
c	593	21	0.7	21	1	AZ611116
c	594	21	0.7	21	1	AZ611423
	595	21	0.7	21	1	AZ615628
	596	21	0.7	21	1	AZ627843
	597	21	0.7	21	1	AZ627845
c	598	21	0.7	21	1	AZ657727
c	599	21	0.7	21	1	AZ766552
c	600	21	0.7	21	1	AZ769976
	601	21	0.7	21	1	AZ793486
c	602	21	0.7	21	1	AZ799327
c	603	21	0.7	21	1	AZ810054
c	604	21	0.7	21	1	AZ815424
c	605	21	0.7	21	1	AZ819181
c	606	21	0.7	21	1	AZ832198
c	607	21	0.7	21	1	AZ843603
c	608	21	0.7	21	1	AZ960063
c	609	21	0.7	21	1	BH000837
	610	21	0.7	22	1	AW332181
	611	21	0.7	22	1	AW332399
	612	21	0.7	22	1	CF282024
	613	21	0.7	22	1	CF299342
	614	21	0.7	22	1	CF300133
	615	21	0.7	22	1	CF310366
c	616	21	0.7	22	1	CF310486
	617	21	0.7	22	1	CF311269

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c	618	21	0.7	22	1	CF311713
c	619	21	0.7	22	1	CF312498
	620	21	0.7	22	1	CF330679
	621	21	0.7	22	1	CF333430
	622	21	0.7	22	1	CF334781
	623	21	0.7	22	1	CF336250
c	624	21	0.7	22	1	CF337580
	625	21	0.7	22	1	CF338524
c	626	21	0.7	22	1	AZ304806
	627	21	0.7	22	1	AZ310066
c	628	21	0.7	22	1	AZ351527
c	629	21	0.7	22	1	AZ357630
c	630	21	0.7	22	1	AZ374487
c	631	21	0.7	22	1	AZ388103
	632	21	0.7	22	1	AZ401908
	633	21	0.7	22	1	AZ424307
	634	21	0.7	22	1	AZ428818
	635	21	0.7	22	1	AZ459654
	636	21	0.7	22	1	AZ463503
	637	21	0.7	22	1	AZ463652
c	638	21	0.7	22	1	AZ505769
c	639	21	0.7	22	1	AZ582403
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c	641	21	0.7	22	1	AZ654691
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	645	21	0.7	22	1	AZ787098
	646	21	0.7	22	1	AZ787606
	647	21	0.7	22	1	AZ792704
	648	21	0.7	22	1	AZ810674
	649	21	0.7	22	1	AZ820439
c	650	21	0.7	22	1	AZ841661
	651	21	0.7	22	1	AZ843514
c	652	21	0.7	22	1	AZ946102
c	653	21	0.7	22	1	BH000233
c	654	21	0.7	22	1	TA131B09P
c	655	21	0.7	22	1	TA329F10P
	656	21	0.7	22	1	TA35C12Q
c	657	21	0.7	22	1	TA380A07P
	658	21	0.7	23	1	CF279238
	659	21	0.7	23	1	CF297943
	660	21	0.7	23	1	CF310501
	661	21	0.7	23	1	CF319212
c	662	21	0.7	23	1	CF322953
c	663	21	0.7	23	1	CF329042
	664	21	0.7	23	1	CF334077
c	665	21	0.7	23	1	CF334657
	666	21	0.7	23	1	AZ309219
c	667	21	0.7	23	1	AZ309851
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c	670	21	0.7	23	1	AZ351354
c	671	21	0.7	23	1	AZ357645
	672	21	0.7	23	1	AZ419236
c	673	21	0.7	23	1	AZ425710
c	674	21	0.7	23	1	AZ461220
	675	21	0.7	23	1	AZ465327
	676	21	0.7	23	1	AZ481702
	677	21	0.7	23	1	AZ588254
	678	21	0.7	23	1	AZ593540
c	679	21	0.7	23	1	AZ610785
	680	21	0.7	23	1	AZ647637
c	681	21	0.7	23	1	AZ654903
c	682	21	0.7	23	1	AZ778751
c	683	21	0.7	23	1	AZ787184
	684	21	0.7	23	1	AZ792751
c	685	21	0.7	23	1	AZ859570
c	686	21	0.7	23	1	AZ939608
	687	21	0.7	23	1	BH000534
c	688	21	0.7	23	1	TA151C02Q
	689	21	0.7	23	1	TA274B03P
c	690	21	0.7	23	1	TA353A10P

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c	399	22.6	0.8	30	1	DR31A15T
	400	22.6	0.8	32	1	R16114
c	401	22.6	0.8	34	1	BU431802
c	402	22.6	0.8	34	1	C21199
	403	22.6	0.8	34	1	CF319950
	404	22.6	0.8	34	1	CF328492
c	405	22.6	0.8	37	1	CF332027
	406	22.6	0.8	38	1	BG778513
c	407	22.6	0.8	40	1	CF332441
	408	22.6	0.8	50	1	AA966391
c	409	22.4	0.8	25	1	AZ330737
	410	22.4	0.8	28	1	AZ809971
c	411	22.4	0.8	32	1	AL036826
	412	22.4	0.8	32	1	CF298526
	413	22.4	0.8	32	1	CF334956
c	414	22.4	0.8	33	1	AL048719
c	415	22.4	0.8	33	1	AL048733
	416	22.4	0.8	33	1	AV859963
c	417	22.4	0.8	33	1	BX554821
	418	22.4	0.8	33	1	CF335736
c	419	22.4	0.8	33	1	AZ504854
c	420	22.4	0.8	34	1	BX553519
c	421	22.4	0.8	34	1	BX562266
c	422	22.2	0.8	27	1	AW327923
	423	22.2	0.8	27	1	CF291968
	424	22.2	0.8	27	1	CF299084
	425	22.2	0.8	27	1	CF329725
	426	22.2	0.8	27	1	CF330557
	427	22.2	0.8	27	1	CF335229
	428	22.2	0.8	27	1	N89936
	429	22.2	0.8	27	1	AZ344642
	430	22.2	0.8	27	1	AZ401672
c	431	22.2	0.8	27	1	AZ434285
	432	22.2	0.8	27	1	AZ486791
	433	22.2	0.8	27	1	AZ511894
	434	22.2	0.8	27	1	AZ580921
	435	22.2	0.8	27	1	AZ616094
	436	22.2	0.8	27	1	AZ623186
	437	22.2	0.8	27	1	AZ627847
c	438	22.2	0.8	27	1	AZ809295
c	439	22.2	0.8	27	1	TA355B06P
	440	22.2	0.8	29	1	CF328988
	441	22.2	0.8	30	1	CF299716
c	442	22.2	0.8	31	1	AZ579477
c	443	22.2	0.8	33	1	AV743346
	444	22.2	0.8	34	1	BQ594010
c	445	22.2	0.8	44	1	CF302212
c	446	22	0.8	22	1	AZ823875
	447	22	0.8	23	1	CF332379
c	448	22	0.8	23	1	AZ801003
c	449	22	0.8	25	1	CF638767
	450	22	0.8	26	1	BQ583199
	451	22	0.8	26	1	AZ358846
	452	22	0.8	27	1	CF333518
c	453	22	0.8	27	1	R59382
c	454	22	0.8	30	1	AL048796
	455	22	0.8	30	1	CF331804
c	456	22	0.8	32	1	CF332296
	457	22	0.8	32	1	BX554291
	458	22	0.8	32	1	BX555135
	459	22	0.8	32	1	BX556161
c	460	22	0.8	33	1	AU013658
	461	22	0.8	33	1	AU269499
	462	22	0.8	33	1	BX565664
	463	22	0.8	37	1	BJ054011
	464	22	0.8	39	1	BJ049570
	465	22	0.8	40	1	BJ082856
c	466	22	0.8	45	1	CF331757
c	467	22	0.8	46	1	CF321820
c	468	22	0.8	47	1	CF317896
c	469	22	0.8	47	1	AW250836
c	470	22	0.8	47	1	CF321993
c	471	22	0.8	48	1	BQ590523

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ACCESSION:CF331757
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ACCESSION:CF317896
ACCESSION:AW250836
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c	472	21.8	0.8	25	1	AZ404078
	473	21.8	0.8	27	1	N29432
	474	21.8	0.8	28	1	CF307749
	475	21.8	0.8	28	1	AZ481286
	476	21.8	0.8	33	1	CF300359
c	477	21.8	0.8	33	1	AZ346849
	478	21.8	0.8	34	1	TA318H06P
	479	21.8	0.8	49	1	AA116935
	480	21.6	0.8	28	1	CF337400
	481	21.6	0.8	28	1	AW332443
	482	21.6	0.8	29	1	AU284377
	483	21.6	0.8	29	1	BQ583967
c	484	21.6	0.8	29	1	AZ819924
c	485	21.6	0.8	32	1	R59306
c	486	21.6	0.8	32	1	AZ326012
c	487	21.6	0.8	33	1	BI152241
	488	21.6	0.8	34	1	AZ345610
c	489	21.6	0.8	34	1	AW334249
c	490	21.6	0.8	34	1	AV674152
	491	21.6	0.8	35	1	BE894837
c	492	21.6	0.8	37	1	CF328866
c	493	21.6	0.8	39	1	AW248768
c	494	21.6	0.8	45	1	AW249952
c	495	21.6	0.8	46	1	CF314394
c	496	21.6	0.8	49	1	AI270095
c	497	21.4	0.8	23	1	AL048776
c	498	21.4	0.8	24	1	AL048765
c	499	21.4	0.8	25	1	N59260
	500	21.4	0.8	25	1	AZ330737
	501	21.4	0.8	25	1	CF317378
	502	21.4	0.8	25	1	N27663
c	503	21.4	0.8	26	1	CF299646
	504	21.4	0.8	27	1	R59382
	505	21.4	0.8	27	1	N34459
	506	21.4	0.8	27	1	R31539
	507	21.4	0.8	27	1	AZ382581
	508	21.4	0.8	28	1	AL587582
	509	21.4	0.8	28	1	TA327D04P
c	510	21.4	0.8	29	1	AL048694
	511	21.4	0.8	29	1	AU267990
c	512	21.4	0.8	29	1	BX627582
c	513	21.4	0.8	29	1	TA239G06Q
c	514	21.4	0.8	30	1	AL048729
c	515	21.4	0.8	31	1	CF297930
	516	21.4	0.8	31	1	CF319504
c	517	21.4	0.8	32	1	BI693086
	518	21.4	0.8	32	1	BX556940
	519	21.4	0.8	32	1	AZ451251
	520	21.4	0.8	33	1	BX554821
c	521	21.4	0.8	38	1	CF302184
c	522	21.4	0.8	38	1	CF321807
	523	21.2	0.8	26	1	AL587774
	524	21.2	0.8	26	1	AW327613
	525	21.2	0.8	26	1	CF278359
c	526	21.2	0.8	26	1	CF282426
c	527	21.2	0.8	26	1	CF297087
	528	21.2	0.8	26	1	CF299701
	529	21.2	0.8	26	1	CF302874
	530	21.2	0.8	26	1	CF311369
	531	21.2	0.8	26	1	CF331439
c	532	21.2	0.8	26	1	AZ355083
c	533	21.2	0.8	26	1	AZ359871
c	534	21.2	0.8	26	1	AZ376664
c	535	21.2	0.8	26	1	AZ389765
c	536	21.2	0.8	26	1	AZ414673
c	537	21.2	0.8	26	1	AZ593300
	538	21.2	0.8	26	1	AZ612722
	539	21.2	0.8	26	1	AZ623156
	540	21.2	0.8	26	1	AZ624441
	541	21.2	0.8	26	1	AZ627846
c	542	21.2	0.8	26	1	AZ652515
	543	21.2	0.8	26	1	AZ800453
	544	21.2	0.8	26	1	AZ963974

ACCESSION:AZ404078
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ACCESSION:CF307749
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ACCESSION:AZ612722
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ACCESSION:AZ624441
ACCESSION:AZ627846
ACCESSION:AZ652515
ACCESSION:AZ800453
ACCESSION:AZ963974

	253	26	0.9	40	1	AA852205
c	254	25.8	0.9	30	1	AU267300
	255	25.8	0.9	32	1	AZ627842
	256	25.8	0.9	35	1	BJ036312
	257	25.8	0.9	38	1	CF321807
c	258	25.6	0.9	32	1	CF302459
	259	25.6	0.9	32	1	AZ314322
	260	25.6	0.9	32	1	AZ579652
	261	25.6	0.9	33	1	CF334899
	262	25.6	0.9	34	1	CF315464
c	263	25.6	0.9	34	1	AZ307192
c	264	25.6	0.9	34	1	DR41A4T
	265	25.6	0.9	37	1	AL587823
c	266	25.4	0.9	34	1	CF319784
	267	25.4	0.9	37	1	CF332027
	268	25.4	0.9	38	1	BX556487
	269	25.4	0.9	39	1	BX555173
c	270	25.4	0.9	39	1	CF642215
	271	25.4	0.9	39	1	AZ346794
c	272	25.2	0.9	30	1	BG666435
	273	25.2	0.9	30	1	CF280699
c	274	25.2	0.9	30	1	CF292086
	275	25.2	0.9	30	1	CF299555
	276	25.2	0.9	30	1	CF312417
	277	25.2	0.9	30	1	CF322226
c	278	25.2	0.9	30	1	CF327835
	279	25.2	0.9	30	1	CF336555
	280	25.2	0.9	30	1	AZ357603
c	281	25.2	0.9	30	1	AZ455741
	282	25.2	0.9	30	1	AZ481739
	283	25.2	0.9	30	1	AZ582114
c	284	25.2	0.9	31	1	BG292912
	285	25.2	0.9	32	1	R59306
	286	25.2	0.9	32	1	DR1F7S
	287	25.2	0.9	36	1	BI094774
c	288	25	0.9	35	1	AZ351309
	289	25	0.9	38	1	CF315043
	290	24.8	0.9	31	1	AW245279
	291	24.6	0.9	31	1	AW249485
	292	24.6	0.9	31	1	BQ591372
	293	24.6	0.9	31	1	AZ486763
	294	24.6	0.9	32	1	AW250841
	295	24.6	0.9	32	1	CF332296
	296	24.6	0.9	37	1	CF301193
c	297	24.6	0.9	48	1	CF330635
	298	24.4	0.9	26	1	BM658913
	299	24.4	0.9	32	1	AL587570
	300	24.4	0.9	37	1	BX556312
	301	24.4	0.9	37	1	BX562242
c	302	24.4	0.9	40	1	AA852205
	303	24.2	0.9	29	1	CF279536
c	304	24.2	0.9	29	1	CF299920
c	305	24.2	0.9	29	1	CF312601
c	306	24.2	0.9	29	1	AZ389566
	307	24.2	0.9	29	1	AZ414283
	308	24.2	0.9	29	1	AZ451930
	309	24.2	0.9	29	1	AZ468402
	310	24.2	0.9	29	1	AZ486793
	311	24.2	0.9	29	1	AZ661709
c	312	24.2	0.9	29	1	AZ784208
c	313	24.2	0.9	29	1	AZ806470
c	314	24.2	0.9	29	1	AZ812242
c	315	24.2	0.9	29	1	AZ825156
c	316	24.2	0.9	29	1	AZ868731
	317	24.2	0.9	29	1	TA334G09Q
c	318	24.2	0.9	30	1	BG865511
c	319	24.2	0.9	30	1	AZ443322
c	320	24.2	0.9	32	1	AZ397471
	321	24.2	0.9	34	1	BQ587432
c	322	24.2	0.9	37	1	BG430173
c	323	24.2	0.9	37	1	TA369C05P
	324	24	0.9	29	1	CF314795
	325	24	0.9	32	1	CF318239

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ACCESSION:AU267300
ACCESSION:AZ627842
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ACCESSION:AZ314322
ACCESSION:AZ579652
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	326	24	0.9	33	1	R38731
c	327	24	0.9	34	1	AU265130
c	328	24	0.9	35	1	BF239380
	329	24	0.9	36	1	BX565764
	330	24	0.9	40	1	CF332442
c	331	23.8	0.8	27	1	CF311022
	332	23.8	0.8	27	1	AZ941721
	333	23.8	0.8	27	1	AZ970621
	334	23.8	0.8	28	1	AZ824574
	335	23.6	0.8	30	1	AZ458127
c	336	23.6	0.8	30	1	AZ962183
c	337	23.6	0.8	31	1	AU268044
	338	23.6	0.8	32	1	CA853459
	339	23.6	0.8	32	1	AL941390
	340	23.6	0.8	33	1	AU266959
	341	23.6	0.8	33	1	AZ759642
c	342	23.6	0.8	34	1	BG531309
c	343	23.6	0.8	34	1	BG612023
	344	23.4	0.8	25	1	N59260
	345	23.4	0.8	26	1	CF337311
	346	23.4	0.8	28	1	AU257468
	347	23.4	0.8	32	1	BX555194
	348	23.4	0.8	33	1	AZ310096
c	349	23.4	0.8	36	1	AW059764
c	350	23.4	0.8	39	1	CF328529
c	351	23.2	0.8	28	1	AL048439
	352	23.2	0.8	28	1	CF282351
	353	23.2	0.8	28	1	CF321885
	354	23.2	0.8	28	1	CF322082
	355	23.2	0.8	28	1	CF330748
c	356	23.2	0.8	28	1	CF330938
c	357	23.2	0.8	28	1	CF337400
	358	23.2	0.8	28	1	AZ399637
c	359	23.2	0.8	28	1	AZ401766
	360	23.2	0.8	28	1	AZ471744
c	361	23.2	0.8	28	1	AZ493138
	362	23.2	0.8	28	1	AZ653365
	363	23.2	0.8	28	1	AZ785035
	364	23.2	0.8	28	1	AZ824519
c	365	23.2	0.8	28	1	AZ833425
	366	23.2	0.8	28	1	AZ836072
	367	23.2	0.8	28	1	AZ866569
c	368	23.2	0.8	28	1	TA291A01Q
	369	23.2	0.8	28	1	TA29A09P
	370	23.2	0.8	28	1	TA379D11P
	371	23.2	0.8	29	1	BQ590537
c	372	23.2	0.8	29	1	CF328476
c	373	23.2	0.8	33	1	AZ759642
c	374	23.2	0.8	35	1	AZ475373
c	375	23.2	0.8	37	1	CF293279
c	376	23.2	0.8	45	1	CF332233
	377	23	0.8	23	1	CF329694
	378	23	0.8	25	1	CF317007
	379	23	0.8	26	1	CF299646
	380	23	0.8	26	1	R26779
	381	23	0.8	29	1	CF299155
	382	23	0.8	29	1	TA378G07P
	383	23	0.8	32	1	BF032851
	384	23	0.8	34	1	AL047464
c	385	23	0.8	34	1	BJ054454
c	386	23	0.8	34	1	TA318H06P
c	387	23	0.8	35	1	AV834098
	388	23	0.8	35	1	CF310898
c	389	23	0.8	35	1	CF310898
c	390	23	0.8	46	1	CF298283
	391	22.8	0.8	27	1	N51845
	392	22.8	0.8	27	1	AZ862643
	393	22.8	0.8	28	1	T56352
	394	22.8	0.8	28	1	AZ514352
	395	22.8	0.8	33	1	AU252805
c	396	22.8	0.8	37	1	CF301193
c	397	22.8	0.8	40	1	CF331029
c	398	22.8	0.8	50	1	CF332589

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107	28.4	1.0	40	1	CF336399
c 108	28.4	1.0	40	1	AZ831983
109	28.4	1.0	41	1	CF291539
110	28.4	1.0	41	1	CF305364
111	28.4	1.0	41	1	CF318677
112	28.4	1.0	41	1	CF320203
113	28.4	1.0	41	1	CF330464
114	28.4	1.0	41	1	CF334638
c 115	28.4	1.0	41	1	AZ775066
c 116	28.4	1.0	41	1	AZ827008
117	28.2	1.0	33	1	AL587609
118	28.2	1.0	34	1	AL587876
c 119	28.2	1.0	34	1	AZ345610
120	28.2	1.0	36	1	AL587891
121	28.2	1.0	36	1	AZ945733
122	28.2	1.0	37	1	CF329026
123	28.2	1.0	39	1	CF300591
124	28.2	1.0	42	1	CF318540
c 125	28	1.0	36	1	BE876160
126	28	1.0	36	1	CF317028
127	28	1.0	36	1	CF331983
128	28	1.0	36	1	AZ470916
129	28	1.0	36	1	AZ628484
130	28	1.0	36	1	AZ793484
131	28	1.0	36	1	AZ949866
132	28	1.0	36	1	AZ957867
c 133	28	1.0	37	1	BG033620
134	28	1.0	37	1	CF291818
135	28	1.0	37	1	CF293279
c 136	28	1.0	37	1	CF300002
c 137	28	1.0	37	1	CF300328
138	28	1.0	37	1	CF301864
139	28	1.0	37	1	CF307971
c 140	28	1.0	37	1	CF316114
c 141	28	1.0	37	1	CF321294
142	28	1.0	37	1	CF326975
143	28	1.0	37	1	CF333624
144	28	1.0	37	1	CF336769
c 145	28	1.0	37	1	AZ321759
146	28	1.0	37	1	AZ463801
c 147	28	1.0	37	1	AZ831214
148	28	1.0	37	1	DR102P24T
c 149	28	1.0	37	1	DR102P2T
c 150	28	1.0	38	1	BF526154
c 151	28	1.0	39	1	BG287495
152	28	1.0	39	1	CNS004NT
c 153	28	1.0	40	1	BG166502
c 154	28	1.0	40	1	BJ082856
c 155	28	1.0	40	1	DR85H22T
c 156	28	1.0	41	1	CF328487
157	28	1.0	42	1	CF330825
158	27.8	1.0	35	1	T50295
159	27.6	1.0	34	1	AW334249
c 160	27.6	1.0	37	1	CF301560
161	27.6	1.0	38	1	CF302184
162	27.6	1.0	40	1	CF331029
163	27.4	1.0	37	1	CF299167
c 164	27.2	1.0	32	1	AW327277
165	27.2	1.0	32	1	CF291773
166	27.2	1.0	32	1	CF299386
c 167	27.2	1.0	32	1	CF309233
168	27.2	1.0	32	1	CF309345
169	27.2	1.0	32	1	CF313717
170	27.2	1.0	32	1	CF321046
171	27.2	1.0	32	1	CF328471
172	27.2	1.0	32	1	CF331270
173	27.2	1.0	32	1	AZ459536
c 174	27.2	1.0	32	1	AZ470832
175	27.2	1.0	32	1	AZ611890
c 176	27.2	1.0	32	1	AZ778018
c 177	27.2	1.0	32	1	DR85L21T
178	27.2	1.0	33	1	BU431798
179	27.2	1.0	33	1	CF291613

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ACCESSION:CF291539
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2004, 13:01:45 ; Search time 67 Seconds
(without alignments)
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Perfect score: 2804
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Searched: 1870 seqs, 45352 residues

Total number of hits satisfying chosen parameters: 3740

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3699 summaries

Database : rst3.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	4	33	1.2	49	1	AA116935	ACCESSION:AA116935
	5	32.8	1.2	46	1	CF321820	ACCESSION:CF321820
	6	32.4	1.2	45	1	CF332233	ACCESSION:CF332233
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	8	32.4	1.2	47	1	CF317896	ACCESSION:CF317896
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	13	31.6	1.1	48	1	CF329281	ACCESSION:CF329281
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	15	31.2	1.1	48	1	AV950753	ACCESSION:AV950753
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  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Sarkanen,S. and Ford,J.D.
  TITLE     Nucleotide sequences encoding pinoresinol/lariciresinol reductase
            proteins and their methods of use
  JOURNAL   Patent: US 6635459-A 122 21-OCT-2003;
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VERSION     AX191970.1  GI:15210119
KEYWORDS    .
SOURCE      synthetic construct
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            artificial sequences.
REFERENCE   1
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Ford,J.D. and Sarkanen,S.
  TITLE     Recombinant pinoresinol/lariciresinol reductase, recombinant
            dirigent protein, and methods of use
  JOURNAL   Patent: WO 0149833-A 122 12-JUL-2001;
            Washington State University Research Foundation (US) ; REGENTS OF
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RESULT 4611
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SOURCE      unidentified
  ORGANISM  unidentified
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REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 141 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
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            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
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  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 27 17-MAY-2001;
            Rigshospitalet (DK)
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VERSION     AX723850.1  GI:30503193
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 1537 27-MAR-2003;
            Molecular Engines Laboratories (FR)
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  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 141 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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RESULT 4607
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KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 141 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1598 CCCCTCCTGGCC 1609
              ||||||||||||
Db         13 CCCCTCCTGGCC 2


RESULT 4608
AR144877/c
LOCUS       AR144877                18 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 122 from patent US 6210942.
ACCESSION   AR144877
VERSION     AR144877.1  GI:15106744
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Sarkanen,S. and Ford,J.D.
  TITLE     Recombinant pinoresinol/lariciresinol reductase, recombinant
            dirigent protein, and methods of use
  JOURNAL   Patent: US 6210942-A 122 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .18
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                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAA 2797
              ||||||||||||
Db         18 AAAAAAAAAAAA 7


RESULT 4609
AR410329/c
LOCUS       AR410329                18 bp    DNA     linear   PAT 18-DEC-2003
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VERSION     AX394753.1  GI:21065832
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Molecules involved in the regulation of insulin resistance syndrome
            (irs)
  JOURNAL   Patent: WO 0218568-A 4 07-MAR-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="H-T11-C PRIMER"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4601
AX394784/c
LOCUS       AX394784                  16 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 8 from Patent WO0218421.
ACCESSION   AX394784
VERSION     AX394784.1  GI:21065858
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Human and mouse e2-protein, nucleic acids coding therefor and uses
            thereof
  JOURNAL   Patent: WO 0218421-A 8 07-MAR-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="H-T11-C"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4602
BD073879/c
LOCUS       BD073879                  16 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Isolation of novel aging factor gene P23.
ACCESSION   BD073879
VERSION     BD073879.1  GI:22619482
KEYWORDS    JP 2001512698-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Suishelm,K., Hosier,S. and Kubbies,M.
  TITLE     Isolation of novel aging factor gene P23
  JOURNAL   Patent: JP 2001512698-A 4 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS   Unidentified
            PN   JP 2001512698-A/4
            PD   28-AUG-2001
            PF   05-AUG-1998 JP 2000506375
            PR   08-AUG-1997 US    08/908873
            PI   KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02,
            PC   C12P21/08,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Isolation of novel aging factor gene P23
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4603
AX146684/c
LOCUS       AX146684                  17 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 26 from Patent WO0134834.
ACCESSION   AX146684
VERSION     AX146684.1  GI:14285077
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 26 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.4%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4604
AX146685/c
LOCUS       AX146685                  17 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 27 from Patent WO0134834.
ACCESSION   AX146685
VERSION     AX146685.1  GI:14285078
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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  JOURNAL   Patent: US 6642438-A 17 04-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4596
AX127439/c
LOCUS       AX127439                  16 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 82 from Patent WO0130999.
ACCESSION   AX127439
VERSION     AX127439.1  GI:14133906
KEYWORDS    .
SOURCE      Bruguiera gymnorrhiza
  ORGANISM  Bruguiera gymnorrhiza
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Malpighiales; Rhizophoraceae; Bruguiera.
REFERENCE   1
  AUTHORS   Karube,I. and Hanagata,N.
  TITLE     Salt tolerance genes
  JOURNAL   Patent: WO 0130999-A 82 03-MAY-2001;
            EBARA CORPORATION (JP)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Bruguiera gymnorrhiza"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:39984"
                     /note="Artificially Synthesized Primer Sequence"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4597
AX146678/c
LOCUS       AX146678                  16 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 20 from Patent WO0134834.
ACCESSION   AX146678
VERSION     AX146678.1  GI:14285071
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 20 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4598
AX253410/c
LOCUS       AX253410                  16 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 22 from Patent WO0171013.
ACCESSION   AX253410
VERSION     AX253410.1  GI:16073944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Clendennen,S.K. and Kellogg,J.A.
  TITLE     Melon promoters for expression of transgenes in plants
  JOURNAL   Patent: WO 0171013-A 22 27-SEP-2001;
            Exelixis Plant Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4599
AX391466/c
LOCUS       AX391466                  16 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 2 from Patent WO0216632.
ACCESSION   AX391466
VERSION     AX391466.1  GI:19700076
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Pharmaceutical compositions comprising a modulator of adamts-1
  JOURNAL   Patent: WO 0216632-A 2 28-FEB-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4600
AX394753/c
LOCUS       AX394753                  16 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 4 from Patent WO0218568.
ACCESSION   AX394753
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REFERENCE   1  (bases 1 to 16)
  AUTHORS   Clendennen,S.K., Kellogg,J.A., Phan,C.B., Mathews,H.V. and
            Webb,N.M.
  TITLE     Banana promoter and melon promoter for expression of transgene in
  JOURNAL   Patent: JP 2002539779-A 17 26-NOV-2002;
            EXELIXIS PLANT SCIENCES INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002539779-A/17
            PD   26-NOV-2002
            PF   17-MAR-2000 JP 2000606722
            PR   19-MAR-1999 US    60/125310
            PI   STEPHANIE K CLENDENNEN,JILL A KELLOGG,CHAU B PHAN,HELENA V  PI
              MATHEWS,
            PI   NANCY M WEBB
            PC   C12N15/09,A01H1/00,C12N5/10,C12Q1/68//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC   oligonucleotide primer
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4592
BD274864/c
LOCUS       BD274864                 16 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Bioassay for Identifying Estrogen Receptor beta/alpha Selective
            Modulators.
ACCESSION   BD274864
VERSION     BD274864.1  GI:33084632
KEYWORDS    JP 2002533098-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Harris,H. and But,R.A.
  TITLE     Bioassay for Identifying Estrogen Receptor beta/alpha Selective
            Modulators
  JOURNAL   Patent: JP 2002533098-A 14 08-OCT-2002;
            WYETH HOLDINGS CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002533098-A/14
            PD   08-OCT-2002
            PF   17-DEC-1999 JP 2000589734
            PR   18-DEC-1998 US    60/112790
            PI   heather harris,ramesh a but
            CC   Description of Artificial Sequence:oligonucleotide FH   Key
                 Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4593
AR266620/c
LOCUS       AR266620                 16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 58 from patent US 6495319.
ACCESSION   AR266620
VERSION     AR266620.1  GI:29695684
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 58 17-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4594
AR266646/c
LOCUS       AR266646                 16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 84 from patent US 6495319.
ACCESSION   AR266646
VERSION     AR266646.1  GI:29695710
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 84 17-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
             ||||||||||||
Db         16 GAAAAAAAAAAA 5


RESULT 4595
AR429379/c
LOCUS       AR429379                 16 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 17 from patent US 6642438.
ACCESSION   AR429379
VERSION     AR429379.1  GI:40189572
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Clendennen,S.K., Kellogg,J.A., Phan,C.B., Mathews,H.V. and
            Webb,N.M.
  TITLE     Melon promoters for expression of transgenes in plants
```

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FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2452 AGACATGGGATCCAATT 2468
              || ||||| |||| |||
Db          2 AGCCATGGAATCCCATT 18


RESULT 4587
AR430984
LOCUS       AR430984                  22 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 58 from patent US 6649742.
ACCESSION   AR430984
VERSION     AR430984.1  GI:40192815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 6649742-A 58 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2452 AGACATGGGATCCAATT 2468
              || ||||| |||| |||
Db          2 AGCCATGGAATCCCATT 18


RESULT 4588
AX038544
LOCUS       AX038544                  23 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 301 from Patent WO0061795.
ACCESSION   AX038544
VERSION     AX038544.1  GI:11227892
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   De Canck,I.D., Rossau,R. and Rombout,A.
  TITLE     Method for the amplification of hla class i alleles
  JOURNAL   Patent: WO 0061795-A 301 19-OCT-2000;
            CANCK ILSE DE (BE) ; ROSSAU RUDI (BE) ; INNOGENETICS NV (BE) ;
            ROMBOUT ANNELIES (BE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.4%;  Score 12.2;  DB 1;  Length 23;
  Best Local Similarity   66.7%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        959 GTTCTCAGAAGAGCCAAATCG 979
              :|||||||  | :| || || |
Db          1 RTTCTCAGGATRGTCACATGG 21


RESULT 4589
AX460877/c
LOCUS       AX460877                  15 bp    DNA     linear   PAT 08-JUL-2002
DEFINITION  Sequence 8 from Patent WO0212470.
ACCESSION   AX460877
VERSION     AX460877.1  GI:21726123
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Evans,M.J., Scicchitano,M.S., Bapat,A.R., Beer,E., Bhat,R.A.,
            Ferris,E., Mastroeni,R., Zhang,J. and Karathanasis,S.K.
  TITLE     A member of the lysyl oxidase gene family
  JOURNAL   Patent: WO 0212470-A 8 14-FEB-2002;
            Wyeth (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match              0.4%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAA 2796
              ||||||||||||
Db         15 GAAAAAAAAAAA 4


RESULT 4590
I25868
LOCUS       I25868                    15 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 2 from patent US 5552535.
ACCESSION   I25868
VERSION     I25868.1  GI:1605738
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   McLean,M.J., Holland,D., Garman,A.J. and Sheppard,R.C.
  TITLE     Multiple oligonucleotide containing oligomers and the cleanable
            linkers used in their preparation
  JOURNAL   Patent: US 5552535-A 2 03-SEP-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.4%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2177
              ||||||||||||
Db          1 TTTTTTTTTTTT 12


RESULT 4591
BD268991/c
LOCUS       BD268991                  16 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Banana promoter and melon promoter for expression of transgene in
            plant.
ACCESSION   BD268991
VERSION     BD268991.1  GI:33078759
KEYWORDS    JP 2002539779-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
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VERSION     AR141474.1  GI:15100990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D. and Carroll,S.F.
  TITLE     Proteins encoding gelonin sequences
  JOURNAL   Patent: US 6146850-A 58 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2452 AGACATGGGATCCAATT 2468
              || ||||| |||| |||
Db          2 AGCCATGGAATCCCATT 18


RESULT 4583
BD243946
LOCUS       BD243946                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  TREX, a novel gene of TRAF-interacting EXT gene family and
            diagnostic and therapeutic uses thereof.
ACCESSION   BD243946
VERSION     BD243946.1  GI:33053716
KEYWORDS    JP 2002525126-A/22.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Sato,T.
  TITLE     TREX, a novel gene of TRAF-interacting EXT gene family and
            diagnostic and therapeutic uses thereof
  JOURNAL   Patent: JP 2002525126-A 22 13-AUG-2002;
            THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT     OS   Linear
            PN   JP 2002525126-A/22
            PD   13-AUG-2002
            PF   17-SEP-1999 JP 2000572406
            PR   17-SEP-1998 US    09/156191
            PI   TAKAAKI SATO
            PC
            C12N15/09,A61K31/711,A61K39/395,A61K39/395,A61K45/00,A61K48/00, PC
             A61P35/00,
            PC   A61P35/04,A61P37/02,C07K14/47,C07K16/18,C12P21/02,C12Q1/68, PC
              G01N33/15,
            PC
            G01N33/50,G01N33/566,G01N33/574//C12P21/08,(C12P21/02,C12R1:91) PC
             ,C12N15/00
            CC   TREX, a novel gene of TRAF-interacting EXT gene family and  CC
                 diagnostic and
            CC   therapeutic uses thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Linear'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        790 CTGTCAGAAGGAGCTGG 806
              ||||||| |  ||||||
Db          5 CTGTCAGTATTAGCTGG 21


RESULT 4584
I11948
LOCUS       I11948                   22 bp    DNA     linear   PAT 26-JUL-1995
DEFINITION  Sequence 60 from Patent US 5416202.
ACCESSION   I11948
VERSION     I11948.1  GI:909391
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Bernhard,S.L., Better,M.D., Carroll,S.F., Lane,J.A. and Lei,S.-P.
  TITLE     Materials comprising and methods of preparation and use for
            ribosome-inactivating proteins
  JOURNAL   Patent: US 5416202-A 60 16-MAY-1995;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2452 AGACATGGGATCCAATT 2468
              || ||||| |||| |||
Db          2 AGCCATGGAATCCCATT 18


RESULT 4585
I40519
LOCUS       I40519                   22 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 58 from patent US 5621083.
ACCESSION   I40519
VERSION     I40519.1  GI:2082811
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 5621083-A 58 15-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2452 AGACATGGGATCCAATT 2468
              || ||||| |||| |||
Db          2 AGCCATGGAATCCCATT 18


RESULT 4586
AR368003
LOCUS       AR368003                 22 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 58 from patent US 6376217.
ACCESSION   AR368003
VERSION     AR368003.1  GI:34601514
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D. and Carroll,S.F.
  TITLE     Fusion proteins and polynucleotides encoding gelonin sequences
  JOURNAL   Patent: US 6376217-A 58 23-APR-2002;
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COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/9
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| |||||  ||
Db         20 AAAAAAAAAAAAGCTTG 4


RESULT 4578
AR003766
LOCUS       AR003766                 22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 58 from patent US 5744580.
ACCESSION   AR003766
VERSION     AR003766.1  GI:3965025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 5744580-A 58 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2452 AGACATGGGATCCAATT 2468
              || ||||| |||| |||
Db          2 AGCCATGGAATCCCATT 18


RESULT 4579
AR010102
LOCUS       AR010102                 22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 58 from patent US 5756699.
ACCESSION   AR010102
VERSION     AR010102.1  GI:3968907
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 5756699-A 58 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2452 AGACATGGGATCCAATT 2468
              || ||||| |||| |||
Db          2 AGCCATGGAATCCCATT 18


RESULT 4580
AR055308
LOCUS       AR055308                 22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 58 from patent US 5837491.
ACCESSION   AR055308
VERSION     AR055308.1  GI:5980885
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Polynucleotides encoding gelonin sequences
  JOURNAL   Patent: US 5837491-A 58 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2452 AGACATGGGATCCAATT 2468
              || ||||| |||| |||
Db          2 AGCCATGGAATCCCATT 18


RESULT 4581
AR141237
LOCUS       AR141237                 22 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 58 from patent US 6146631.
ACCESSION   AR141237
VERSION     AR141237.1  GI:15100754
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 6146631-A 58 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2452 AGACATGGGATCCAATT 2468
              || ||||| |||| |||
Db          2 AGCCATGGAATCCCATT 18


RESULT 4582
AR141474
LOCUS       AR141474                 22 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 58 from patent US 6146850.
ACCESSION   AR141474
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I30198/c
LOCUS       I30198                  22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 27 from patent US 5580726.
ACCESSION   I30198
VERSION     I30198.1  GI:1820989
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 27 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| |||||  ||
Db         20 AAAAAAAAAAAAGCTTG 4


RESULT 4574
BD206200/c
LOCUS       BD206200                22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206200
VERSION     BD206200.1  GI:33015970
KEYWORDS    JP 2002515252-A/13.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 13 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/13
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                      Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| |||||  ||
Db         20 AAAAAAAAAAAAGCTTG 4


RESULT 4575
AR003283/c
LOCUS       AR003283                22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5744300.
ACCESSION   AR003283
VERSION     AR003283.1  GI:3964542
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 5 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| |||||  ||
Db         20 AAAAAAAAAAAAGCTTG 4


RESULT 4576
I30194/c
LOCUS       I30194                  22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 23 from patent US 5580726.
ACCESSION   I30194
VERSION     I30194.1  GI:1820985
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 23 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| |||||  ||
Db         20 AAAAAAAAAAAAGCTTG 4


RESULT 4577
BD206196/c
LOCUS       BD206196                22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206196
VERSION     BD206196.1  GI:33015966
KEYWORDS    JP 2002515252-A/9.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 9 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 73 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTT 2172
              ||||||||| ||  |||
Db          3 TTTTTTCTCTTTCATTT 19


RESULT 4569
AR241709
LOCUS       AR241709                  21 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 16 from patent US 6472153.
ACCESSION   AR241709
VERSION     AR241709.1  GI:27287521
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dempcy,R.O., Afonina,I.A. and Vermeulen,N.M.J.
  TITLE     Hybridization-triggered fluorescent detection of nucleic acids
  JOURNAL   Patent: US 6472153-A 16 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTT 2173
              | ||||| ||||| |||
Db          1 TCTTTCTTCTTTTCTTT 17


RESULT 4570
AX023419/c
LOCUS       AX023419                  21 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 34 from Patent WO0014217.
ACCESSION   AX023419
VERSION     AX023419.1  GI:10183819
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lipford,G.B., Heeg,K. and Wagner,H.
  TITLE     G-motif oligonucleotides and uses thereof
  JOURNAL   Patent: WO 0014217-A 34 16-MAR-2000;
            LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;
            CPG IMMUNOPHARMACEUTICALS GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic, no natural origin"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2798
              || | |||||||||| |
Db         21 ATAGGAAAAAAAAAATA 5


RESULT 4571
AX555818
LOCUS       AX555818                  21 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 414 from Patent WO02070755.
ACCESSION   AX555818
VERSION     AX555818.1  GI:25899292
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lyamichev,V.I., Kaiser,M.W. and Lyamicheva,N.
  TITLE     Fen endonucleases
  JOURNAL   Patent: WO 02070755-A 414 12-SEP-2002;
            Third Wave Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAA 2796
              ||||| ||||| ||| |
Db          1 GAATTCAAAAAGAAAGA 17


RESULT 4572
AR003287/c
LOCUS       AR003287                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 9 from patent US 5744300.
ACCESSION   AR003287
VERSION     AR003287.1  GI:3964546
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 9 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 22;
  Best Local Similarity   82.4%;  Pred. No. 5.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| |||||  ||
Db         20 AAAAAAAAAAAAGCTTG 4


RESULT 4573
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RESULT 4564
AR100323/c
LOCUS       AR100323                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 54 from patent US 6080580.
ACCESSION   AR100323
VERSION     AR100323.1  GI:12810771
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-.alpha. (TNF-.alpha.) expression
  JOURNAL   Patent: US 6080580-A 54 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1494 AGAAAATGGAGAAACAC 1510
              | || |||||||||  ||
Db         18 AAAACATGGAGAAAGAC 2


RESULT 4565
AR149978/c
LOCUS       AR149978                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 54 from patent US 6228642.
ACCESSION   AR149978
VERSION     AR149978.1  GI:15114569
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-(.alpha.) (TNF-.alpha.) expression
  JOURNAL   Patent: US 6228642-A 54 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1494 AGAAAATGGAGAAACAC 1510
              | || |||||||||  ||
Db         18 AAAACATGGAGAAAGAC 2


RESULT 4566
BD227851/c
LOCUS       BD227851                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha).
ACCESSION   BD227851
VERSION     BD227851.1  GI:33037621
KEYWORDS    JP 2002526125-A/54.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,F.C., Butler,M.M. and Jr,W.J.S.
  TITLE     Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha)
  JOURNAL   Patent: JP 2002526125-A 54 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526125-A/54
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574737
            PR   05-OCT-1998 US    09/166186,18-MAY-1999 US    09/313932 PI
            BRENDA F BAKER,FRANK C BENNETT,MADELINE M BUTLER,WILLIAM J  PI
            SHANAHAN JR
            PC   C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/
            PC   00,A61P1/16,
            PC   A61P1/18,A61P3/10,A61P17/00,A61P17/04,A61P29/00,A61P31/00, PC
             C07H21/02,
            PC   C07H21/04,C12N15/00
            CC   Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1494 AGAAAATGGAGAAACAC 1510
              | || |||||||||  ||
Db         18 AAAACATGGAGAAAGAC 2


RESULT 4567
AX148870
LOCUS       AX148870                 20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 72 from Patent WO0136625.
ACCESSION   AX148870
VERSION     AX148870.1  GI:14347394
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 72 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTT 2172
              |||||||||  ||  |||
Db          2 TTTTTTCTCTTTCATTT 18


RESULT 4568
AX148871
LOCUS       AX148871                 20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 73 from Patent WO0136625.
ACCESSION   AX148871
VERSION     AX148871.1  GI:14347395
KEYWORDS    .
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REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 5201 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1626 TACCTACCTTACTATTT 1642
              | ||| |||| ||||||
Db          2 TTCCTTCCTTCCTATTT 18


RESULT 4560
AX149223/c
LOCUS       AX149223                 20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 425 from Patent WO0136625.
ACCESSION   AX149223
VERSION     AX149223.1  GI:14347747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 425 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAA 2795
              | | ||||||| |||||
Db         17 AAAGTTGAAAATAAAAA 1


RESULT 4561
AX148869
LOCUS       AX148869                 20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 71 from Patent WO0136625.
ACCESSION   AX148869
VERSION     AX148869.1  GI:14347393
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 71 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTT 2172
              |||||||||  ||  |||
Db          1 TTTTTTCTCTTTCATTT 17


RESULT 4562
AX477137/c
LOCUS       AX477137                 20 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 228 from Patent WO0220848.
ACCESSION   AX477137
VERSION     AX477137.1  GI:22216390
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,
            Lusis,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
  TITLE     Gene and sequence variation associated with cancer
  JOURNAL   Patent: WO 0220848-A 228 14-MAR-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Primer"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        683 CAGATGGACGAGGTGCA 699
              || ||||| || |||||
Db         20 CAAATGGAAGAAGTGCA 4


RESULT 4563
AX526513/c
LOCUS       AX526513                 20 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 228 from Patent WO0220847.
ACCESSION   AX526513
VERSION     AX526513.1  GI:25171320
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,
            Lusis,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
  TITLE     Gene and sequence variation associated with lipid disorder
  JOURNAL   Patent: WO 0220847-A 228 14-MAR-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Primer"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        683 CAGATGGACGAGGTGCA 699
              || ||||| || |||||
Db         20 CAAATGGAAGAAGTGCA 4
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FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1546 GTAGGGAAGGAACAGGA 1562
              ||||||  ||  | |||||
Db         17 GTAGGGCAGAAGCAGGA 1


RESULT 4555
AR098789/c
LOCUS       AR098789                 18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 44 from patent US 6077672.
ACCESSION   AR098789
VERSION     AR098789.1  GI:12808555
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of TRADD expression
  JOURNAL   Patent: US 6077672-A 44 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        407 GAAGCGTACGCCGCCGC 423
              |||||   |||||||||
Db         17 GAAGCCGCCGCCGCCGC 1


RESULT 4556
AX131090
LOCUS       AX131090                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2308 from Patent WO0130362.
ACCESSION   AX131090
VERSION     AX131090.1  GI:14137395
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 2308 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin E ribozyme binding site"

  Query Match              0.4%;  Score 12.2;  DB 1;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 4.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        500 GCGGGGCTGCCCTCGCA 516
              ||| ||||  |||||||
Db          2 GCGTGGCTCTCCTCGCA 18


RESULT 4557
AX148872
LOCUS       AX148872                 19 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 74 from Patent WO0136625.
ACCESSION   AX148872
VERSION     AX148872.1  GI:14347396
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 74 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match              0.4%;  Score 12.2;  DB 1;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 4.6e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTT 2172
              |||||||||  ||  |||
Db          2 TTTTTTCTCTTTCATTT 18


RESULT 4558
AR137400/c
LOCUS       AR137400                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 15 from patent US 6197507.
ACCESSION   AR137400
VERSION     AR137400.1  GI:14478909
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Berg,T., Tollersrud,O.Kristien. and Nilssen,O.
  TITLE     Genetic test for .alpha.-mannosidosis
  JOURNAL   Patent: US 6197507-A 15 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.4%;  Score 12.2;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        434 CTGCACCAGCCGGCGCC 450
              ||||| | |||| ||||
Db         19 CTGCAGCCGCCGCCGCC 3


RESULT 4559
AR293466
LOCUS       AR293466                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5201 from patent US 6537751.
ACCESSION   AR293466
VERSION     AR293466.1  GI:31680750
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db         18 AAAAAAAAAAAAGGGGG 2


RESULT 4552
BD145063/c
LOCUS       BD145063                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145063
VERSION     BD145063.1  GI:27850821
KEYWORDS    JP 2002119291-A/44.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 44 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/44
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db         18 AAAAAAAAAAAAGGGGG 2


RESULT 4553
BD166063/c
LOCUS       BD166063                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166063
VERSION     BD166063.1  GI:27871875
KEYWORDS    JP 2002191372-A/43.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 43 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/43
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566,  PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db         18 AAAAAAAAAAAAGGGGG 2


RESULT 4554
BD089251/c
LOCUS       BD089251                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089251
VERSION     BD089251.1  GI:22634861
KEYWORDS    JP 2001321190-A/1495.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 1495 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/1495
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,  PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
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  JOURNAL   Patent: US 6492121-A 43 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db         18 AAAAAAAAAAAAGGGGG 2


RESULT 4549
AR264963
LOCUS       AR264963                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 47 from patent US 6492121.
ACCESSION   AR264963
VERSION     AR264963.1  GI:29693350
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 47 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db          1 AAAAAAAAAAAAGGGGG 17


RESULT 4550
BD072904/c
LOCUS       BD072904                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072904
VERSION     BD072904.1  GI:22618507
KEYWORDS    JP 2001286300-A/42.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 42 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/42
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTG 1995
              ||||||| ||||| | |
Db         18 AAAAAAAAAAAAGGGGG 2


RESULT 4551
BD107531/c
LOCUS       BD107531                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107531
VERSION     BD107531.1  GI:23202349
KEYWORDS    JP 2002000275-A/40.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 40 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/40
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.3e+03;
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REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sivaraman,V.S., Wang,H.-y. and Malbon,C.C.
  TITLE     Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for cancer
  JOURNAL   Patent: US 6271210-A 3 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        410 GCGTACGCCGCCGCCAT 426
              ||   ||||||||||||
Db          1 GCCGCCGCCGCCGCCAT 17


RESULT 4545
AR164081
LOCUS       AR164081                 17 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 4 from patent US 6271210.
ACCESSION   AR164081
VERSION     AR164081.1  GI:16235020
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sivaraman,V.S., Wang,H.-y. and Malbon,C.C.
  TITLE     Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for cancer
  JOURNAL   Patent: US 6271210-A 4 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        410 GCGTACGCCGCCGCCAT 426
              ||   ||||||||||||
Db          1 GCCGCCGCCGCCGCCAT 17


RESULT 4546
BD058091
LOCUS       BD058091                 17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for breast cancer.
ACCESSION   BD058091
VERSION     BD058091.1  GI:22603697
KEYWORDS    JP 2001518881-A/3.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sivaraman,V.S., Wang,H.Y. and Malbon,C.C.
  TITLE     Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for breast cancer
  JOURNAL   Patent: JP 2001518881-A 3 16-OCT-2001;
            THE RESEARCH FOUNDATION OF STATE UNIV OF NEW YORK
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001518881-A/3
            PD   16-OCT-2001
            PF   19-MAR-1998 JP 1998541700
            PI   VIMALA S SIVARAMAN,HSIEN YU WANG,CRAIG C MALBON PC
            C12N15/11,A61K31/70,C12Q1/68//A61K48/00
            CC   The molecular type is mRNA which is antisense. FH   Key
                 Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        410 GCGTACGCCGCCGCCAT 426
              ||   ||||||||||||
Db          1 GCCGCCGCCGCCGCCAT 17


RESULT 4547
BD058092
LOCUS       BD058092                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for breast cancer.
ACCESSION   BD058092
VERSION     BD058092.1  GI:22603698
KEYWORDS    JP 2001518881-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sivaraman,V.S., Wang,H.Y. and Malbon,C.C.
  TITLE     Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for breast cancer
  JOURNAL   Patent: JP 2001518881-A 4 16-OCT-2001;
            THE RESEARCH FOUNDATION OF STATE UNIV OF NEW YORK
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001518881-A/4
            PD   16-OCT-2001
            PF   19-MAR-1998 JP 1998541700
            PI   VIMALA S SIVARAMAN,HSIEN YU WANG,CRAIG C MALBON PC
            C12N15/11,A61K31/70,C12Q1/68//A61K48/00
            CC   The molecular type is cDNA which is antisense. FH   Key
                 Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        410 GCGTACGCCGCCGCCAT 426
              ||   ||||||||||||
Db          1 GCCGCCGCCGCCGCCAT 17


RESULT 4548
AR264959/c
LOCUS       AR264959                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 43 from patent US 6492121.
ACCESSION   AR264959
VERSION     AR264959.1  GI:29693346
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
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REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1080 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACT 2190
              ||||||||||||  || |
Db          1 TTTTTTTTTTTCCAAAT 17


RESULT 4541
AX214795
LOCUS       AX214795                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 237 from Patent WO0159103.
ACCESSION   AX214795
VERSION     AX214795.1  GI:15524838
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 237 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||  | ||  ||||
Db          1 AAAAAAAATAGAAGAAAA 17


RESULT 4542
AX216730
LOCUS       AX216730                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 2172 from Patent WO0159103.
ACCESSION   AX216730
VERSION     AX216730.1  GI:15526791
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 2172 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||  | ||  ||||
Db          1 AAAAAAAATAGAAGAAAA 17


RESULT 4543
BD202793/c
LOCUS       BD202793                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD202793
VERSION     BD202793.1  GI:33012563
KEYWORDS    JP 2002509721-A/5819.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 5819 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/5819
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              ||||||  ||| |||||
Db         17 AAAAAAGGAAAGAAAAA 1


RESULT 4544
AR164080
LOCUS       AR164080                  17 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 3 from patent US 6271210.
ACCESSION   AR164080
VERSION     AR164080.1  GI:16235018
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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  TITLE     Plant promoter
  JOURNAL   Patent: US 6218598-A 9 17-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 25;
  Best Local Similarity   72.7%;  Pred. No. 5e+03;
  Matches   16;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2484 AATGGTGATGGGGTAATCTATA 2505
              |||| ||| | | | ||||| |
Db         24 AATGTTGAGGTGTTGATCTAGA 3


RESULT 4537
E55072/c
LOCUS       E55072                    25 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Plant promoter.
ACCESSION   E55072
VERSION     E55072.1  GI:18625258
KEYWORDS    JP 2000083679-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ishige,I., Nishikawa,S. and Oeda,K.
  TITLE     Plant promoter
  JOURNAL   Patent: JP 2000083679-A 9 28-MAR-2000;
            SUMITOMO CHEM CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000083679-A/9
            PD   28-MAR-2000
            PF   12-JUL-1999 JP 1999197240
            PR
            PI   IKUHARU ISHIGE,SATOMI NISHIKAWA,KENJI OEDA
            PC   C12N15/09,A01H5/00,C12N1/21,C12N5/10//(C12N15/09,C12R1:91), PC
              (C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N15/00,C12R1:91), PC
            (C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 25;
  Best Local Similarity   72.7%;  Pred. No. 5e+03;
  Matches   16;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2484 AATGGTGATGGGGTAATCTATA 2505
              |||| ||| | | | ||||| |
Db         24 AATGTTGAGGTGTTGATCTAGA 3


RESULT 4538
BD258579/c
LOCUS       BD258579                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258579
VERSION     BD258579.1  GI:33068349
KEYWORDS    JP 2002541795-A/6372.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6372 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6372
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              | ||||  |||||||||
Db         17 ACAAAATTAAAAAAAAA 1


RESULT 4539
AR187068
LOCUS       AR187068                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2556 from patent US 6346398.
ACCESSION   AR187068
VERSION     AR187068.1  GI:20233033
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2556 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACT 2190
              ||||||||||  || |
Db          1 TTTTTTTTTTCCAAAT 17


RESULT 4540
AR323678
LOCUS       AR323678                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1080 from patent US 6566127.
ACCESSION   AR323678
VERSION     AR323678.1  GI:33709486
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 16 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/16
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              | ||||||||||||
Db         22 GCAAAAAAAAAAAA 9


RESULT 4533
BD225572
LOCUS       BD225572                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Assay for methylation in the GST-Pi gene.
ACCESSION   BD225572
VERSION     BD225572.1  GI:33035342
KEYWORDS    JP 2002512810-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Clark,S.J., Millar,D.S. and Molloy,P.L.
  TITLE     Assay for methylation in the GST-Pi gene
  JOURNAL   Patent: JP 2002512810-A 17 08-MAY-2002;
            COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
COMMENT     OS   Artificial Sequence
            PN   JP 2002512810-A/17
            PD   08-MAY-2002
            PF   23-APR-1999 JP 2000546048
            PR   23-APR-1998 AU      PP 3129
            PI   SUSAN JOY CLARK,DOUGLAS S MILLAR,PETER LAURENCE MOLLOY PC
            C12Q1/68,C12N15/09,C12Q1/48,C12N15/00
            CC   Description of Artificial Sequence:Oligonucleotide which binds
            CC   bisulfite-converted human GST-Pi gene
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 23;
  Best Local Similarity   72.7%;  Pred. No. 5.1e+03;
  Matches   16;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAA 2802
              ||   |||||| ||| ||| ||
Db          2 AACCTAAAAAATAAACAAACAA 23


RESULT 4534
AR078307/c
LOCUS       AR078307                 24 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 17 from patent US 5962332.
ACCESSION   AR078307
VERSION     AR078307.1  GI:10005053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Singer,R.H. and Taneja,K.L.
  TITLE     Detection of trinucleotide repeats by in situ hybridization
  JOURNAL   Patent: US 5962332-A 17 05-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 24;
  Best Local Similarity   66.7%;  Pred. No. 5.1e+03;
  Matches   16;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        429 ACCCCCTGCACCAGCCGGCGCCCA 452
              | || | ||  | |||| |||| |
Db         24 ANCCGCCGCCGCCGCCGCCGCCNA 1


RESULT 4535
AX043218/c
LOCUS       AX043218                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 784 from Patent WO0065088.
ACCESSION   AX043218
VERSION     AX043218.1  GI:11341826
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 784 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 25;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAA 2796
              || ||||||||||
Db         14 TTAAAAAAAAAAAA 1


RESULT 4536
AR146859/c
LOCUS       AR146859                 25 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 9 from patent US 6218598.
ACCESSION   AR146859
VERSION     AR146859.1  GI:15110048
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ishige,F., Nishikawa,S. and Oeda,K.
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Db         22 ACAAAAAAAAAAAA 9


RESULT 4528
AR003290/c
LOCUS       AR003290                 22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 12 from patent US 5744300.
ACCESSION   AR003290
VERSION     AR003290.1  GI:3964549
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 12 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
             | ||||||||||||
Db         22 GCAAAAAAAAAAAA 9


RESULT 4529
I30193/c
LOCUS       I30193                   22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 22 from patent US 5580726.
ACCESSION   I30193
VERSION     I30193.1  GI:1820984
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 22 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
             | ||||||||||||
Db         22 ACAAAAAAAAAAAA 9


RESULT 4530
I30201/c
LOCUS       I30201                   22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 30 from patent US 5580726.
ACCESSION   I30201
VERSION     I30201.1  GI:1820992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 30 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
             | ||||||||||||
Db         22 GCAAAAAAAAAAAA 9


RESULT 4531
BD206195/c
LOCUS       BD206195                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206195
VERSION     BD206195.1  GI:33015965
KEYWORDS    JP 2002515252-A/8.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 8 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/8
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. PH   Key
                      Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
             | ||||||||||||
Db         22 ACAAAAAAAAAAAA 9


RESULT 4532
BD206203/c
LOCUS       BD206203                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206203
VERSION     BD206203.1  GI:33015973
KEYWORDS    JP 2002515252-A/16.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
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RESULT 4524
I30197/c
LOCUS       I30197                  22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 26 from patent US 5580726.
ACCESSION   I30197
VERSION     I30197.1  GI:1820988
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 26 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              | ||||||||||||
Db         22 GTAAAAAAAAAAAA 9


RESULT 4525
BD206198/c
LOCUS       BD206198                22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206198
VERSION     BD206198.1  GI:33015968
KEYWORDS    JP 2002515252-A/11.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 11 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/11
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                      Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              | ||||||||||||
Db         22 ATAAAAAAAAAAAA 9


RESULT 4526
BD206199/c
LOCUS       BD206199                22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206199
VERSION     BD206199.1  GI:33015969
KEYWORDS    JP 2002515252-A/12.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 12 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/12
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                      Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              | ||||||||||||
Db         22 GTAAAAAAAAAAAA 9


RESULT 4527
AR003282/c
LOCUS       AR003282                22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 4 from patent US 5744300.
ACCESSION   AR003282
VERSION     AR003282.1  GI:3964541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 4 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              | ||||||||||||
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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              |||||||| |||||
Db         19 TTTTTTTTCTTTTT 6


RESULT 4520
DOGP41401/c
LOCUS       DOGP41401                 21 bp    DNA     linear   MAM 07-MAR-1996
DEFINITION  Dog (Clone: CXX.414) primer for STS 414, 5' end.
ACCESSION   L24302
VERSION     L24302.1  GI:401996
KEYWORDS    PCR identification; PCR primer; STS.
SEGMENT     1 of 2
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
  TITLE     One hundred and one new simple sequence repeat-based markers for
            the canine genome
  JOURNAL   Mamm. Genome 6 (3), 192-195 (1995)
  MEDLINE   95268214
   PUBMED   7749226
COMMENT     Original source text: Canis familiaris (library: E. Ostrander, in
            pBluescript+) adult spleen DNA.
            Submitted by:
            Fred Hutchinson Cancer Research Center
            Transplantation Biology Dept
            1124 Columbia; Mailstop M318
            Seattle, WA 98104, USA
            e-mail: EAOstrander@lbl.gov
            PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
            PCR Profile:  Denaturation:    94 degrees C for 1.00 minute
            Annealing:       55 or 59 degrees C for 0.45 minutes
            Polymerization:  74 degrees C for 1.00 minutes
            PCR Cycles:      33
            Final Extension:  74 degrees C for 5.00 minutes.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
                     /tissue_type="spleen"
                     /dev_stage="adult"
                     /tissue_lib="E. Ostrander, in pBluescript+"
     primer_bind     1. .21

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 21;
  Best Local Similarity   92.9%;  Pred. No. 4.9e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              |||||||||||| |
Db         19 GAAAAAAAAAAATA 6


RESULT 4521
AR003285/c
LOCUS       AR003285                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 7 from patent US 5744300.
ACCESSION   AR003285
VERSION     AR003285.1  GI:3964544
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 7 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              | ||||||||||||
Db         22 ATAAAAAAAAAAAA 9


RESULT 4522
AR003286/c
LOCUS       AR003286                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 8 from patent US 5744300.
ACCESSION   AR003286
VERSION     AR003286.1  GI:3964545
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 8 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              | ||||||||||||
Db         22 GTAAAAAAAAAAAA 9


RESULT 4523
I30196/c
LOCUS       I30196                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 25 from patent US 5580726.
ACCESSION   I30196
VERSION     I30196.1  GI:1820987
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 25 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 5e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              | ||||||||||||
Db         22 ATAAAAAAAAAAAA 9
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ACCESSION   AX078832
VERSION     AX078832.1  GI:13158449
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Fundytus,M.E., Coderre,T.J., Cohen,S.R., Henry,J.L. and Vainio,A.
  TITLE     Antisense oligonucleotides for metabotropic glutamate receptor type
            1 (mglur1)
  JOURNAL   Patent: WO 0105963-A 6 25-JAN-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              ||||||||| ||||
Db          1 GAAAAAAAACAAAA 14


RESULT 4516
AX685128
LOCUS       AX685128                 18 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 5 from Patent WO0222889.
ACCESSION   AX685128
VERSION     AX685128.1  GI:29371479
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lieber,C.M., Woolley,A.T., Hahm,J.I. and Housman,D.
  TITLE     Direct haplotyping using carbon nanotube probes
  JOURNAL   Patent: WO 0222889-A 5 21-MAR-2002;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US) ; Massachusetts
            Institute Of Technology (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic PNA label"
     misc_feature    7. .8
                     /note="Lys"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   81.2%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2181
              ||||||  |||||| |
Db          1 TTTTTTNNTTTTTTGT 16


RESULT 4517
AR174366
LOCUS       AR174366                 20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 26 from patent US 6306655.
ACCESSION   AR174366
VERSION     AR174366.1  GI:17914686
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP alpha expression
  JOURNAL   Patent: US 6306655-A 26 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 4.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        378 AGTCGGCCGACCCC 391
              ||||||||||| ||
Db          7 AGTCGGCCGACTCC 20


RESULT 4518
AX590963/c
LOCUS       AX590963                 20 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 403 from Patent WO02086113.
ACCESSION   AX590963
VERSION     AX590963.1  GI:27949513
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Cookson,W.O., Moffat,M.F., Allen,M. and Lench,N.
  TITLE     Enzyme and snp marker for disease
  JOURNAL   Patent: WO 02086113-A 403 31-OCT-2002;
            Isis Innovation Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 4.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2414 GGTCTGTAAATACT 2427
              ||||| ||||||||
Db         20 GGTCTTTAAATACT 7


RESULT 4519
AX148814/c
LOCUS       AX148814                 20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 16 from Patent WO0136625.
ACCESSION   AX148814
VERSION     AX148814.1  GI:14347338
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 16 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 4.7e+03;
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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGT 1992
              ||||||| ||||||
Db         17 AAAAAAAAAAAAGT 4


RESULT 4511
BD255421/c
LOCUS       BD255421                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255421
VERSION     BD255421.1  GI:33065191
KEYWORDS    JP 2002541795-A/3214.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 3214 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/3214
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAA 2796
              || ||||||||||||
Db         17 TTCAAAAAAAAAAA 4


RESULT 4512
AX676082
LOCUS       AX676082                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 35 from Patent WO02059381.
ACCESSION   AX676082
VERSION     AX676082.1  GI:29333766
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Slaugenhaupt,S. and Gusella,J.F.
  TITLE     Gene for identifying individuals with familial dysautonomia
  JOURNAL   Patent: WO 02059381-A 35 01-AUG-2002;
            The General Hospital Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10095"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTA 2187
              ||||||||||||| |
Db          1 TTTTTTTTTTTCA 14


RESULT 4513
AR047114/c
LOCUS       AR047114                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1907 from patent US 5817796.
ACCESSION   AR047114
VERSION     AR047114.1  GI:5968579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 1907 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTT 2191
              |||||||||||| ||
Db         17 TTTTTTTTTAAATT 4


RESULT 4514
I54166/c
LOCUS       I54166                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1907 from patent US 5646042.
ACCESSION   I54166
VERSION     I54166.1  GI:2475369
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 1907 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTT 2191
              |||||||||||| ||
Db         17 TTTTTTTTTAAATT 4


RESULT 4515
AX078832
LOCUS       AX078832                  18 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 6 from Patent WO0105963.
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RESULT 4506
AR056161
LOCUS       AR056161                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 365 from patent US 5837542.
ACCESSION   AR056161
VERSION     AR056161.1  GI:5981738
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 365 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.8e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTA 2187
              ||||||||||||  |
Db          1 TTTTTTTTTTTTCA 14


RESULT 4507
AR113919
LOCUS       AR113919                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 365 from patent US 6132967.
ACCESSION   AR113919
VERSION     AR113919.1  GI:14094241
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 365 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.8e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTA 2187
              ||||||||||||  |
Db          1 TTTTTTTTTTTTCA 14


RESULT 4508
AX633205
LOCUS       AX633205                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 344 from Patent EP1260586.
ACCESSION   AX633205
VERSION     AX633205.1  GI:28468819
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 344 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 15;
  Best Local Similarity   92.9%;  Pred. No. 2.8e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTA 2187
              ||||||||||||  |
Db          1 TTTTTTTTTTTTCA 14


RESULT 4509
AR187058/c
LOCUS       AR187058                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2546 from patent US 6346398.
ACCESSION   AR187058
VERSION     AR187058.1  GI:20233023
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2546 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.7e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGT 1992
              |||||||  ||||||
Db         17 AAAAAAAAAAAAGT 4


RESULT 4510
AR323668/c
LOCUS       AR323668                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1070 from patent US 6566127.
ACCESSION   AR323668
VERSION     AR323668.1  GI:33709476
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1070 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 3.7e+03;
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RESULT 4502
AR174027/c
LOCUS       AR174027                  14 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 17 from patent US 6306624.
ACCESSION   AR174027
VERSION     AR174027.1  GI:17914347
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
  TITLE     Retinoid metabolizing protein
  JOURNAL   Patent: US 6306624-A 17 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.4e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAA 2796
              || ||||||||||
Db         14 TTAAAAAAAAAAAA 1


RESULT 4503
AR174031
LOCUS       AR174031                  14 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 21 from patent US 6306624.
ACCESSION   AR174031
VERSION     AR174031.1  GI:17914351
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
  TITLE     Retinoid metabolizing protein
  JOURNAL   Patent: US 6306624-A 21 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.4e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTA 2187
              ||||||||||||
Db          1 TTTTTTTTTTTCA 14


RESULT 4504
BD073880/c
LOCUS       BD073880                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Isolation of novel aging factor gene P23.
ACCESSION   BD073880
VERSION     BD073880.1  GI:22619483
KEYWORDS    JP 2001512698-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Suishelm,K., Hosier,S. and Kubbies,M.
  TITLE     Isolation of novel aging factor gene P23
  JOURNAL   Patent: JP 2001512698-A 5 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS   Unidentified
            PN   JP 2001512698-A/5
            PD   28-AUG-2001
            PF   05-AUG-1998 JP 2000506375
            PR   08-AUG-1997 US    08/908873
            PI   KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02,
            PC   C12P21/08,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Isolation of novel aging factor gene P23
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.4e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAA 2796
              || ||||||||||
Db         14 TTAAAAAAAAAAAA 1


RESULT 4505
BD073882
LOCUS       BD073882                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Isolation of novel aging factor gene P23.
ACCESSION   BD073882
VERSION     BD073882.1  GI:22619485
KEYWORDS    JP 2001512698-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Suishelm,K., Hosier,S. and Kubbies,M.
  TITLE     Isolation of novel aging factor gene P23
  JOURNAL   Patent: JP 2001512698-A 7 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS   Unidentified
            PN   JP 2001512698-A/7
            PD   28-AUG-2001
            PF   05-AUG-1998 JP 2000506375
            PR   08-AUG-1997 US    08/908873
            PI   KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02,
            PC   C12P21/08,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Isolation of novel aging factor gene P23
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12.4;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 2.4e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTA 2187
              ||||||||||||
Db          1 TTTTTTTTTTTCA 14
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                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 22;
  Best Local Similarity   78.9%;  Pred. No. 4.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              | ||||||| ||||| ||
Db         22 TCAAAAAAAAAAAAGCTTG 4


RESULT 4498
BD206197/c
LOCUS       BD206197                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206197
VERSION     BD206197.1  GI:33015967
KEYWORDS    JP 2002515252-A/10.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 10 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/10
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Aspergillus oryzae"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:5062"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 22;
  Best Local Similarity   78.9%;  Pred. No. 4.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              | ||||||| ||||| ||
Db         22 TCAAAAAAAAAAAAGCTTG 4


RESULT 4499
AX377075/c
LOCUS       AX377075                 24 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 33 from Patent WO0212557.
ACCESSION   AX377075
VERSION     AX377075.1  GI:19573369
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cailloux,F. and Gobron,S.
  TITLE     Method for detecting known mutations in tube
  JOURNAL   Patent: WO 0212557-A 33 14-FEB-2002;
            Nucleica (FR)
FEATURES              Location/Qualifiers
     source           1. .24
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
                      /note="Amorce pour la detection de mutations responsables
                      de la mucoviscidose."

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 24;
  Best Local Similarity   78.9%;  Pred. No. 5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | |||||| |||| || ||
Db         24 GCAAAAAAGAAAAGAAGAA 6


RESULT 4500
AR028195/c
LOCUS       AR028195                 30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 44 from patent US 5858661.
ACCESSION   AR028195
VERSION     AR028195.1  GI:5940168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Shiloh,Y.
  TITLE     Ataxia-telangiectasia gene and its genomic organization
  JOURNAL   Patent: US 5858661-A 44 12-JAN-1999;
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 30;
  Best Local Similarity   78.9%;  Pred. No. 4.3e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| |||| || || ||
Db         30 AAAAACAAAACAAGAAGAA 12


RESULT 4501
AR138598/c
LOCUS       AR138598                 30 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 123 from patent US 6200749.
ACCESSION   AR138598
VERSION     AR138598.1  GI:14480943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Shiloh,Y.
  TITLE     Mutated forms of the ataxia-telangiectasia gene and method to
            screen for a partial A-T phenotype
  JOURNAL   Patent: US 6200749-A 123 13-MAR-2001;
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 30;
  Best Local Similarity   78.9%;  Pred. No. 4.3e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| |||| || || ||
Db         30 AAAAACAAAACAAGAAGAA 12
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DEFINITION  Sequence 10 from patent US 5744300.
ACCESSION   AR003288
VERSION     AR003288.1  GI:3964547
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 10 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 22;
  Best Local Similarity   78.9%;  Pred. No. 4.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              | ||||||| |||||  ||
Db         22 TTAAAAAAAAAAAAGCTTG 4


RESULT 4494
I30199/c
LOCUS       I30199                   22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 28 from patent US 5580726.
ACCESSION   I30199
VERSION     I30199.1  GI:1820990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 28 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 22;
  Best Local Similarity   78.9%;  Pred. No. 4.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              | ||||||| |||||  ||
Db         22 TTAAAAAAAAAAAAGCTTG 4


RESULT 4495
BD206201/c
LOCUS       BD206201                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206201
VERSION     BD206201.1  GI:33015971
KEYWORDS    JP 2002515252-A/14.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 14 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/14
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 22;
  Best Local Similarity   78.9%;  Pred. No. 4.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              | ||||||| |||||  ||
Db         22 TTAAAAAAAAAAAAGCTTG 4


RESULT 4496
AR003284/c
LOCUS       AR003284                 22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5744300.
ACCESSION   AR003284
VERSION     AR003284.1  GI:3964543
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 6 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 22;
  Best Local Similarity   78.9%;  Pred. No. 4.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              | ||||||| |||||  ||
Db         22 TCAAAAAAAAAAAAGCTTG 4


RESULT 4497
I30195/c
LOCUS       I30195                   22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 24 from patent US 5580726.
ACCESSION   I30195
VERSION     I30195.1  GI:1820986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 24 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
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           FH   Key             Location/Qualifiers
           FT   source          1. .20
           FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| ||||  || |||||
Db         20 AAAACAAAAGTAAGAAAAA 2


RESULT 4489
AX149168
LOCUS       AX149168                 20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 370 from Patent WO0136625.
ACCESSION   AX149168
VERSION     AX149168.1  GI:14347692
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 370 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAAC 2189
              |||  ||||| |||| |||
Db          2 TTTCATTTTTATTTTCAAC 20


RESULT 4490
AX149224
LOCUS       AX149224                 20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 426 from Patent WO0136625.
ACCESSION   AX149224
VERSION     AX149224.1  GI:14347748
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 426 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAAC 2189
              |||  ||||| |||| |||
Db          2 TTTCATTTTTATTTTCAAC 20


RESULT 4491
AR236360/c
LOCUS       AR236360                 21 bp    RNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6465176.
ACCESSION   AR236360
VERSION     AR236360.1  GI:27280288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Giordano,T., Beach,D.L. and Temeles,G.L.
  TITLE     Method for identifying compounds RNA/RNA binding protein
            interactions
  JOURNAL   Patent: US 6465176-A 8 15-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 21;
  Best Local Similarity   78.9%;  Pred. No. 4.7e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||| ||| ||| ||| |||
Db         20 AAATAAATAAATAAATAAA 2


RESULT 4492
AX183997
LOCUS       AX183997                 21 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 1750 from Patent WO0142511.
ACCESSION   AX183997
VERSION     AX183997.1  GI:15135332
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
  TITLE     Ibd-related polymorphisms
  JOURNAL   Patent: WO 0142511-A 1750 14-JUN-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
            Biotherapeutics Corporation (CA)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 4.7e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTG 2193
              ||||||||  |||   ||||
Db          1 TTTTTTTTGNTTTCCATTTG 20


RESULT 4493
AR003288/c
LOCUS       AR003288                 22 bp    DNA     linear   PAT 04-DEC-1998
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  JOURNAL   Patent: WO 0206531-A 12 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Complement DNA oligo AGT02009"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTTTAAAAAA 19


RESULT 4485
AX441510
LOCUS       AX441510                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 14 from Patent WO0206531.
ACCESSION   AX441510
VERSION     AX441510.1  GI:21690471
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 14 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02021"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTGTAAAAAA 19


RESULT 4486
AX441513
LOCUS       AX441513                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 17 from Patent WO0206531.
ACCESSION   AX441513
VERSION     AX441513.1  GI:21690474
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 17 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02024"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTCTAAAAAA 19


RESULT 4487
BD065818
LOCUS       BD065818                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065818
VERSION     BD065818.1  GI:22611421
KEYWORDS    JP 2001511000-A/453.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 453 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/453
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              || |||| |||||||  ||
Db          1 AACAAAACAAAAAAAGTAA 19


RESULT 4488
BD144137/c
LOCUS       BD144137                 20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Oligonucleotide for detecting HIV-1 and detection method.
ACCESSION   BD144137
VERSION     BD144137.1  GI:27849895
KEYWORDS    JP 2002125687-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ishizuka,T., Ishiguro,T. and Saito,J.
  TITLE     Oligonucleotide for detecting HIV-1 and detection method
  JOURNAL   Patent: JP 2002125687-A 7 08-MAY-2002;
            TOSOH CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002125687-A/7
            PD   08-MAY-2002
            PF   30-OCT-2000 JP 2000334937
            PI   TETSUYA ISHIZUKA,TAKAHIKO ISHIGURO,JUICHI SAITO PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Oligonucleotide capable of binding specifically to a specified

            CC           site of
            CC   HIV-1 RNA
```

```
  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| ||||  || |||||
Db         20 AAAACAAAAGTAAGAAAAA 2


RESULT 4480
AX441504/c
LOCUS       AX441504                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 8 from Patent WO0206531.
ACCESSION   AX441504
VERSION     AX441504.1  GI:21690465
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 8 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide AGT02008"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 4481
AX441505/c
LOCUS       AX441505                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 9 from Patent WO0206531.
ACCESSION   AX441505
VERSION     AX441505.1  GI:21690466
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 9 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide AGT02012"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 4482
AX441506/c
LOCUS       AX441506                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 10 from Patent WO0206531.
ACCESSION   AX441506
VERSION     AX441506.1  GI:21690467
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 10 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide AGT02013"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 4483
AX441507/c
LOCUS       AX441507                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 11 from Patent WO0206531.
ACCESSION   AX441507
VERSION     AX441507.1  GI:21690468
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 11 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide AGT02014"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 4484
AX441508
LOCUS       AX441508                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 12 from Patent WO0206531.
ACCESSION   AX441508
VERSION     AX441508.1  GI:21690469
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
```

```
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||    ||||||
Db          1 AAAAAAAAATTGTAAAAAA 19


RESULT 4475
AR360429
LOCUS       AR360429                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 17 from patent US 6596490.
ACCESSION   AR360429
VERSION     AR360429.1  GI:33767459
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 17 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||    ||||||
Db          1 AAAAAAAAATTCTAAAAAA 19


RESULT 4476
AR382158/c
LOCUS       AR382158                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from patent US 6610481.
ACCESSION   AR382158
VERSION     AR382158.1  GI:40090567
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Koch,J.E.
  TITLE     Cascade nucleic acid amplification reaction
  JOURNAL   Patent: US 6610481-A 5 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              ||| ||| ||| ||| |||
Db         20 TTTCTTTCTTTCTTTCTTT 2


RESULT 4477
AR382159
LOCUS       AR382159                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6610481.
ACCESSION   AR382159
VERSION     AR382159.1  GI:40090568
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Koch,J.E.
  TITLE     Cascade nucleic acid amplification reaction
  JOURNAL   Patent: US 6610481-A 6 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              ||| ||| ||| ||| |||
Db          1 TTTCTTTCTTTCTTTCTTT 19


RESULT 4478
AX136904/c
LOCUS       AX136904                  20 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 6 from Patent EP1065278.
ACCESSION   AX136904
VERSION     AX136904.1  GI:14273253
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Makino,Y., Abe,Y., Ogawa,M., Takagi,M., Takenaka,S. and
            Yamashita,K.
  TITLE     Detection of partly complementary nucleic acid fragment
  JOURNAL   Patent: EP 1065278-A 6 03-JAN-2001;
            FUJI PHOTO FILM CO., LTD. (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sample nucleic acid fragment"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||    |||||||
Db         20 AAAAAAAATTTTAAAAAAA 2


RESULT 4479
AX429779/c
LOCUS       AX429779                  20 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 7 from Patent EP1203826.
ACCESSION   AX429779
VERSION     AX429779.1  GI:21540955
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ishizuka,T., Ishiguro,T. and Saitoh,J.
  TITLE     Oligonucleotide for detection of hiv-1 and detection method
  JOURNAL   Patent: EP 1203826-A 7 08-MAY-2002;
            Tosoh Corporation (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide hybridizable with a specific site
                     of HIV-1 RNA"
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     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 4470
AR360421/c
LOCUS       AR360421                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6596490.
ACCESSION   AR360421
VERSION     AR360421.1  GI:33767451
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 9 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 4471
AR360422/c
LOCUS       AR360422                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 10 from patent US 6596490.
ACCESSION   AR360422
VERSION     AR360422.1  GI:33767452
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 10 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 4472
AR360423/c
LOCUS       AR360423                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6596490.
ACCESSION   AR360423
VERSION     AR360423.1  GI:33767453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 11 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 4473
AR360424
LOCUS       AR360424                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 12 from patent US 6596490.
ACCESSION   AR360424
VERSION     AR360424.1  GI:33767454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 12 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTTTAAAAAA 19


RESULT 4474
AR360426
LOCUS       AR360426                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 14 from patent US 6596490.
ACCESSION   AR360426
VERSION     AR360426.1  GI:33767456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 14 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
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  JOURNAL   Patent: US 6596489-A 10 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 4465
AR360396/c
LOCUS       AR360396                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6596489.
ACCESSION   AR360396
VERSION     AR360396.1  GI:33767426
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JCURNAL   Patent: US 6596489-A 11 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db         20 AAAAAAAAATTTTAAAAAA 2


RESULT 4466
AR360397
LOCUS       AR360397                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 12 from patent US 6596489.
ACCESSION   AR360397
VERSION     AR360397.1  GI:33767427
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 12 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTTTAAAAAA 19


RESULT 4467
AR360399
LOCUS       AR360399                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 14 from patent US 6596489.
ACCESSION   AR360399
VERSION     AR360399.1  GI:33767429
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 14 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTGTAAAAAA 19


RESULT 4468
AR360402
LOCUS       AR360402                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 17 from patent US 6596489.
ACCESSION   AR360402
VERSION     AR360402.1  GI:33767432
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 17 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTCTAAAAAA 19


RESULT 4469
AR360420/c
LOCUS       AR360420                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6596490.
ACCESSION   AR360420
VERSION     AR360420.1  GI:33767450
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 8 22-JUL-2003;
FEATURES             Location/Qualifiers
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```
            necrosis factor-alpha (TNF-alpha).
ACCESSION   BD228014
VERSION     BD228014.1  GI:33037784
KEYWORDS    JP 2002526125-A/217.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,F.C., Butler,M.M. and Jr,W.J.S.
  TITLE     Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha)
  JOURNAL   Patent: JP 2002526125-A 217 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526125-A/217
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574737
            PR   05-OCT-1998 US    09/166186,18-MAY-1999 US    09/313932 PI
            BRENDA F BAKER,FRANK C BENNETT,MADELINE M BUTLER,WILLIAM J  PI
            SHANAHAN JR
            PC   C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/
            PC   00,A61P1/16,
            PC   A61P1/18,A61P3/10,A61P17/00,A61P17/04,A61P29/00,A61P31/00, PC
             C07H21/02,
            PC   C07H21/04,C12N15/00
            CC   Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1449 TGAACCCTGGAGACCAGAG 1467
              ||  |  |||||||||||  |
Db         19 TGGAATCTGGAGACCAGGG 1


RESULT 4461
AR211368/c
LOCUS       AR211368                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6399305.
ACCESSION   AR211368
VERSION     AR211368.1  GI:21514671
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Makino,Y., Abe,Y., Takagi,M., Takenaka,S., Yamashita,K. and
            Ogawa,M.
  TITLE     Protection of partial complementary nucleic acid fragment using a
            electroconductive chip and intercalator
  JOURNAL   Patent: US 6399305-A 6 04-JUN-2002;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match              0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||    |||||||
Db         20 AAAAAAAATTTTAAAAAAA 2


RESULT 4462
AR360393/c
LOCUS       AR360393                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6596489.
ACCESSION   AR360393
VERSION     AR360393.1  GI:33767423
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 8 22-JUL-2003;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match              0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||    |||||||
Db         20 AAAAAAAATTTTAAAAAAA 2


RESULT 4463
AR360394/c
LOCUS       AR360394                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6596489.
ACCESSION   AR360394
VERSION     AR360394.1  GI:33767424
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 9 22-JUL-2003;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match              0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||    |||||||
Db         20 AAAAAAAATTTTAAAAAAA 2


RESULT 4464
AR360395/c
LOCUS       AR360395                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 10 from patent US 6596489.
ACCESSION   AR360395
VERSION     AR360395.1  GI:33767425
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
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ACCESSION   A88305
VERSION     A88305.1  GI:6736875
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 453 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              || |||| ||||||| ||
Db          1 AACAAAACAAAAAAAGTAA 19


RESULT 4456
A90272
LOCUS       A90272                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 453 from Patent EP0856579.
ACCESSION   A90272
VERSION     A90272.1  GI:6738786
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 453 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              || |||| ||||||| ||
Db          1 AACAAAACAAAAAAAGTAA 19


RESULT 4457
AR100486/c
LOCUS       AR100486                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 217 from patent US 6080580.
ACCESSION   AR100486
VERSION     AR100486.1  GI:12810934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-.alpha. (TNF-.alpha.) expression
  JOURNAL   Patent: US 6080580-A 217 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1449 TGAACCCTGGAGACCAGAG 1467
              || |  |||||||||| |
Db         19 TGGAATCTGGAGACCAGGG 1


RESULT 4458
AR150141/c
LOCUS       AR150141                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 217 from patent US 6228642.
ACCESSION   AR150141
VERSION     AR150141.1  GI:15114732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-(.alpha.) (TNF-.alpha.) expression
  JOURNAL   Patent: US 6228642-A 217 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1449 TGAACCCTGGAGACCAGAG 1467
              || |  |||||||||| |
Db         19 TGGAATCTGGAGACCAGGG 1


RESULT 4459
AR164029
LOCUS       AR164029                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 228 from patent US 6271030.
ACCESSION   AR164029
VERSION     AR164029.1  GI:16234940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP beta expression
  JOURNAL   Patent: US 6271030-A 228 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              | ||||| |||| |||||
Db          2 ACAAAAACAAAACCAAAAA 20


RESULT 4460
BD228014/c
LOCUS       BD228014                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide regulation of expression of tumor
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  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 13 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02020"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTTGAAAAAA 19


RESULT 4451
AR158935/c
LOCUS       AR158935                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 557 from patent US 6251588.
ACCESSION   AR158935
VERSION     AR158935.1  GI:16221349
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 557 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              ||  || ||||| ||||||
Db         20 AGGGTTAAAAAAGAAAAAA 2


RESULT 4452
AR086217/c
LOCUS       AR086217                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 38 from patent US 5985558.
ACCESSION   AR086217
VERSION     AR086217.1  GI:10012983
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
  TITLE     Antisense oligonucleotide compositions and methods for the
            inibition of c-Jun and c-Fos
  JOURNAL   Patent: US 5985558-A 38 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1000 GCGGGAGAAGTTGGACAAG 1018
              ||||  |||||||| | ||
Db         19 GCGGCTGAAGTTGGGCGAG 1


RESULT 4453
AR176783/c
LOCUS       AR176783                  20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 38 from patent US 6312900.
ACCESSION   AR176783
VERSION     AR176783.1  GI:17919138
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of activating protein 1
  JOURNAL   Patent: US 6312900-A 38 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1000 GCGGGAGAAGTTGGACAAG 1018
              ||||  |||||||| | ||
Db         19 GCGGCTGAAGTTGGGCGAG 1


RESULT 4454
AX462490
LOCUS       AX462490                  20 bp    DNA     linear   PAT 15-JUL-2002
DEFINITION  Sequence 234 from Patent EP1217079.
ACCESSION   AX462490
VERSION     AX462490.1  GI:21885703
KEYWORDS    .
SOURCE      Aegilops tauschii
  ORGANISM  Aegilops tauschii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Aegilops.
REFERENCE   1
  AUTHORS   Bernard,M., Sourdille,P. and Guyomarch,H.
  TITLE     Microsatellite markers from Triticum tauschii
  JOURNAL   Patent: EP 1217079-A 234 26-JUN-2002;
            INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Aegilops tauschii"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:37682"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        829 TGAGGTCTTCTGCTCAGTC 847
              |||| ||||||| | || |
Db          1 TGAGTTCTTCTGGTGAGGC 19


RESULT 4455
A88305
LOCUS       A88305                    20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 453 from Patent WO9833904.
```

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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 16 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATGTGAAAAAA 19


RESULT 4446
AX441512
LOCUS       AX441512                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 16 from Patent WO0206531.
ACCESSION   AX441512
VERSION     AX441512.1  GI:21690473
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 16 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02023"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATGTGAAAAAA 19


RESULT 4447
AR158936/c
LOCUS       AR158936                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 558 from patent US 6251588.
ACCESSION   AR158936
VERSION     AR158936.1  GI:16221351
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JCURNAL   Patent: US 6251588-A 558 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              ||  || ||||| ||||||
Db         19 AGGGTTAAAAAAGAAAAAA 1


RESULT 4448
AR360398
LOCUS       AR360398                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 13 from patent US 6596489.
ACCESSION   AR360398
VERSION     AR360398.1  GI:33767428
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 13 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTTGAAAAAA 19


RESULT 4449
AR360425
LOCUS       AR360425                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 13 from patent US 6596490.
ACCESSION   AR360425
VERSION     AR360425.1  GI:33767455
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 13 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||    ||||||
Db          1 AAAAAAAAATTTGAAAAAA 19


RESULT 4450
AX441509
LOCUS       AX441509                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 13 from Patent WO0206531.
ACCESSION   AX441509
VERSION     AX441509.1  GI:21690470
KEYWORDS    .
SOURCE      synthetic construct
```

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  Best Local Similarity   87.5%;  Pred. No. 4.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1398 CCCTGCAGAACTACAT 1413
              ||||||||  || ||||
Db          5 CCCTGCAGCACCACAT 20


RESULT 4441
AR211895/c
LOCUS       AR211895                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 105 from patent US 6399373.
ACCESSION   AR211895
VERSION     AR211895.1  GI:21515338
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bougueleret,L.
  TITLE     Nucleic acid encoding a retinoblastoma binding protein (RBP-7) and
            polymorphic markers associated with said nucleic acid
  JOURNAL   Patent: US 6399373-A 105 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGAAAG 2197
              ||||||||||  | | | ||
Db         19 TTTTTTTTAATTATAAGAG 1


RESULT 4442
AR241724
LOCUS       AR241724                 19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 12 from patent US 6472154.
ACCESSION   AR241724
VERSION     AR241724.1  GI:27287536
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 12 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||  |||  |||  |||||  |
Db          1 TTTCTTTCTTTCTTTTTCT 19


RESULT 4443
BD221965/c
LOCUS       BD221965                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Nucleic acid encoding retinoblastoma-binding protein (RBP-7) and
            polymorphic marker relating to the nucleic acid.
ACCESSION   BD221965
VERSION     BD221965.1  GI:33031735
KEYWORDS    JP 2002519027-A/104.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bougueleret,L.
  TITLE     Nucleic acid encoding retinoblastoma-binding protein (RBP-7) and
            polymorphic marker relating to the nucleic acid
  JOURNAL   Patent: JP 2002519027-A 104 02-JUL-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002519027-A/104
            PD   02-JUL-2002
            PF   30-JUN-1999 JP 2000557360
            PR   30-JUN-1998 US    60/091315,10-DEC-1998 US    60/111909 PI
            LYDIE BOUGUELERET
            PC   C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N5/10,
            PC   C12Q1/68,
            PC   G01N33/53,G01N33/566,C12N15/00,C12N5/00,C12N15/00 CC
            potential microsequencing oligo for 5-129-144.mis1 FH   Key
                Location/Qualifiers
            FT   primer_bind     1. .19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGAAAG 2197
              ||||||||||  | | | ||
Db         19 TTTTTTTTAATTATAAGAG 1


RESULT 4444
AR360401
LOCUS       AR360401                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 16 from patent US 6596489.
ACCESSION   AR360401
VERSION     AR360401.1  GI:33767431
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 16 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.4%;  Score 12.6;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||     ||||||
Db          1 AAAAAAAAATGTGAAAAAA 19


RESULT 4445
AR360428
LOCUS       AR360428                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 16 from patent US 6596490.
ACCESSION   AR360428
VERSION     AR360428.1  GI:33767458
KEYWORDS    .
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RESULT 4437
AX011523
LOCUS       AX011523                  22 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 20 from Patent WO9955892.
ACCESSION   AX011523
VERSION     AX011523.1  GI:9998073
KEYWORDS    .
SOURCE      Visna virus
  ORGANISM  Visna virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Ovine/caprine
            lentivirus.
REFERENCE   1
  AUTHORS   Charneau,P., Firat,H. and Zennou,V.
  TITLE     Use of triplex structure dna sequences for transferring nucleotide
            sequences
  JOURNAL   Patent: WO 9955892-A 20 04-NOV-1999;
            CHARNEAU PIERRE (FR); FIRAT HUESEYIN (FR); PASTEUR INSTITUT (FR);
            ZENNOU VERONIQUE (FR)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Visna virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11741"
     misc_feature    complement(1. .22)
                     /note="Sequence a double brin"
     misc_feature    4
                     /note="A peut etre T"
     misc_feature    6
                     /note="G peut etre T"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 22;
  Best Local Similarity   87.5%;  Pred. No. 4.7e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||| |||||| |||
Db          1 AAAAAGAAAAAAGAAA 16


RESULT 4438
BD226410
LOCUS       BD226410                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Use of triplex structure DNA sequences for transferring nucleotide
            sequences.
ACCESSION   BD226410
VERSION     BD226410.1  GI:33036180
KEYWORDS    JP 2002512804-A/20.
SOURCE      Visna virus
  ORGANISM  Visna virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Ovine/caprine
            lentivirus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Charneau,P., Zennou,V. and Firat,H.
  TITLE     Use of triplex structure DNA sequences for transferring nucleotide
            sequences
  JOURNAL   Patent: JP 2002512804-A 20 08-MAY-2002;
            INSTITUT PASTEUR
COMMENT     OS   Visna virus
            PN   JP 2002512804-A/20
            PD   08-MAY-2002
            PF   23-APR-1999 JP 2000546035
            PR   24-APR-1998 FR     98/05197
            PI   PIERRE CHARNEAU,VERONIQUE ZENNOU,HUESEYIN FIRAT PC
            C12N15/09,A61K48/00,C12N5/10,C12N7/00//A61K35/12,C07K14/16, PC
            C12N15/00,
            PC   C12N5/00
            CC   Strandedness: Double;
            CC   A can be T
            CC   G can be T
            CC   Sequence of double strand
            FH   Key             Location/Qualifiers
            FT   misc_feature    (4)
            FT   misc_feature    (6)
            FT   misc_feature    complement(1. .22).
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Visna virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:11741"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 22;
  Best Local Similarity   87.5%;  Pred. No. 4.7e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||| |||||| |||
Db          1 AAAAAGAAAAAAGAAA 16


RESULT 4439
AR409907/c
LOCUS       AR409907                  23 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 20 from patent US 6635422.
ACCESSION   AR409907
VERSION     AR409907.1  GI:40161042
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 20 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 23;
  Best Local Similarity   87.5%;  Pred. No. 4.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||  ||||||
Db         23 AAAAAAAATTAAAAAA 8


RESULT 4440
AX591818
LOCUS       AX591818                  23 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 179 from Patent WO0246409.
ACCESSION   AX591818
VERSION     AX591818.1  GI:27950087
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Guo,X., Li,L., Patturajan,M., Shimkets,R.A., Casman,S.J.,
            Malyankar,U.M., Tchernev,V.T., Vernet,C.A., Spytek,K.A.,
            Shenoy,S.G., Alsobrook,J.P., Edinger,S., Peyman,J.A., Stone,D.J.,
            Ellerman,K., Gangolli,E.A., Boldog,F.L., Colman,S.D., Eisen,A.J.,
            Liu,X., Padigaru,M., Spaderna,S.K. and Zerhusen,B.D.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0246409-A 179 13-JUN-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="CHEMICALLY SYNTHESIZED"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 23;
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Krieg,A.M. and Hartmann,G.
  TITLE     Immunostimulatory nucleic acid molecules for activating dendritic
            cells
  JOURNAL   Patent: US 6429199-A 99 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 4433
AX104584/c
LOCUS       AX104584                 20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 776 from Patent WO0122972.
ACCESSION   AX104584
VERSION     AX104584.1  GI:13920781
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 776 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 4434
AX354981/c
LOCUS       AX354981                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 9 from Patent WO0197843.
ACCESSION   AX354981
VERSION     AX354981.1  GI:18619648
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 9 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-chimeric
                     phosphorothioate/phosphodiester backbone with
                     phosphorothioate at 5' and 3' ends"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 4435
AX547637/c
LOCUS       AX547637                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 776 from Patent WO02053141.
ACCESSION   AX547637
VERSION     AX547637.1  GI:25812781
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 776 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGA 2194
              ||||||| ||| ||||
Db         20 TTTTTTTCAACGTTGA 5


RESULT 4436
AR297993/c
LOCUS       AR297993                 21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 9728 from patent US 6537751.
ACCESSION   AR297993
VERSION     AR297993.1  GI:31685277
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 9728 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 4.5e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              |||  ||||||||||
Db         21 GAAGGAAAAAAAAAAA 6
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  Best Local Similarity   87.5%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        461 CAGCAGCAGGCCTGGC 476
              ||||||||||  | |||
Db          2 CAGCAGCAGGTCAGGC 17


RESULT 4428
BD217399
LOCUS       BD217399                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of TNFR1 expression.
ACCESSION   BD217399
VERSION     BD217399.1  GI:33027169
KEYWORDS    JP 2002519015-A/22.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense modulation of TNFR1 expression
  JOURNAL   Patent: JP 2002519015-A 22 02-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002519015-A/22
            PD   02-JUL-2002
            PF   17-JUN-1999 JP 2000557265
            PR   26-JUN-1998 US    09/106038
            PI   BRENDA F BAKER,LEX M COWSERT
            PC
            C12N15/09,A61K31/7105,A61K31/711,A61K48/00,A61P29/00,A61P43/00, PC
             C12Q1/68,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense modulation of TNFR1 expression
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 18;
  Best Local Similarity   87.5%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        461 CAGCAGCAGGCCTGGC 476
              ||||||||||  | |||
Db          2 CAGCAGCAGGTCAGGC 17


RESULT 4429
AR228127
LOCUS       AR228127                 19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 28 from patent US 6448003.
ACCESSION   AR228127
VERSION     AR228127.1  GI:27266873
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Guida,M. and Kurth,J.
  TITLE     Genotyping the human phenol sulfotransferbase 2 gene STP2
  JOURNAL   Patent: US 6448003-A 28 10-SEP-2002;
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||  ||
Db          3 GAAAAAAAAAAAGGAA 18


RESULT 4430
AR429749/c
LOCUS       AR429749                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 29 from patent US 6645745.
ACCESSION   AR429749
VERSION     AR429749.1  GI:40190087
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wojnowski,L., Gellner,K. and Eiselt,R.
  TITLE     Identification of a new member of the cytochrome P450 3A (CYP3A)
            gene family: CYP3AX
  JOURNAL   Patent: US 6645745-A 29 11-NOV-2003;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        757 CATTTCCATGACCAAG 772
              ||||||||||  | |||
Db         20 CATTTCCATGGCAAAG 5


RESULT 4431
AR107643
LOCUS       AR107643                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 83 from patent US 6110664.
ACCESSION   AR107643
VERSION     AR107643.1  GI:12823130
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 83 29-AUG-2000;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2268 TTATTTCAGATGTTTC 2283
              ||||||||  ||||||
Db          1 TTATTTCATTTGTTTC 16


RESULT 4432
AR222265/c
LOCUS       AR222265                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 99 from patent US 6429199.
ACCESSION   AR222265
VERSION     AR222265.1  GI:23329730
KEYWORDS    .
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  AUTHORS   Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Oligoribonucleotides with enzymatic activity
  JOURNAL   Patent: US 6617438-A 557 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||| |||| |||||||
Db         17 AAACAAAACAAAAAAA 2


RESULT 4424
AR398177/c
LOCUS       AR398177                  17 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 558 from patent US 6617438.
ACCESSION   AR398177
VERSION     AR398177.1  GI:40135776
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Oligoribonucleotides with enzymatic activity
  JOURNAL   Patent: US 6617438-A 558 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||| |||| |||
Db         16 AAAAAAACAAAACAAA 1


RESULT 4425
AR434060/c
LOCUS       AR434060                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 483 from patent US 6656700.
ACCESSION   AR434060
VERSION     AR434060.1  GI:40196903
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 483 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTT 2178
              | |||| |||||||||
Db         17 TTCTTTCTTTTTTTT 2


RESULT 4426
BD203175
LOCUS       BD203175                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD203175
VERSION     BD203175.1  GI:33012945
KEYWORDS    JP 2002509721-A/6201.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 6201 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/6201
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            PT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              |||||  |||||||||
Db          2 AAAAATTAAAAAAAAA 17


RESULT 4427
AR096351
LOCUS       AR096351                  18 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 22 from patent US 6007995.
ACCESSION   AR096351
VERSION     AR096351.1  GI:10025085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense inhibition of TNFR1 expression
  JOURNAL   Patent: US 6007995-A 22 28-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 18;
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RESULT 4419
AR323677
LOCUS       AR323677                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1079 from patent US 6566127.
ACCESSION   AR323677
VERSION     AR323677.1  GI:33709485
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1079 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAA 2188
              ||||||||||||  ||
Db          1 TTTTTTTTTTTCCAA 16


RESULT 4420
BD254586
LOCUS       BD254586                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD254586
VERSION     BD254586.1  GI:33064356
KEYWORDS    JP 2002541795-A/2379.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2379 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/2379
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2801
              || |||| ||||||||
Db          1 AAGAAAATAAAAAAAA 16


RESULT 4421
AR286186/c
LOCUS       AR286186                 17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 558 from patent US 6528640.
ACCESSION   AR286186
VERSION     AR286186.1  GI:29723782
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 558 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2801
              ||| |||| |||||||
Db         17 AAACAAAACAAAAAAA 2


RESULT 4422
AR286187/c
LOCUS       AR286187                 17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 559 from patent US 6528640.
ACCESSION   AR286187
VERSION     AR286187.1  GI:29723783
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 559 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2801
              ||||||| |||| |||
Db         16 AAAAAAACAAAACAAA 1


RESULT 4423
AR398176/c
LOCUS       AR398176                 17 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 557 from patent US 6617438.
ACCESSION   AR398176
VERSION     AR398176.1  GI:40135774
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
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ACCESSION   AX043237
VERSION     AX043237.1  GI:11341845
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 803 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 13;  DB 1;  Length 25;
  Best Local Similarity   76.2%;  Pred. No. 4.8e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGAA 2195
              ||||||||||||  | |  ||
Db          1 TTTTTTTTTTTTCCCCTCCAA 21


RESULT 4416
AX042933/c
LOCUS       AX042933                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 499 from Patent WO0065088.
ACCESSION   AX042933
VERSION     AX042933.1  GI:11341541
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 499 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 13;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 4417
AJ588309/c
LOCUS       AJ588309                 25 bp    DNA     linear   PLN 23-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, right border, clone
            530A11.
ACCESSION   AJ588309
VERSION     AJ588309.1  GI:37937933
KEYWORDS    right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 25)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="530A11"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .25
                     /note="T-DNA flanking sequence
                     right border"

  Query Match             0.5%;  Score 13;  DB 1;  Length 25;
  Best Local Similarity   76.2%;  Pred. No. 4.8e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | |||| | ||||| ||| ||
Db         25 TAAAAAGACAAAAACAAACAA 5


RESULT 4418
AR187067
LOCUS       AR187067                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2555 from patent US 6346398.
ACCESSION   AR187067
VERSION     AR187067.1  GI:20233032
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2555 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAA 2188
              ||||||||||||  ||
Db          1 TTTTTTTTTTTTCCAA 16
```

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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
            Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
            Imbach,J.Louis.
  TITLE     Oligonucleotides having a conserved G4 core sequence
  JOURNAL   Patent: US 5952490-A 142 14-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 4411
I21708/c
LOCUS       I21708                  21 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 4 from patent US 5523389.
ACCESSION   I21708
VERSION     I21708.1  GI:1602062
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Ecker,D.J., Wyatt,J.R. and Imbach,J.L.
  TITLE     Inhibitors of human immunodeficiency virus
  JOURNAL   Patent: US 5523389-A 4 04-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 4412
AX032696/c
LOCUS       AX032696                21 bp    DNA     linear   PAT 20-SEP-2000
DEFINITION  Sequence 142 from Patent EP1016715.
ACCESSION   AX032696
VERSION     AX032696.1  GI:10279634
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
            Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
            Wyatt,J.R.
  TITLE     Oligonucleotides having a conserved g4 core sequence
  JOURNAL   Patent: EP 1016715-A 142 05-JUL-2000;
            ISIS PHARMACEUTICALS INC (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 4413
AR043093/c
LOCUS       AR043093                22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5814445.
ACCESSION   AR043093
VERSION     AR043093.1  GI:5964101
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Belyavsky,A.V. and Ivanova,N.B.
  TITLE     Method of identification and cloning differentially expressed
            messenger RNAs
  JOURNAL   Patent: US 5814445-A 1 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         22 AAAAAAAAAAAAA 10


RESULT 4414
AX043137/c
LOCUS       AX043137                24 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 703 from Patent WO0065088.
ACCESSION   AX043137
VERSION     AX043137.1  GI:11341745
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 703 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 13;  DB 1;  Length 24;
  Best Local Similarity   76.2%;  Pred. No. 4.8e+03;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAA 2796
              | | | | | ||||||||||
Db         21 GCTCGTAGTTAAAAAAAAAA 1


RESULT 4415
AX043237
LOCUS       AX043237                25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 803 from Patent WO0065088.
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Db          1 AAAAAAAAAAAAA 13


RESULT 4406
AR087163/c
LOCUS       AR087163                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 33 from patent US 5986053.
ACCESSION   AR087163
VERSION     AR087163.1  GI:10013926
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and
            Mollegaard,N.E.
  TITLE     Peptide nucleic acids complexes of two peptide nucleic acid strands
            and one nucleic acid strand
  JOURNAL   Patent: US 5986053-A 33 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   68.4%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||       ||||||
Db         20 AAAAAAANNNNNNAAAAAA 2


RESULT 4407
E36062/c
LOCUS       E36062                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Higher-order structure and binding of peptide nucleic acid.
ACCESSION   E36062
VERSION     E36062.1  GI:13022464
KEYWORDS    JP 1999236396-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bushato,O., Eguhorumu,M., Nielsen,P.A., Berg,R.H., Ekka,D.J. and
            Morugado,N.A.
  TITLE     Higher-order structure and binding of peptide nucleic acid
  JOURNAL   Patent: JP 1999236396-A 7 31-AUG-1999;
            ISIS PHARMACEUTICALS INC,BUCHARDT DORUTE,EGUHORUMU MICHAEL, IELSEN
            PATER A, BERGH RORUFU HO
COMMENT     OS   Unidentified
            PN   JP 1999236396-A/7
            PD   31-AUG-1999
            PF   14-OCT-1998 JP 1998291590
            PR   02-JUL-1993 US       088658
            PI   BUSHATO ORE,EGUHORUMU MICHAEL,NIELSEN PATER A,BERG RORUFU HO,
            PI   EKKA DAVID JAY,MORUGADO NILUS A
            PC   C07H21/04,A61K31/00,A61K31/00,A61K31/00,A61K31/70,A61K48/00,
            PC   C07H21/02,
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   68.4%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||       ||||||
Db         20 AAAAAAANNNNNNAAAAAA 2


RESULT 4408
I49618/c
LOCUS       I49618                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 33 from patent US 5641625.
ACCESSION   I49618
VERSION     I49618.1  GI:2471838
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and
            Mollegaard,N.E.
  TITLE     Cleaving double-stranded DNA with peptide nucleic acids
  JOURNAL   Patent: US 5641625-A 33 24-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   68.4%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||       ||||||
Db         20 AAAAAAANNNNNNAAAAAA 2


RESULT 4409
AR297173/c
LOCUS       AR297173                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 8908 from patent US 6537751.
ACCESSION   AR297173
VERSION     AR297173.1  GI:31684457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 8908 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1096 TGTTCATTTGGCT 1108
              |||||||||||||
Db         13 TGTTCATTTGGCT 1


RESULT 4410
AR074334/c
LOCUS       AR074334                  21 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 142 from patent US 5952490.
ACCESSION   AR074334
VERSION     AR074334.1  GI:10001089
KEYWORDS    .
SOURCE      Unknown.
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A17773
LOCUS       A17773                  20 bp    DNA     linear   PAT 30-SEP-1994
DEFINITION  Nucleotide sequence 12 from patent number EP0488900.
ACCESSION   A17773
VERSION     A17773.1  GI:641136
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Caput,D., Ferrara,P., Miloux,B., Minty,A. and Vita,N.
  TITLE     Protein with cytokine activity, recombinant DNA, expression vector
            and hosts for obtaining it
  JOURNAL   Patent: EP 0488900-A 12 03-JUN-1992;
            ELF SANOFI
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 4402
A29944
LOCUS       A29944                  20 bp    DNA     linear   PAT 23-JUN-1995
DEFINITION  Oligonucleotide primer sequence.
ACCESSION   A29944
VERSION     A29944.1  GI:1249025
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le
            Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
  TITLE     Protein having cytokin type activity, recombinant DNA coding for
            this protein, transformed cells and microorganisms
  JOURNAL   Patent: EP 0506574-A 17 30-SEP-1992;
            ELF SANOFI
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 4403
AR094462
LOCUS       AR094462                20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 20 from patent US 6001649.
ACCESSION   AR094462
VERSION     AR094462.1  GI:10021407
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Caput,D., Ferrara,P., Miloux,B., Minty,A. and Vita,N.
  TITLE     Chemokine NC28 (monocyte chemotactic protein-3, MCP-3) polypeptides
            and their recombinant production
  JOURNAL   Patent: US 6001649-A 20 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 4404
AR164799
LOCUS       AR164799                20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 6 from patent US 6274333.
ACCESSION   AR164799
VERSION     AR164799.1  GI:16237994
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Caput,D., Chalon,P., Ferrara,P. and Vita,N.
  TITLE     Type-2 neurotensin receptor (NT-R2)
  JOURNAL   Patent: US 6274333-A 6 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 4405
I58491
LOCUS       I58491                  20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 19 from patent US 5652123.
ACCESSION   I58491
VERSION     I58491.1  GI:2477729
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Caput,D., Ferrara,P., Guillemot,J.-C., Kaghad,M., Labit-Le
            Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
  TITLE     Protein having interleukin 13 activity, recombinant DNA coding for
            this protein, transformed cells and microorganisms
  JOURNAL   Patent: US 5652123-A 19 29-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
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COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/41
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAA 2797
              |||||||||||||
Db          6 GAAAAAAAAAAAA 18


RESULT 4399
BD145064
LOCUS       BD145064                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145064
VERSION     BD145064.1  GI:27850822
KEYWORDS    JP 2002119291-A/45.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 45 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/45
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAA 2797
              |||||||||||||
Db          6 GAAAAAAAAAAAA 18


RESULT 4400
BD166064
LOCUS       BD166064                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166064
VERSION     BD166064.1  GI:27871876
KEYWORDS    JP 2002191372-A/44.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 44 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/44
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13;  DB 1;  Length 18;
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAA 2797
              |||||||||||||
Db          6 GAAAAAAAAAAAA 18


RESULT 4401
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VERSION     BD096968.1  GI:22642556
KEYWORDS    JP 2001526063-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Sun,Y.
  TITLE     SAG:apoptosis sensitivity gene
  JOURNAL   Patent: JP 2001526063-A 3 18-DEC-2001;
            WARNER LAMBERT CO
COMMENT     OS   Unidentified
            PN   JP 2001526063-A/3
            PD   18-DEC-2001
            PF   15-DEC-1998 JP 2000525451
            PR   19-DEC-1997 US    60/068179,11-SEP-1998 US    60/099840 PI
            YI SUN
            PC   C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
            PC   A61P39/06,
            PC   A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12Q1/68,
            PC   G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   /desc = 'oligonucleotide P1 downstream primer' FH   Key
                 Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 4396
AR264964/c
LOCUS       AR264964                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 48 from patent US 6492121.
ACCESSION   AR264964
VERSION     AR264964.1  GI:29693351
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 48 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAA 2797
              |||||||||||||
Db         13 GAAAAAAAAAAAA 1


RESULT 4397
BD072905
LOCUS       BD072905                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072905
VERSION     BD072905.1  GI:22618508
KEYWORDS    JP 2001286300-A/43.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 43 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/43
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAA 2797
              |||||||||||||
Db          6 GAAAAAAAAAAAA 18


RESULT 4398
BD107532
LOCUS       BD107532                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107532
VERSION     BD107532.1  GI:23202350
KEYWORDS    JP 2002000275-A/41.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 41 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
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ACCESSION   BD176801
VERSION     BD176801.1  GI:29122513
KEYWORDS    WO 02074951-A/48.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 48 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/48
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         13 AAAAAAAAAAAAA 1


RESULT 4392
BD176802
LOCUS       BD176802                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176802
VERSION     BD176802.1  GI:29122514
KEYWORDS    WO 02074951-A/49.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 49 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/49
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2178
              |||||||||||||
Db          1 TTTTTTTTTTTTT 13


RESULT 4393
AR187059/c
LOCUS       AR187059                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2547 from patent US 6346398.
ACCESSION   AR187059
VERSION     AR187059.1  GI:20233024
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2547 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 4394
AR323669/c
LOCUS       AR323669                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1071 from patent US 6566127.
ACCESSION   AR323669
VERSION     AR323669.1  GI:33709477
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1071 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         17 AAAAAAAAAAAAA 5


RESULT 4395
BD096968/c
LOCUS       BD096968                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  SAG:apoptosis sensitivity gene.
ACCESSION   BD096968
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
  TITLE     Ibd-related polymorphisms
  JOURNAL   Patent: WO 0142511-A 1880 14-JUN-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
            Biotherapeutics Corporation (CA)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 28;
  Best Local Similarity   78.9%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||   || ||||||
Db         27 AAAAAAAANGGAAGAAAAAA 9


RESULT 4388
AR241806
LOCUS       AR241806                 14 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 94 from patent US 6472154.
ACCESSION   AR241806
VERSION     AR241806.1  GI:27287618
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 94 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTT 2178
              ||||||||||||
Db          1 TTTTTTTTTTTT 13


RESULT 4389
BD084126/c
LOCUS       BD084126                 14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION   BD084126
VERSION     BD084126.1  GI:22629736
KEYWORDS    JP 2001525663-A/14.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Polymorphisms and new genes in the region of the human
            hemochromatosis gene
  JOURNAL   Patent: JP 2001525663-A 14 11-DEC-2001;
            PROGENTIOR INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001525663-A/14
            PD   11-DEC-2001
            PF   30-SEP-1997 JP 1998516815
            PR   01-OCT-1996 US    08/724394,07-MAY-1997 US    08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC   Polymorphisms
            and new genes in the region of the human CC   hemochromatosis gene
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db         14 AAAAAAAAAAAAA 2


RESULT 4390
BD176797
LOCUS       BD176797                 14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176797
VERSION     BD176797.1  GI:29122509
KEYWORDS    WO 02074951-A/44.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 44 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/44
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2798
              |||||||||||||
Db          1 AAAAAAAAAAAAA 13


RESULT 4391
BD176801/c
LOCUS       BD176801                 14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||| |||| ||||| ||
Db         22 AAAACAAAACAAAAACAA 5


RESULT 4383
AX084400/c
LOCUS       AX084400                  23 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 6 from Patent WO0112830.
ACCESSION   AX084400
VERSION     AX084400.1  GI:13185851
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hallenbeck,P.L. and Chen,C.T.
  TITLE     Adenoviral vectors including dna sequences encoding angiogenic
            inhibitors
  JOURNAL   Patent: WO 0112830-A 6 22-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 23;
  Best Local Similarity   83.3%;  Pred. No. 4.5e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1970 TTTACCTTGAAAAAAAGA 1987
              |||||  ||||||||| |
Db         18 TTTACACTGAAAAAAAAA 1


RESULT 4384
AX494260/c
LOCUS       AX494260                  25 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 25 from Patent WO02059256.
ACCESSION   AX494260
VERSION     AX494260.1  GI:23339870
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 25 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTG 2193
              |||||||||||  ||  ||
Db         25 TTTTTTTTTTTGACAATG 8


RESULT 4385
AX494261/c
LOCUS       AX494261                  25 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 26 from Patent WO02059256.
ACCESSION   AX494261
VERSION     AX494261.1  GI:23339871
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 26 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTG 2193
              |||||||||||  ||  ||
Db         25 TTTTTTTTTTTGACAATG 8


RESULT 4386
AX494264/c
LOCUS       AX494264                  25 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 29 from Patent WO02059256.
ACCESSION   AX494264
VERSION     AX494264.1  GI:23339874
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 29 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 4.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTG 2193
              |||||||||||  ||  ||
Db         25 TTTTTTTTTTTGACAATG 8


RESULT 4387
AX184127/c
LOCUS       AX184127                  28 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 1880 from Patent WO0142511.
ACCESSION   AX184127
VERSION     AX184127.1  GI:15135467
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/5
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                   Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Aspergillus oryzae"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:5062"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1978 GAAAAAAAGAAAAGTGTG 1995
              ||||||||  |||||  ||
Db         21 GAAAAAAAAAAAAAGCTTG 4


RESULT 4380
BD206193/c
LOCUS       BD206193                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206193
VERSION     BD206193.1  GI:33015963
KEYWORDS    JP 2002515252-A/6.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 6 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/6
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                   Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Aspergillus oryzae"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:5062"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1978 GAAAAAAAGAAAAGTGTG 1995
              ||||||||  |||||  ||
Db         21 GAAAAAAAAAAAAAGCTTG 4


RESULT 4381
BD206194/c
LOCUS       BD206194                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206194
VERSION     BD206194.1  GI:33015964
KEYWORDS    JP 2002515252-A/7.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 7 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/7
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                   Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Aspergillus oryzae"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:5062"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1978 GAAAAAAAGAAAAGTGTG 1995
              ||||||||  |||||  ||
Db         21 GAAAAAAAAAAAAAGCTTG 4


RESULT 4382
A63568/c
LOCUS       A63568                    22 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 9 from Patent WO9720924.
ACCESSION   A63568
VERSION     A63568.1  GI:3717223
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Scaggiante,B. and Quadrifoglio,F.
  TITLE     A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMOURAL
            AGENTS
  JOURNAL   Patent: WO 9720924-A 9 12-JUN-1997;
            SAICOM S R L (IT)
COMMENT     Other publication IT MI952539 19970604
            Other publication AU 1175497 19970627.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="unidentified"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+03;
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  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 2 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1978 GAAAAAAAGAAAAGTGTG 1995
              ||||||||  |||||  ||
Db         21 GAAAAAAAAAAAAAGCTTG 4


RESULT 4375
AR003281/c
LOCUS       AR003281                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5744300.
ACCESSION   AR003281
VERSION     AR003281.1  GI:3964540
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 3 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1978 GAAAAAAAGAAAAGTGTG 1995
              ||||||||  |||||  ||
Db         21 GAAAAAAAAAAAAAGCTTG 4


RESULT 4376
I30190/c
LOCUS       I30190                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 19 from patent US 5580726.
ACCESSION   I30190
VERSION     I30190.1  GI:1820981
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 19 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1978 GAAAAAAAGAAAAGTGTG 1995
              ||||||||  |||||  ||
Db         21 GAAAAAAAAAAAAAGCTTG 4


RESULT 4377
I30191/c
LOCUS       I30191                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 20 from patent US 5580726.
ACCESSION   I30191
VERSION     I30191.1  GI:1820982
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 20 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1978 GAAAAAAAGAAAAGTGTG 1995
              ||||||||  |||||  ||
Db         21 GAAAAAAAAAAAAAGCTTG 4


RESULT 4378
I30192/c
LOCUS       I30192                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 21 from patent US 5580726.
ACCESSION   I30192
VERSION     I30192.1  GI:1820983
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 21 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1978 GAAAAAAAGAAAAGTGTG 1995
              ||||||||  |||||  ||
Db         21 GAAAAAAAAAAAAAGCTTG 4


RESULT 4379
BD206192/c
LOCUS       BD206192                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206192
VERSION     BD206192.1  GI:33015962
KEYWORDS    JP 2002515252-A/5.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 5 28-MAY-2002;
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            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="140F08"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .21
                     /note="T-DNA flanking sequence
                     left border"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||||| ||  |||||
Db         20 AAAAAAAAGAAGCAAAAA 3


RESULT 4371
AX521617/c
LOCUS       AX521617                 21 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 123 from Patent WO0222874.
ACCESSION   AX521617
VERSION     AX521617.1  GI:23572664
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Utermohlen,J.G. and Connaughton,J.
  TITLE     Oligonucleotides for labeling oligonucleotide probes and proteins
  JOURNAL   Patent: WO 0222874-A 123 21-MAR-2002;
            VENTANA MEDICAL SYSTEMS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide probe"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||| ||||| | |||||
Db         21 AAAAGAAAAATAGAAAAA 4


RESULT 4372
AR342463/c
LOCUS       AR342463                 21 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 13 from patent US 6576423.
ACCESSION   AR342463
VERSION     AR342463.1  GI:33737473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Batra,S.K., Brand,R.E., Ringel,J., Faulmann,G., Lohr,M. and
            Varshney,G.C.
  TITLE     Specific mucin expression as a marker for pancreatic cancer
  JOURNAL   Patent: US 6576423-A 13 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        718 CCTGTTGCTGCACGATCA 735
              |||| ||||| | |||||
Db         18 CCTGCTGCTGGATGATCA 1


RESULT 4373
AR003279/c
LOCUS       AR003279                 22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5744300.
ACCESSION   AR003279
VERSION     AR003279.1  GI:3964538
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 1 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 22;
  Best Local Similarity   83.3%;  Pred. No. 4.4e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1978 GAAAAAAAGAAAAGTGTG 1995
              |||||||| |||||  ||
Db         21 GAAAAAAAAAAAAGCTTG 4


RESULT 4374
AR003280/c
LOCUS       AR003280                 22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 2 from patent US 5744300.
ACCESSION   AR003280
VERSION     AR003280.1  GI:3964539
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
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            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        683 CAGATGGACGAGGTGCAG 700
              ||| | ||||||||||
Db         20 CAGGAGCACGAGGTGCAG 3


RESULT 4368
AJ590206
LOCUS       AJ590206                 20 bp    DNA     linear   PLN 23-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            565B12.
ACCESSION   AJ590206
VERSION     AJ590206.1  GI:37939830
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="565B12"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .20
                     /note="T-DNA flanking sequence
                     left border"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1757 TTTATTCATTAAGCTTTT 1774
              |||||| || | ||||||
Db          3 TTTATTTATGAGGCTTTT 20


RESULT 4369
AB068687/c
LOCUS       AB068687                 20 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, reverse primer for human STS sts-X82877 at
            1p36.
ACCESSION   AB068687
VERSION     AB068687.1  GI:15129491
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .20
                     /note="reverse primer for human STS sts-X82877 at 1p36
                     sts-X82877 obtained from clones B126K2, B288J19, B288I21,
                     Human BAC library RPCI-11"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1157 GCAGAATATTTAACCAGA 1174
              ||||||| || | |||||
Db         20 GCAGAATGTTGAGCCAGA 3


RESULT 4370
ATH527468/c
LOCUS       ATH527468                21 bp    DNA     linear   PLN 29-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            140F08.
ACCESSION   AJ527468
VERSION     AJ527468.1  GI:26795728
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
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KEYWORDS    WO 03000902-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Oikawa,H., Sassa,T. and Toyomasu,T.
  TITLE     Aphidicolin biosynthetic gene cluster
  JOURNAL   Patent: WO 03000902-A 17 03-JAN-2003;
            JAPAN SCIENCE AND TECHNOLOGY CORP,HIDEAKI OIKAWA,TAKESHI SASSA,
            TOMONOBU TOYOMASU
COMMENT     OS   Artificial Sequence
            PN   WO 03000902-A/17
            PD   03-JAN-2003
            PF   02-MAY-2002 WO 2002JP004381
            PR   21-JUN-2001 JP 01P   188465
            PI   HIDEAKI OIKAWA,TAKESHI SASSA,TOMONOBU TOYOMASU PC
            C12N15/52,C12N5/53,C12N9/02,C12P21/02,C12N1/21,C12N9/00,C12N9/ PC
            10,C12N15/54
            CC   Aphidicolin biosynthetic gene cluster
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1908 AGATCAACAATACCTTTT 1925
              ||||||| || ||||||
Db          1 AGATCAAGTATTCCTTTT 18


RESULT 4365
BD204803/c
LOCUS       BD204803                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel human chromosome 16 genes, compositions, methods of making
            and using same.
ACCESSION   BD204803
VERSION     BD204803.1  GI:33014573
KEYWORDS    JP 2002514903-A/34.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Landes,G.M., Burn,T.C., Connors,T.D., Dackowski,W.R., Raay,T.J.V.
            and Klinger,K.W.
  TITLE     Novel human chromosome 16 genes, compositions, methods of making
            and using same
  JOURNAL   Patent: JP 2002514903-A 34 21-MAY-2002;
            GENZYME CORP
COMMENT     OS   Synthetic construct
            PN   JP 2002514903-A/34
            PD   21-MAY-2002
            PF   16-JAN-1997 JP 1998502904
            PR   17-JUN-1996 US    08/665259,01-OCT-1996 US    08/720614 PR
            09-DEC-1996 US    08/762500
            PI   GREGORY M LANDES,TIMOTHY C BURN,TIMOTHY D CONNORS,WILLIAM R
            PI   DACKOWSKI,
            PI   TERENCE J VAN RAAY,KATHERINE W KLINGER
            PC   C12N15/12,C12N15/85,C07K14/47,C07K14/475,C07K16/18,A01K67/027
            CC   Oligonucleotide Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Synthetic construct'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        602 TCCGACCTGCTGCTGCCC 619
              | || ||||| |||||||
Db         19 TGCGGCCTGCGGCTGCCC 2


RESULT 4366
BD211411/c
LOCUS       BD211411                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Immunomodulator polypeptide ZSIG57.
ACCESSION   BD211411
VERSION     BD211411.1  GI:33021181
KEYWORDS    JP 2002518009-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sheppard,P.O.
  TITLE     Immunomodulator polypeptide ZSIG57
  JOURNAL   Patent: JP 2002518009-A 4 25-JUN-2002;
            ZYMOGENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002518009-A/4
            PD   25-JUN-2002
            PF   20-MAY-1999 JP 2000554849
            PR   18-JUN-1998 US    09/099600
            PI   PAUL O SHEPPARD
            PC   C12N15/09,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/08//(C12N1/19,C12R1:84),C12N15/00,C12N5/00 CC
            Oligonucleotide primer ZC16495
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        401 CTGGGGGAAGCGTACGCC 418
              ||| | ||| ||||||||
Db         20 CTGTGAGAAACGTACGCC 3


RESULT 4367
BD224921/c
LOCUS       BD224921                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224921
VERSION     BD224921.1  GI:33034691
KEYWORDS    JP 2002526095-A/56.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 56 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/56
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Qy        307 CCACACTGGAGTCGCCGA 324
              ||||||||  |||  ||||
Db          2 CCACACTGCAGTATCCGA 19


RESULT 4361
BD178842/c
LOCUS       BD178842                  20 bp    DNA     linear   PAT 16-APR-2003
DEFINITION  Gene panel for genes involving liver regeneration.
ACCESSION   BD178842
VERSION     BD178842.1  GI:30016109
KEYWORDS    WO 02077222-A/180.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Yokoya,F., Okutsu,T., Mori,M., Yoshiyuki, Takahara, Fukuda,H.,
            Aburatani,H. and Sonaka,I.
  TITLE     Gene panel for genes involving liver regeneration
  JOURNAL   Patent: WO 02077222-A 180 03-OCT-2002;
            AJINOMOTO CO INC,FUMIHIKO YOKOYA,TOMOHISA OKUTSU,MAIKO MORI,
            YOSHIYUKI TAKAHARA,HISAO FUKUDA,HIROYUKI ABURATANI,ICHIRO SONAKA
COMMENT     OS   Artificial Sequence
            PN   WO 02077222-A/180
            PD   03-OCT-2002
            PF   13-MAR-2002 WO 2002JP002372
            PR   13-MAR-2001 JP 01P   070940
            PI   FUMIHIKO YOKOYA,TOMOHISA OKUTSU,MAIKO MORI,YOSHIYUKI PI
            TAKAHARA,HISAO FUKUDA,
            PI   HIROYUKI ABURATANI,ICHIRO SONAKA
            PC   C12N15/09,C12Q1/68,G01N33/15,G01N33/50,G01N37/00 CC
            Description of Artificial Sequence: primer
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        770 AAGAACCCTCTGAACCTC 787
              |||||  ||||||||  | |
Db         19 AAGAAGCCTCTGAAGCCC 2


RESULT 4362
BD179443/c
LOCUS       BD179443                  20 bp    DNA     linear   PAT 16-APR-2003
DEFINITION  Genomic DNA participating in rheumatoid arthritis, method of
            diagnosing the same, method of judging the onset risk of the same
            and diagnostic for detecting the same.
ACCESSION   BD179443
VERSION     BD179443.1  GI:30016761
KEYWORDS    WO 02079466-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shiozawa,S., Komai,K., Yagi,H. and Matsuura,N.
  TITLE     Genomic DNA participating in rheumatoid arthritis, method of
            diagnosing the same, method of judging the onset risk of the same
            and diagnostic for detecting the same
  JOURNAL   Patent: WO 02079466-A 8 10-OCT-2002;
            SHUNICHI SHIOZAWA,KOICHIRO KOMAI,HIROFUMI YAGI,NAO MATSUURA
COMMENT     OS   Artificial Sequence
            PN   WO 02079466-A/8
            PD   10-OCT-2002
            PF   29-MAR-2002 WO 2002JP003191
            PR   30-MAR-2001 JP 01P   102006
            PI   SHUNICHI SHIOZAWA,KOICHIRO KOMAI,HIROFUMI YAGI,NAO MATSUURA PC
              C12N15/09,C12Q1/68,G01N33/566,G01N33/50
            CC   Synthesized oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1730 TTATCAGAAGGTGACAAG 1747
              |||  ||  |||||||  |||
Db         18 TTACCACAAGGTGAGAAG 1


RESULT 4363
BD182024
LOCUS       BD182024                  20 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Polypeptide serving as angiogenic marker and DNA thereof.
ACCESSION   BD182024
VERSION     BD182024.1  GI:30792942
KEYWORDS    WO 02090546-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sato,Y., Sonoda,H. and Ota,H.
  TITLE     Polypeptide serving as angiogenic marker and DNA thereof
  JOURNAL   Patent: WO 02090546-A 4 14-NOV-2002;
            SHIONOGI AND CO LTD,YASUFUMI SATO,HIKARU SONODA,HIDEKI OTA
COMMENT     OS   Artificial Sequence
            PN   WO 02090546-A/4
            PD   14-NOV-2002
            PF   26-APR-2002 WO 2002JP004251
            PR   07-MAY-2001 JP 01P   136179
            PI   YASUFUMI SATO,HIKARU SONODA,HIDEKI OTA
            PC   C12N15/12,C12Q1/68,A61K38/02,A61P35/00,A61P43/00,A61K39/395,
            PC   A61P9/00,
            PC   A61P27/02,A61P29/00,A61P15/00,G01N33/574,G01N33/50,G01N33/15,
            PC   G01N33/566
            CC   Description of Artificial Sequence:primer2
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2419 GTAAATACTGGTGCACTT 2436
              ||  |||||||  ||  ||||
Db          1 GTCAATACTGATGGACTT 18


RESULT 4364
BD189560
LOCUS       BD189560                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Aphidicolin biosynthetic gene cluster.
ACCESSION   BD189560
VERSION     BD189560.1  GI:32999299
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            PR   05-FEB-1998 US    60/073767
            PI   QINGYUN LIU,TERENCE MACDONALD,TIMOTHY P
            BONNERT,GORDON YU QUAN
            PI   NG,
            PI   LEE F KOLAKOWSKI JR,JANET CLARK,TOM I BONNER
            PC   C07K14/705,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/09, PC
            C12P21/02,
            PC   G01N33/53,G01N33/566,C12N5/00,C12N15/00
            CC   Novel GABAB receptor DNA sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        657 ACCTGGGGCTCCACGACA 674
              ||||| ||||| | ||||
Db         19 ACCTGCGGCTCTATGACA 2


RESULT 4358
BD136467/c
LOCUS       BD136467                 20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Antisense modulation of PECAM-1.
ACCESSION   BD136467
VERSION     BD136467.1  GI:23231412
KEYWORDS    JP 2002506659-A/46.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,F.C., Condon,T.P., Flournoy,S.C. and Zhang,H.
  TITLE     Antisense modulation of PECAM-1
  JOURNAL   Patent: JP 2002506659-A 46 05-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002506659-A/46
            PD   05-MAR-2002
            PF   18-MAR-1999 JP 2000536890
            PR   19-MAR-1998 US    09/044506
            PI   FRANK C BENNETT,THOMAS P CONDON,SHIN CHENG FLOURNOY,HONG ZHANG
            PC   C12Q1/68,A61K31/711,A61K48/00,A61P1/04,A61P9/00,A61P19/02, PC
             A61P29/00,
            PC   A61P35/00,A61P37/06,A61P43/00,C12N15/09,C12P19/34,C12N15/00 CC
              Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense modulation of PECAM-1
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2628 TGTCTCGTTCCTGTTGGG 2645
              || || |||| |||||||
Db         18 TGCCTTGTTCATGTTGGG 1


RESULT 4359
BD175161/c
LOCUS       BD175161                 20 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Random insertion and deletion DNA mutagenesis.
ACCESSION   BD175161
VERSION     BD175161.1  GI:29120855
KEYWORDS    JP 2002253255-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shishido,M., Yoshisaka,T. and Murakami,H.
  TITLE     Random insertion and deletion DNA mutagenesis
  JOURNAL   Patent: JP 2002253255-A 5 10-SEP-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002253255-A/5
            PD   10-SEP-2002
            PF   01-MAR-2001 JP 2001057478
            PI   MASAHIKO SHISHIDO,TAKAHIRO YOSHISAKA,HIROSHI MURAKAMI PC
            C12N15/09,C12P21/02,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: 3' anchor FH   Key
                Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        307 CCACACTGGAGTCGCCGA 324
              |||||||| |||  ||||
Db         19 CCACACTGCAGTATCCGA 2


RESULT 4360
BD175163
LOCUS       BD175163                 20 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Random insertion and deletion DNA mutagenesis.
ACCESSION   BD175163
VERSION     BD175163.1  GI:29120857
KEYWORDS    JP 2002253255-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shishido,M., Yoshisaka,T. and Murakami,H.
  TITLE     Random insertion and deletion DNA mutagenesis
  JOURNAL   Patent: JP 2002253255-A 7 10-SEP-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002253255-A/7
            PD   10-SEP-2002
            PF   01-MAR-2001 JP 2001057478
            PI   MASAHIKO SHISHIDO,TAKAHIRO YOSHISAKA,HIROSHI MURAKAMI PC
            C12N15/09,C12P21/02,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: Biotin labeled primer CC
            BIotin-labeled deoxythymidine
            FH   Key             Location/Qualifiers
            FT   modified_base   (1).
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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            PF   23-APR-1998 JP 1998546351
            PR   23-APR-1997 US    08/842385
            PI   PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA

            PI   N FRIEDMAN,
            PI   JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R  PI
             KLASS,
            PI   JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D
            PI   STROUPE
            PC   C12Q1/68,C07K14/47,C12N5/10,C07K16/00,G01N33/574,A61K38/17 CC
             Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Chlamydia sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:35827"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        546 ACCTCTCCGGGCTGGAGG 563
              | | || ||||||||||
Db         18 AACACTGCGGGCTGGAGG 1


RESULT 4355
BD107224/c
LOCUS       BD107224                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Base sequence for detecting Lactobacillus bacteria and Pediococcus
            bacteria, and method for detecting these bacteria.
ACCESSION   BD107224
VERSION     BD107224.1  GI:23202042
KEYWORDS    JP 2002034578-A/69.
SOURCE      Pediococcus damnosus
  ORGANISM  Pediococcus damnosus
            Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
            Pediococcus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Yasuhara,T., Takahashi,K. and Motoyama,Y.
  TITLE     Base sequence for detecting Lactobacillus bacteria and Pediococcus
            bacteria, and method for detecting these bacteria
  JOURNAL   Patent: JP 2002034578-A 69 05-FEB-2002;
            ASAHI BREWERIES LTD
COMMENT     OS   Pediococcus damnosus
            PN   JP 2002034578-A/69
            PD   05-FEB-2002
            PF   31-JUL-2000 JP 2000230241
            PI   TAKAOMI YASUHARA,KYOKO TAKAHASHI,YASURO MOTOYAMA PC
            C12N15/09,C12Q1/68//(C12Q1/68,C12R1:24),(C12Q1/68,C12R1:25), PC
            (C12Q1/68,C12R1:225),(C12Q1/68,C12R1:01),C12N15/00 CC   Base
            sequence for detecting Lactobacillus bacteria and  CC
            Pediococcus
            CC   bacteria, and method for detecting these bacteria FH   Key
                    Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Pediococcus damnosus'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Pediococcus damnosus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:51663"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2126 AACTTGTAGAAACGAAGC 2143
              || ||| ||||||| |||
Db         18 AAGTTGAAGAAACGGAGC 1


RESULT 4356
BD123448/c
LOCUS       BD123448                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Stress-responsive gene and method of detecting stress by using
            stress-responsive gene.
ACCESSION   BD123448
VERSION     BD123448.1  GI:23218393
KEYWORDS    JP 2002017355-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wariishi,H., Tanaka,H., Kurihara,H. and Okada,K.
  TITLE     Stress-responsive gene and method of detecting stress by using
            stress-responsive gene
  JOURNAL   Patent: JP 2002017355-A 4 22-JAN-2002;
            HIROYUKI WARIISHI,KUBOTA CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002017355-A/4
            PD   22-JAN-2002
            PF   30-JUN-2000 JP 2000199783
            PI   HIROYUKI WARIISHI,HIROO TANAKA,HIROMASA KURIHARA,KOICHI OKADA
            PC
            C12N15/09,C12N1/19,C12N1/21,C12N9/02,C12Q1/68,G01N33/00,G01N33/ PC
             15,
            PC
            G01N33/50,G01N33/53//(C12N15/09,C12R1:645),(C12N9/02,C12R1:645) PC
            ,
            PC   (C12Q1/68,C12R1:645),C12N15/00,(C12N15/00,C12R1:645) CC
            Stress-responsive gene and method of detecting stress by using CC
            stress-responsive gene
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        900 CTGAAGTACAGAGGCGAC 917
              | ||| |||||| |||||
Db         19 CAGAAATACAGACGCGAC 2


RESULT 4357
BD124115/c
LOCUS       BD124115                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel GABAB receptor DNA sequence.
ACCESSION   BD124115
VERSION     BD124115.1  GI:23219060
KEYWORDS    JP 2002502859-A/12.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Liu,Q., Macdonald,T., Bonnert,T.P., Ng,G.Y.Q., Jr,L.F.K., Clark,J.
            and Bonner,T.I.
  TITLE     Novel GABAB receptor DNA sequence
  JOURNAL   Patent: JP 2002502859-A 12 29-JAN-2002;
            MERCK & CO INC,MERCK FROST CANADA & CO, UNIVERSITY OF TEXAS HEALTH
            SCIENCE CENTER AT SAN ANTONIO, NATIONAL INSTITUTES OF HEALTH,MERCK
            SHARP & DOHME LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002502859-A/12
            PD   29-JAN-2002
            PF   03-FEB-1999 JP 2000530542
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DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065669
VERSION     BD065669.1  GI:22611272
KEYWORDS    JP 2001511000-A/304.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 304 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/304
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unknown'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        160 GGACGCCATGTTGTGGAA 177
              |||| | || ||||||||
Db         20 GGACACGATTTTGTGGAA 3


RESULT 4352
BD082177/c
LOCUS       BD082177                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Vascular endothelial growth factor C (VEGF-C) protein and gene,
            mutants thereof, and uses thereof.
ACCESSION   BD082177
VERSION     BD082177.1  GI:22627787
KEYWORDS    JP 2001523951-A/23.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Alitalo,K. and Joukov,V.
  TITLE     Vascular endothelial growth factor C (VEGF-C) protein and gene,
            mutants thereof, and uses thereof
  JOURNAL   Patent: JP 2001523951-A 23 27-NOV-2001;
            THE LUDWIG INSTITUTE FOR CANCER RESEARCH, HELSINKI UNIVERSITY
            LICENSING LTD
COMMENT     PN   JP 2001523951-A/23
            PD   27-NOV-2001
            PF   02-FEB-1998 JP 1998533178
            PR   05-FEB-1997 US    08/795430
            PI   KARI ALITALO,VLADIMIR JOUKOV
            PC   C12N15/12,C07K14/52,C12N15/10,C07K16/24,C12Q1/68,C12N15/62, PC
                 G01N33/50,
            PC   A01K67/027
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Zea mays"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:4577"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2593 TTAATTGAAACTCTCTGT 2610
              |||||| | |||| ||||
Db         20 TTAATTCATACTCACTGT 3


RESULT 4353
BD087972/c
LOCUS       BD087972                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD087972
VERSION     BD087972.1  GI:22633582
KEYWORDS    JP 2001321190-A/216.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 216 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/216
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
                 C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                  Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1157 GCAGAATATTTAACCAGA 1174
              ||||||| || | |||||
Db         20 GCAGAATGTTGAGCCAGA 3


RESULT 4354
BD106449/c
LOCUS       BD106449                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Reagents and methods useful for detecting diseases of the prostate.
ACCESSION   BD106449
VERSION     BD106449.1  GI:23201267
KEYWORDS    JP 2002503956-A/16.
SOURCE      Chlamydia sp.
  ORGANISM  Chlamydia sp.
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
            Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,
            Russell,J.C. and Stroupe,S.D.
  TITLE     Reagents and methods useful for detecting diseases of the prostate
  JOURNAL   Patent: JP 2002503956-A 16 05-FEB-2002;
            ABBOTT LABORATORIES
COMMENT     PN   JP 2002503956-A/16
            PD   05-FEB-2002
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Ag2954 Forward"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        328 TCAGCCGCCACCCTACTT 345
              |||||| | ||||| |||
Db          3 TCAGCCACTACCCTCCTT 20


RESULT 4348
BD013225/c
LOCUS       BD013225                  20 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  P21(cip1) used for treatment of rheumatoid arthritis.
ACCESSION   BD013225
VERSION     BD013225.1  GI:22093414
KEYWORDS    WO 0121793-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Miyasaka,N. and Kosaka,H.
  TITLE     P21(cip1) used for treatment of rheumatoid arthritis
  JOURNAL   Patent: WO 0121793-A 6 29-MAR-2001;
            NOBUYUKI MIYASAKA,HITOSHI KOSAKA
COMMENT     OS   Artificial Sequence
            PN   WO 0121793-A/6
            PD   29-MAR-2001
            PF   22-SEP-2000 WO 2000JP006511
            PR   22-SEP-1999 JP 99P   269579
            PI   NOBUYUKI MIYASAKA,HITOSHI KOSAKA
            PC   C12N15/12,C12Q1/68,C12N9/12,C07K14/47,A61K45/00,A61K38/17, PC
             A61P29/00,
            PC   A61P19/02,A61P43/00,G01N33/50,G01N33/15
            CC   Description of Artificial Sequence: artificially synthesized
            primer
            CC            A61P29/00,
            CC   sequence
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        896 GTGGCTGAAGTACAGAGG 913
              | |||||||||| |||| |
Db         18 GAGGCTGAAGTTCAGATG 1


RESULT 4349
BD013841/c
LOCUS       BD013841                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Lentivirus belonging to the group of Mandrillus leucophaeus
            immunodeficiency virus and utilization thereof.
ACCESSION   BD013841
VERSION     BD013841.1  GI:22554170
KEYWORDS    JP 2001103983-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Guertler,L.G., Hauser,H.P., Deroco,I.B.D., Zekeng,L. and Kaptue,L.
  TITLE     Lentivirus belonging to the group of Mandrillus leucophaeus
            immunodeficiency virus and utilization thereof
  JOURNAL   Patent: JP 2001103983-A 1 17-APR-2001;
            DADE BEHRING MARBURG GMBH
COMMENT     OS   Unknown
            PN   JP 2001103983-A/1
            PD   17-APR-2001
            PF   03-AUG-2000 JP 2000236066
            PR   03-AUG-1999 DE   19936003.0
            PI   LUTZ GARHALT GUERTLER,HANS PATER HAUSER,IBETT BEATRIS DOMMO
            PI   DEROCO,
            PI   LEOPOLD ZEKENG,LAZARE KAPTUE
            PC
            C12N15/09,C07K14/155,C12N7/02,G01N33/569,G06F17/30//(C12N15/09, PC
             C12R1:93),
            PC   (C12N7/02,C12R1:93),C12N15/00,(C12N15/00,C12R1:93) CC
            description of the unknown organism: primer,non-genomic DNA FH
            Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unknown'.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2442 GACTTTTTTGAGACATGG 2459
              ||| |||| || ||||||
Db         19 GACATTTTGGACACATGG 2


RESULT 4350
BD061540/c
LOCUS       BD061540                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for detecting Rett symdrome and detection kit.
ACCESSION   BD061540
VERSION     BD061540.1  GI:22607145
KEYWORDS    JP 2001292775-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Yamakawa,K.
  TITLE     Method for detecting Rett symdrome and detection kit
  JOURNAL   Patent: JP 2001292775-A 7 23-OCT-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
COMMENT     OS   Artificial Sequence
            PN   JP 2001292775-A/7
            PD   23-OCT-2001
            PF   11-APR-2000 JP 2000109638
            PI   KAZUHIRO YAMAKAWA
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Synthetic DNA, forward primer for exon 3 amplification FH
            Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1677 TGGACTTCTTAGTTGTTT 1694
              ||| |||||||| || ||
Db         18 TGGGCTTCTTAGGTGGTT 1


RESULT 4351
BD065669/c
LOCUS       BD065669                  20 bp    DNA     linear   PAT 27-AUG-2002
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AX804914
LOCUS       AX804914                 20 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 1082 from Patent WO03060160.
ACCESSION   AX804914
VERSION     AX804914.1  GI:38522055
KEYWORDS    .
SOURCE      Oreochromis niloticus (Nile tilapia)
  ORGANISM  Oreochromis niloticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Labroidei; Cichlidae; Oreochromis.
REFERENCE   1
  AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
  TITLE     Verification of food origin based on nucleic acid pattern
            recognition
  JOURNAL   Patent: WO 03060160-A 1082 24-JUL-2003;
            Genomar ASA (NO)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oreochromis niloticus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:8128"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        903 AAGTACAGAGGCGACTGT 920
              ||||  |||||| |||||
Db          3 AAGTTGAGAGGCTACTGT 20


RESULT 4344
AX814089/c
LOCUS       AX814089                 20 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 12 from Patent EP1334979.
ACCESSION   AX814089
VERSION     AX814089.1  GI:39103391
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Vossen,E.A. and Allefs,J.J.
  TITLE     Gene conferring resistance to phytophthera infestans (late-blight)
            in solanaceae
  JOURNAL   Patent: EP 1334979-A 12 13-AUG-2003;
            Kweek-en Researchbedrijf Agrico B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: reverse primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2566 CTCTGTTCTTGGCTTGGA 2583
              ||| |||| ||||||| |
Db         20 CTCGGTTCCTGGCTTGAA 3


RESULT 4345
AX816308/c
LOCUS       AX816308                 20 bp    DNA     linear   PAT 09-DEC-2003
DEFINITION  Sequence 25 from Patent WO03066675.
ACCESSION   AX816308
VERSION     AX816308.1  GI:39646799
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Allefs,J.J. and van der Vossen,E.A.
  TITLE     Gene conferring resistance to phytophthera infestans (late-blight)
            in solanaceae
  JOURNAL   Patent: WO 03066675-A 25 14-AUG-2003;
            Kweek- en Researchbedrijf Agrico B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: reverse primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2566 CTCTGTTCTTGGCTTGGA 2583
              ||| |||| ||||||| |
Db         20 CTCGGTTCCTGGCTTGAA 3


RESULT 4346
AX840550
LOCUS       AX840550                 20 bp    DNA     linear   PAT 16-DEC-2003
DEFINITION  Sequence 94 from Patent WO03077643.
ACCESSION   AX840550
VERSION     AX840550.1  GI:39978785
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bauer,J.
  TITLE     Methods for increasing the oil content in plants
  JOURNAL   Patent: WO 03077643-A 94 25-SEP-2003;
            BASF Plant Science GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen Sequenz: sequence
                     motive from plant storage protein"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2449 TTGAGACATGGGATCCAA 2466
              |||||||||| | || |
Db          2 TTGAGACATGGAACCCTA 19


RESULT 4347
AX922669
LOCUS       AX922669                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1009 from Patent WO02068649.
ACCESSION   AX922669
VERSION     AX922669.1  GI:40215619
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   .
  JOURNAL   Patent: WO 02068649-A 1009 06-SEP-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct; forward primer (1) for the
                     amplification of sequences containing the N-terminal
                     ankyrin capping module"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        593 TACCGCCGCTCCGACCTG 610
              | |||| | |||||||||
Db          1 TTCCGCGGATCCGACCTG 18


RESULT 4339
AX797528
LOCUS       AX797528                 20 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 13 from Patent WO03050302.
ACCESSION   AX797528
VERSION     AX797528.1  GI:37518031
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hayes,I., Cotter,T., Murphy,F. and Seery,L.
  TITLE     Tgnp
  JOURNAL   Patent: WO 03050302-A 13 19-JUN-2003;
            Eirx Therapeutics Ltd (IE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        280 CCTCTACAGCCCCGCGCC 297
              ||||| ||| ||||| ||
Db          1 CCTCTCCAGTCCCGCCCC 18


RESULT 4340
AX803658
LOCUS       AX803658                 20 bp    DNA     linear   PAT 24-NOV-2003
DEFINITION  Sequence 21 from Patent EP1331267.
ACCESSION   AX803658
VERSION     AX803658.1  GI:38502200
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Frank,B.L., Goodchild,J., Hamlin,H.A., Kulkuskie,R.E.,
            Roberts,P.C., Roberts,N.A., Walther,D.M. and Wolfe,J.L.
  TITLE     Oligonucleotides specific for Hepatitis C Virus
  JOURNAL   Patent: EP 1331267-A 21 30-JUL-2003;
            HYBRIDON, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        113 GGCTGGGGGGATCCTGGA 130
              || |||||| |||||||
Db          3 GGGAGGGGGGGTCCTGGA 20


RESULT 4341
AX804495
LOCUS       AX804495                 20 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 663 from Patent WO03060160.
ACCESSION   AX804495
VERSION     AX804495.1  GI:38521636
KEYWORDS    .
SOURCE      Oreochromis niloticus (Nile tilapia)
  ORGANISM  Oreochromis niloticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Labroidei; Cichlidae; Oreochromis.
REFERENCE   1
  AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
  TITLE     Verification of food origin based on nucleic acid pattern
            recognition
  JOURNAL   Patent: WO 03060160-A 663 24-JUL-2003;
            Genomar ASA (NO)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oreochromis niloticus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:8128"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1786 CCCATTCTTTCCTTCTCT 1803
              | | ||||| ||||||||
Db          3 CGCCTTCTTCCCTTCTCT 20


RESULT 4342
AX804884
LOCUS       AX804884                 20 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 1052 from Patent WO03060160.
ACCESSION   AX804884
VERSION     AX804884.1  GI:38522025
KEYWORDS    .
SOURCE      Oreochromis niloticus (Nile tilapia)
  ORGANISM  Oreochromis niloticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Labroidei; Cichlidae; Oreochromis.
REFERENCE   1
  AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
  TITLE     Verification of food origin based on nucleic acid pattern
            recognition
  JOURNAL   Patent: WO 03060160-A 1052 24-JUL-2003;
            Genomar ASA (NO)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oreochromis niloticus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:8128"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2709 TCTCTGCCTGTAAATGTT 2726
              |||||||||||    ||||
Db          1 TCTCTGCCTGTGTCTGTT 18


RESULT 4343
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RESULT 4334
AX671164/c
LOCUS       AX671164                  20 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 4 from Patent WO03004511.
ACCESSION   AX671164
VERSION     AX671164.1  GI:29329620
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Renzi,P., Allam,M. and Allakhverdi,Z.
  TITLE     Methods for increasing in vivo efficacy of oligonucleotides and
            inhibiting inflammation in mammals
  JOURNAL   Patent: WO 03004511-A 4 16-JAN-2003;
            Topigen Pharmaceutiques Inc (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence is completely synthesized"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        548 CTCTCCGGGCTGGAGGCG 565
              |||| |||||||  ||||
Db         18 CTCTGCGGGCTGTGGGCG 1


RESULT 4335
AX696916/c
LOCUS       AX696916                  20 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 533 from Patent EP1283264.
ACCESSION   AX696916
VERSION     AX696916.1  GI:29420029
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Bauer,S.C., Abrams,M.A., Braford-Goldberg,S.R., Caparon,M.H.,
            Easton,A.M., Klein,B.K., Mckearn,J.P., Olins,P.O., Paik,K.,
            Polazzi,J.O. and Thomas,J.W.
  TITLE     Interleukin-3 (il-3) mutant polypeptides
  JOURNAL   Patent: EP 1283264-A 533 12-FEB-2003;
            G.D. SEARLE & CO. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1241 TGTAAAGAATTCACAGAA 1258
              ||| |||| || ||||||
Db         18 TGTCAAGAGTTTACAGAA 1


RESULT 4336
AX700802
LOCUS       AX700802                  20 bp    DNA     linear   PAT 03-APR-2003
DEFINITION  Sequence 12 from Patent WO03012084.
ACCESSION   AX700802
VERSION     AX700802.1  GI:29536598
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Perfetti,R.
  TITLE     Human glucose-dependent insulin-secreting cell line
  JOURNAL   Patent: WO 03012084-A 12 13-FEB-2003;
            Cedars-Sinai Medical Center (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        394 CTCGCATCTGGGGGAAGC 411
              ||| || |||| ||||||
Db          1 CTCACACCTGGTGGAAGC 18


RESULT 4337
AX721749
LOCUS       AX721749                  20 bp    DNA     linear   PAT 07-MAY-2003
DEFINITION  Sequence 128 from Patent EP1298221.
ACCESSION   AX721749
VERSION     AX721749.1  GI:30422340
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: EP 1298221-A 128 02-APR-2003;
            PrimaGen Holding B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer 3'TAG011GENE-2"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2527 ATATATATACAGGGTATT 2544
              |||||| |||||| || |
Db          3 ATATATTTACAGGATAGT 20


RESULT 4338
AX756534
LOCUS       AX756534                  20 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 48 from Patent WO0220565.
ACCESSION   AX756534
VERSION     AX756534.1  GI:32251132
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stumpp,M.T., Forrer,P., Binz,H.K. and Plueckthun,A.
  TITLE     Collections of repeat proteins comprising repeat modules
  JOURNAL   Patent: WO 0220565-A 48 14-MAR-2002;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
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           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 4708 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        415 CGCCGCCGCCATCAACCC 432
              | ||||||||||| | |||
Db          1 CCCCGCCGCCATTACCCC 18


RESULT 4330
AX613762
LOCUS       AX613762                  20 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 4787 from Patent WO02072882.
ACCESSION   AX613762
VERSION     AX613762.1  GI:28409191
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 4787 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1584 GCACAGACTGGGAACCCC 1601
              | || |||||||||| ||
Db          1 GGACTGACTGGGAACTCC 18


RESULT 4331
AX613782
LOCUS       AX613782                  20 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 4807 from Patent WO02072882.
ACCESSION   AX613782
VERSION     AX613782.1  GI:28409211
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 4807 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1389 CGGTGTCTGCCCTGCAGA 1406
              | ||| |||||| |||||
Db          3 CTGTGCCTGCCCCGCAGA 20


RESULT 4332
AX613806
LOCUS       AX613806                  20 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 4831 from Patent WO02072882.
ACCESSION   AX613806
VERSION     AX613806.1  GI:28409235
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 4831 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2439 TACGACTTTTTTGAGACA 2456
              || ||||| || ||||||
Db          1 TAGGACTTATTGGAGACA 18


RESULT 4333
AX662935/c
LOCUS       AX662935                  20 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 22 from Patent WO02066681.
ACCESSION   AX662935
VERSION     AX662935.1  GI:29163516
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Poole,J., Roninson,I.B. and Chang,B.D.
  TITLE     Reagents and methods for identifying and modulating expression of
            genes regulated by cdk inhibitors
  JOURNAL   Patent: WO 02066681-A 22 29-AUG-2002;
            THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Antisense PCR primer for CC3 promoter (spec Table
                     IIIa)"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        536 CTACTGCCCCACCTCTCC 553
              |||||  |||||||| ||
Db         20 CTACTAACCCACCTCCCC 3
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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2661 AGTGTGCAGTACAGTGTG 2678
              | |||||||||| ||||
Db         19 ATTGTGCAGTACTTTGTG 2


RESULT 4325
AX555049/c
LOCUS       AX555049                 20 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 12 from Patent WO0233128.
ACCESSION   AX555049
VERSION     AX555049.1  GI:25898604
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stuyver,L. and Watanabe,K.A.
  TITLE     Multiplex quantification of nucleic acids in diseased cells
  JOURNAL   Patent: WO 0233128-A 12 25-APR-2002;
            Pharmasset, Ltd. (BB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonulceotide (probe) used to detect HCV viral .
                     load"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        113 GGCTGGGGGGATCCTGGA 130
              ||  |||||| |||||||
Db         20 GGGAGGGGGGGTCCTGGA 3


RESULT 4326
AX587369
LOCUS       AX587369                 20 bp    DNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 145 from Patent WO0236761.
ACCESSION   AX587369
VERSION     AX587369.1  GI:27656234
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   D'Andrea,A.D., Taniguchi,T., Timmers,C. and Grompe,M.
  TITLE     Methods and compositions for the diagnosis of cancer
            susceptibilities and defective dna repair mechanisms and treatment
            thereof
  JOURNAL   Patent: WO 0236761-A 145 10-MAY-2002;
            DANA FARBER CANCER INSTITUTE (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="MG779"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1917 ATACCTTTTTTTTCAGTG 1934
              ||||||| |||| | |||
Db          2 ATACCTTCTTTTGCTGTG 19


RESULT 4327
AX613368/c
LOCUS       AX613368                 20 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 4393 from Patent WO02072882.
ACCESSION   AX613368
VERSION     AX613368.1  GI:28408797
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 4393 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1388 GCGGTGTCTGCCCTGCAG 1405
              |||||| ||  |||||||
Db         19 GCGGTGGCTTACCTGCAG 2


RESULT 4328
AX613661
LOCUS       AX613661                 20 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 4686 from Patent WO02072882.
ACCESSION   AX613661
VERSION     AX613661.1  GI:28409090
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 4686 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        264 CCTCCGCCGGGCAGCACC 281
              ||||| || | |||||||
Db          2 CCTCCCCCCGTCAGCACC 19


RESULT 4329
AX613683
LOCUS       AX613683                 20 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 4708 from Patent WO02072882.
ACCESSION   AX613683
VERSION     AX613683.1  GI:28409112
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DEFINITION  Sequence 222 from Patent WO0220847.
ACCESSION   AX526507
VERSION     AX526507.1  GI:25171314
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,
            Lusis,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
  TITLE     Gene and sequence variation associated with lipid disorder
  JOURNAL   Patent: WO 0220847-A 222 14-MAR-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2251 AAGCTTTATTTGCATATT 2268
              |||| | |||||||| ||
Db          1 AAGCCTCATTTGCATGTT 18


RESULT 4321
AX530262/c
LOCUS       AX530262                 20 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 2 from Patent WO02056909.
ACCESSION   AX530262
VERSION     AX530262.1  GI:25173208
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Reynaud,C.A. and Weill,J.C.
  TITLE     Method for inducing an immune response to polysaccharide bacterial
            antigens and to protein structures of virus capsids
  JOURNAL   Patent: WO 02056909-A 2 25-JUL-2002;
            Institut Necker (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="amorce nucleotidique"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         73 CCTGGTCACCGTGACCCC 90
              |||||||||||  || |
Db         19 CCTGGTCACCGTCTCCTC 2


RESULT 4322
AX535424/c
LOCUS       AX535424                 20 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 34 from Patent WO02070736.
ACCESSION   AX535424
VERSION     AX535424.1  GI:25262138
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,W., Mundlein,A., Huber,M. and Kroath,H.
  TITLE     Method for the detection of nucleic acid molecules
  JOURNAL   Patent: WO 02070736-A 34 12-SEP-2002;
            Austrian Research Centers GmbH - ARC (AT)
FEATURES             Location/Qualifiers
     source          1. .20
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Oligonukleotid"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        212 GAGGATCGCCACGACGGG 229
              |||||||  || ||||||
Db         18 GAGGATCCACAGGACGGG 1


RESULT 4323
AX546284/c
LOCUS       AX546284                 20 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 33 from Patent EP1243290.
ACCESSION   AX546284
VERSION     AX546284.1  GI:25811475
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Besterman,J.M., Macleod,A.R. and Siders,W.M.
  TITLE     Modulation of gene expression by combination therapy
  JOURNAL   Patent: EP 1243290-A 33 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2661 AGTGTGCAGTACAGTGTG 2678
              | ||||||||||  ||||
Db         19 ATTGTGCAGTACTTTGTG 2


RESULT 4324
AX546374/c
LOCUS       AX546374                 20 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 33 from Patent EP1243289.
ACCESSION   AX546374
VERSION     AX546374.1  GI:25811565
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Besterman,J.M., Macleod,A.R. and Siders,W.M.
  TITLE     Modulation of gene expression by combination therapy
  JOURNAL   Patent: EP 1243289-A 33 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
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  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: EP 1225233-A 126 24-JUL-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3'TAG011GENE-2"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2527 ATATATATACAGGGTATT 2544
              |||||| |||||| || |
Db          3 ATATATTTACAGGATAGT 20


RESULT 4316
AX488382/c
LOCUS       AX488382                 20 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 5682 from Patent WO02053728.
ACCESSION   AX488382
VERSION     AX488382.1  GI:22322462
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 5682 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Candida albicans"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:5476"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1438 CAAATCCTACATGAACCC 1455
              ||||||| ||| ||| ||
Db         19 CAAATCCAACACGAAGCC 2


RESULT 4317
AX488423
LOCUS       AX488423                 20 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 5723 from Patent WO02053728.
ACCESSION   AX488423
VERSION     AX488423.1  GI:22322503
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 5723 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Candida albicans"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:5476"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        244 TCCGCGGGTCCCCCACCT 261
              |||||  |||||||| ||
Db          1 TCCGCTTGTCCCCCATCT 18


RESULT 4318
AX511388
LOCUS       AX511388                 20 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 126 from Patent WO02059558.
ACCESSION   AX511388
VERSION     AX511388.1  GI:23392265
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: WO 02059558-A 126 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3'TAG011GENE-2"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2527 ATATATATACAGGGTATT 2544
              |||||| |||||| || |
Db          3 ATATATTTACAGGATAGT 20


RESULT 4319
AX525194
LOCUS       AX525194                 20 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 1 from Patent EP1236807.
ACCESSION   AX525194
VERSION     AX525194.1  GI:25170157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Vo-Dinh,T., Wntenberg,A. and Ericsson,M.N.
  TITLE     Integrated circuit biochip microsystem
  JOURNAL   Patent: EP 1236807-A 1 04-SEP-2002;
            UT-BATTELLE, LLC (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        347 CCCCCTCCCTACCAGCAG 364
              || ||||| | |||||||
Db          1 CCTCCTCCTTCCCAGCAG 18


RESULT 4320
AX526507
LOCUS       AX526507                 20 bp    DNA     linear   PAT 21-NOV-2002
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Qy        628 CGCCCTGGATGCCGCGGG 645
              |||| || ||||| ||||
Db         18 CGCCGTGCATGCCTCGGG 1


RESULT 4311
AX323446/c
LOCUS       AX323446                  20 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 38 from Patent WO0192578.
ACCESSION   AX323446
VERSION     AX323446.1  GI:18094209
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Roninson,I.B., Dokmanovic,M. and Chang,B.D.
  TITLE     Reagents and methods for identifying and modulating expression of
            genes regulated by retinoids
  JOURNAL   Patent: WO 0192578-A 38 06-DEC-2001;
            Board of Trustees of the University of Illinois (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Sense primer for ring finger protein RNF"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2635 TTCCTGTTGGGCTGAACC 2652
              ||||| |||| ||| |||
Db         20 TTCCTTTTGGACTGCACC 3


RESULT 4312
AX418707
LOCUS       AX418707                  20 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 102 from Patent WO0210378.
ACCESSION   AX418707
VERSION     AX418707.1  GI:21523570
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Cowsert,L.M., Wyatt,J., Freier,S.M., Monia,B.P., Butler,M.M. and
            Mckay,R.
  TITLE     Antisense modulation of ptp1b expression
  JOURNAL   Patent: WO 0210378-A 102 07-FEB-2002;
            ISIS PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense Oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1133 GCCGAATTTCCTAGTAAA 1150
              | ||||| |||| |||||
Db          2 GTCGAATATCCTGGTAAA 19


RESULT 4313
AX418829/c
LOCUS       AX418829                  20 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 224 from Patent WO0210378.
ACCESSION   AX418829
VERSION     AX418829.1  GI:21523692
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Cowsert,L.M., Wyatt,J., Freier,S.M., Monia,B.P., Butler,M.M. and
            Mckay,R.
  TITLE     Antisense modulation of ptp1b expression
  JOURNAL   Patent: WO 0210378-A 224 07-FEB-2002;
            ISIS PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense Oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1287 GGACCAGCAGGCTCGCCC 1304
              || | ||||||| |||||
Db         19 GGGCAAGCAGGCCCGCCC 2


RESULT 4314
AX477131
LOCUS       AX477131                  20 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 222 from Patent WO0220848.
ACCESSION   AX477131
VERSION     AX477131.1  GI:22216384
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,
            Lusis,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
  TITLE     Gene and sequence variation associated with cancer
  JOURNAL   Patent: WO 0220848-A 222 14-MAR-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2251 AAGCTTTATTTGCATATT 2268
              |||| | |||||||| ||
Db          1 AAGCCTCATTTGCATGTT 18


RESULT 4315
AX482149
LOCUS       AX482149                  20 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 126 from Patent EP1225233.
ACCESSION   AX482149
VERSION     AX482149.1  GI:22316871
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 7337 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        690 ACGAGGTGCAGAATGTCG 707
              ||||| ||||||| | ||
Db         20 ACGAGCTGCAGAAAGCCG 3


RESULT 4307
AX295954
LOCUS       AX295954                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 7716 from Patent WO0179548.
ACCESSION   AX295954
VERSION     AX295954.1  GI:17057643
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 7716 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        211 CGAGGATCGCCACGACGG 228
              ||||||||| |  |||||
Db          3 CGAGGATCGTCTTGACGG 20


RESULT 4308
AX296316
LOCUS       AX296316                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 8078 from Patent WO0179548.
ACCESSION   AX296316
VERSION     AX296316.1  GI:17058005
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 8078 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        717 ACCTGTTGCTGCACGATC 734
              ||| ||| ||||||| ||
Db          2 ACCCGTTTCTGCACGGTC 19


RESULT 4309
AX298759/c
LOCUS       AX298759                 20 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 393 from Patent WO0183749.
ACCESSION   AX298759
VERSION     AX298759.1  GI:17128749
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
            Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
  TITLE     Gene and sequence variation associated with sensing carbohydrate
            compounds and other sweeteners
  JOURNAL   Patent: WO 0183749-A 393 08-NOV-2001;
            WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
            (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10095"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1571 ATCCTTCTCCACCGCACA 1588
              |||||| |||||| || |
Db         20 ATCCTTTTCCACCCCAAA 3


RESULT 4310
AX317648/c
LOCUS       AX317648                 20 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 651 from Patent WO0190337.
ACCESSION   AX317648
VERSION     AX317648.1  GI:17900549
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Allawi,H., Bartholomay,C.T., Chehak,L., Curtis,M.L., Eis,P.S.,
            Hall,J.G., Ip,H.S., Kaiser,M., Kwiatkowski,R.W., Lukowiak,A.A.,
            Lyamichev,V., Ma,W., Olson-Munoz,M.C., Olson,S.M., Schaefer,J.J.,
            Skrzypczynski,Z., Takova,T.Y., Vedvik,K.L. and Lyamichev,N.E.
  TITLE     Detection of rna
  JOURNAL   Patent: WO 0190337-A 651 29-NOV-2001;
            THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Db          3 GTGCTCAGGTAGTGGTTG 20


RESULT 4302
AX183993
LOCUS       AX183993                 20 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 1746 from Patent WO0142511.
ACCESSION   AX183993
VERSION     AX183993.1  GI:15135328
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
  TITLE     Ibd-related polymorphisms
  JOURNAL   Patent: WO 0142511-A 1746 14-JUN-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
            Biotherapeutics Corporation (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2265 TATTTATTTCAGATGTTTC 2283
              | || ||||  ||||||||
Db          1 TGTTGATTTTNGATGTTTC 19


RESULT 4303
AX224880/c
LOCUS       AX224880                 20 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 34 from Patent WO0161030.
ACCESSION   AX224880
VERSION     AX224880.1  GI:15554953
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gray,D.M. and Bollon,A.P.
  TITLE     Libraries of optimum subsequence regions of mrna and genomic dna
            for control of gene expression
  JOURNAL   Patent: WO 0161030-A 34 23-AUG-2001;
            Cytoclonal Pharmaceutics, Inc. (US) ; University of Texas at
            Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
            Experimental Carcinogenesis, National Cancer Institute/NIH (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        494 GAGGGAGCGGGGCTGCCC 511
              ||||||||  ||| ||||
Db         19 GAGGGAGCCAGGCCGCCC 2


RESULT 4304
AX224881/c
LOCUS       AX224881                 20 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 35 from Patent WO0161030.
ACCESSION   AX224881
VERSION     AX224881.1  GI:15554954
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gray,D.M. and Bollon,A.P.
  TITLE     Libraries of optimum subsequence regions of mrna and genomic dna
            for control of gene expression
  JOURNAL   Patent: WO 0161030-A 35 23-AUG-2001;
            Cytoclonal Pharmaceutics, Inc. (US) ; University of Texas at
            Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
            Experimental Carcinogenesis, National Cancer Institute/NIH (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        494 GAGGGAGCGGGGCTGCCC 511
              ||||||||  ||| ||||
Db         18 GAGGGAGCCAGGCCGCCC 1


RESULT 4305
AX295243/c
LOCUS       AX295243                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 7005 from Patent WO0179548.
ACCESSION   AX295243
VERSION     AX295243.1  GI:17056932
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 7005 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         988 AGGCCGGTCCTTGCGGGA 1005
               ||   ||||||||||||||
Db          18 AGTAGGGTCCTTGCGGGA 1


RESULT 4306
AX295575/c
LOCUS       AX295575                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 7337 from Patent WO0179548.
ACCESSION   AX295575
VERSION     AX295575.1  GI:17057264
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 426 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              ||||||| |||||  |||
Db         19 TTGAAAATAAAAATGAAA 2

RESULT 4298
AX167874/c
LOCUS       AX167874                 20 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 58 from Patent WO0142307.
ACCESSION   AX167874
VERSION     AX167874.1  GI:14597194
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Saito,K., Ohe,N. and Satoh,H.
  TITLE     Mutant er_g(a) and test systems for transactivation
  JOURNAL   Patent: WO 0142307-A 58 14-JUN-2001;
            Sumitomo Chemical Company, Limited (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Designed oligonucleotide primer for PCR"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        601 CTCCGACCTGCTGCTGCC 618
              || |||| |||||||| |
Db         19 CTTCGACATGCTGCTGGC 2

RESULT 4299
AX167876/c
LOCUS       AX167876                 20 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 60 from Patent WO0142307.
ACCESSION   AX167876
VERSION     AX167876.1  GI:14597196
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Saito,K., Ohe,N. and Satoh,H.
  TITLE     Mutant er_g(a) and test systems for transactivation
  JOURNAL   Patent: WO 0142307-A 60 14-JUN-2001;
            Sumitomo Chemical Company, Limited (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Designed oligonucleotide primer for PCR"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1085 GAAGGTGAAGCTGTTCAT 1102
              ||||||| | ||| ||||
Db         20 GAAGGTGGACCTGATCAT 3

RESULT 4300
AX167955
LOCUS       AX167955                 20 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 139 from Patent WO0142307.
ACCESSION   AX167955
VERSION     AX167955.1  GI:14597275
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Saito,K., Ohe,N. and Satoh,H.
  TITLE     Mutant er_g(a) and test systems for transactivation
  JOURNAL   Patent: WO 0142307-A 139 14-JUN-2001;
            Sumitomo Chemical Company, Limited (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Designed oligonucleotide probe for Southern
                     hybridization"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        466 GCAGGCCTGGCCCGGCCG 483
              ||||||||| ||| || |
Db          3 GCAGGCCTGACCCTGCAG 20

RESULT 4301
AX174999
LOCUS       AX174999                 20 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 9 from Patent WO0143540.
ACCESSION   AX174999
VERSION     AX174999.1  GI:14598471
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schatten,G.
  TITLE     Methods for producing transgenic animals
  JOURNAL   Patent: WO 0143540-A 9 21-JUN-2001;
            Schatten, Gerald (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1932 GTGTTAAGGTAATGGTTG 1949
              ||| | ||||| ||||||
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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAA 2797
              ||| ||||| | |||||||
Db         20 GAAATGAAAGAGAAAAAA 3


RESULT 4293
AX149070
LOCUS       AX149070                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 272 from Patent WO0136625.
ACCESSION   AX149070
VERSION     AX149070.1  GI:14347594
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 272 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1787 CCATTCTTTCCTTCTCTG 1804
              ||||| |||| || ||||
Db          2 CCATTTTTTCATTGTCTG 19


RESULT 4294
AX149130
LOCUS       AX149130                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 332 from Patent WO0136625.
ACCESSION   AX149130
VERSION     AX149130.1  GI:14347654
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 332 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||| || ||| |||
Db          3 AAAAAAACAACAAAGAAA 20


RESULT 4295
AX149130/c
LOCUS       AX149130                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 332 from Patent WO0136625.
ACCESSION   AX149130
VERSION     AX149130.1  GI:14347654
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 332 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||| ||| || |||||||
Db         20 TTTCTTTGTTGTTTTTT 3


RESULT 4296
AX149168/c
LOCUS       AX149168                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 370 from Patent WO0136625.
ACCESSION   AX149168
VERSION     AX149168.1  GI:14347692
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 370 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              ||||||| |||||  |||
Db         19 TTGAAAATAAAAATGAAA 2

RESULT 4297
AX149224/c
LOCUS       AX149224                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 426 from Patent WO0136625.
ACCESSION   AX149224
VERSION     AX149224.1  GI:14347748
KEYWORDS    .
SOURCE      synthetic construct
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ACCESSION   AX039577
VERSION     AX039577.1  GI:11229609
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,X. and Cheng,L.
  TITLE     Genes and expression products from hematopoietic cells
  JOURNAL   Patent: WO 0063382-A 11 26-OCT-2000;
            Osiris Therapeutics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer based on 5'-untranslated region of C17
                     cDNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTT 2168
              ||||||||  || |||||
Db          2 TTGATTTTCATCACCTTT 19


RESULT 4289
AX054681/c
LOCUS       AX054681                  20 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 13 from Patent WO0073788.
ACCESSION   AX054681
VERSION     AX054681.1  GI:12228207
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ng,G. and O'Neil,G.
  TITLE     Use of gabapentin in assays to identify gabab receptor modulators
  JOURNAL   Patent: WO 0073788-A 13 07-DEC-2000;
            Merck Frosst Canada & Co. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        657 ACCTGGGGCTCCACGACA 674
              ||||| ||||| | ||||
Db         19 ACCTGCGGCTCTATGACA 2


RESULT 4290
AX137266/c
LOCUS       AX137266                  20 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 1 from Patent EP1074613.
ACCESSION   AX137266
VERSION     AX137266.1  GI:14273582
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Guertler,L.G., Hauser,H.P., dongmo Deloko,Y.B., Zekeng,L. and
            Kaptue,L.
  TITLE     Lentivirus from the group of immunodeficiency viruses from drill
            apes (mandrillus leucophaeus) and its use
  JOURNAL   Patent: EP 1074613-A 1 07-FEB-2001;
            Dade Behring Marburg GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="Primer, nicht genomische DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2442 GACTTTTTTGAGACATGG 2459
              ||| |||| || ||||||
Db         19 GACATTTTGGACACATGG 2


RESULT 4291
AX148870/c
LOCUS       AX148870                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 72 from Patent WO0136625.
ACCESSION   AX148870
VERSION     AX148870.1  GI:14347394
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 72 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              ||| ||||| | ||||||
Db         19 GAAATGAAAGAGAAAAAA 2


RESULT 4292
AX148871/c
LOCUS       AX148871                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 73 from Patent WO0136625.
ACCESSION   AX148871
VERSION     AX148871.1  GI:14347395
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 73 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"
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FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide inhibiting the common
                     subunit of IL-4 and IL-13 human receptor"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        548 CTCTCCGGGCTGGAGGCG 565
              |||| |||||||  ||||
Db         18 CTCTGCGGGCTGTGGGCG 1


RESULT 4284
AX020523/c
LOCUS       AX020523                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 23 from Patent WO9934016.
ACCESSION   AX020523
VERSION     AX020523.1  GI:10044213
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vider,B.Z.
  TITLE     A method for identifying and characterizing cells and tissues
  JOURNAL   Patent: WO 9934016-A 23 08-JUL-1999;
            GENENA LTD (IL); VIDER BEN ZION (IL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        357 ACCAGCAGCTGGCCTACT 374
              ||| |||| ||||| |||
Db         19 ACCGGCAGATGGCCGACT 2


RESULT 4285
AX020603
LOCUS       AX020603                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 103 from Patent WO9934016.
ACCESSION   AX020603
VERSION     AX020603.1  GI:10044293
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vider,B.Z.
  TITLE     A method for identifying and characterizing cells and tissues
  JOURNAL   Patent: WO 9934016-A 103 08-JUL-1999;
            GENENA LTD (IL); VIDER BEN ZION (IL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1737 AAGGTGACAAGTACTGGC 1754
              || ||||| | |||||||
Db          2 AATGTGACCATTACTGGC 19


RESULT 4286
AX026102
LOCUS       AX026102                  20 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 14 from Patent DE19847779.
ACCESSION   AX026102
VERSION     AX026102.1  GI:10187533
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Mueller-Schilling,M., Krammer,P. and Oren,M.
  TITLE     Novel receptor dna useful for identifying apoptosis-modulating
            substances potentially useful for cancer chemotherapy
  JOURNAL   Patent: DE 19847779-C 14 03-FEB-2000;
            DEUTSCHES KREBSFORSCH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1759 TATTCATTAAGCTTTTTT 1776
              | ||  ||||||||||||
Db          3 TGTTGCTTAAGCTTTTTT 20


RESULT 4287
AX039285
LOCUS       AX039285                  20 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 23 from Patent WO0063359.
ACCESSION   AX039285
VERSION     AX039285.1  GI:11229390
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Roes,J.T.
  TITLE     Gene expression in eukaryotic cells
  JOURNAL   Patent: WO 0063359-A 23 26-OCT-2000;
            University College London (GB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR PRIMER"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        377 CAGTCGGCCGACCCCTAC 394
              |||  |||||||| ||||
Db          2 CAGCTGGCCGACCACTAC 19


RESULT 4288
AX039577
LOCUS       AX039577                  20 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 11 from Patent WO0063382.
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                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        574 GAGCGCCCGCAGGGATGC 591
              || ||| |||||| ||||
Db         19 GAACGCACGCAGGAATGC 2


RESULT 4279
AR404363/c
LOCUS       AR404363                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 21 from patent US 6627745.
ACCESSION   AR404363
VERSION     AR404363.1  GI:40152861
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kastner,D.L., Aksentijevichh,I., Centola,M., Deng,Z., Sood,R.,
            Collins,F.S., Blake,T., Liu,P.P., Fischel-Ghodsian,N.,
            Gumucio,D.L., Richards,R.I., Ricke,D.O., Doggett,N.A. and Pras,M.
  TITLE     Pyrin gene and mutants thereof, which cause familial Mediterranean
            fever
  JOURNAL   Patent: US 6627745-A 21 30-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2600 AAACTCTCTGTTCAGAAA 2617
              |||| ||  |||||||||
Db         20 AAACCCTGCGTTCAGAAA 3


RESULT 4280
AR428434
LOCUS       AR428434                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 12 from patent US 6642003.
ACCESSION   AR428434
VERSION     AR428434.1  GI:40187900
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Perfetti,R.
  TITLE     Human glucose-dependent insulin-secreting cell line
  JOURNAL   Patent: US 6642003-A 12 04-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        394 CTCGCATCTGGGGGAAGC 411
              ||| || |||| ||||||
Db          1 CTCACACCTGGTGGAAGC 18


RESULT 4281
AR437017/c
LOCUS       AR437017                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 69 from patent US 6656732.
ACCESSION   AR437017
VERSION     AR437017.1  GI:40200101
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.F. and Watt,A.T.
  TITLE     Antisense inhibition of src-c expression
  JOURNAL   Patent: US 6656732-A 69 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        426 TCAACCCCCTGCACCAGC 443
              |||||  |||||| ||||
Db         18 TCAACAGCCTGCAGCAGC 1


RESULT 4282
AX004337
LOCUS       AX004337                 20 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 89 from Patent WO9919492.
ACCESSION   AX004337
VERSION     AX004337.1  GI:9927819
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Betzner,A.S. and Doutriaux,M.P.
  TITLE     Methods for obtaining plant varieties
  JOURNAL   Patent: WO 9919492-A 89 22-APR-1999;
            BETZNER ANDREAS STEFAN (AU); DOUTRIAUX MARIE PASCALE (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Reverse primer for PCR amplification of NGA106 SSLP
                     marker in Arabidopsis thaliana subspecies"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1785 CCCCATTCTTTCCTTCTC 1802
              ||||||| | | ||||||
Db          3 CCCCATTTTGTTCTTCTC 20


RESULT 4283
AX008651/c
LOCUS       AX008651                 20 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 4 from Patent WO9966037.
ACCESSION   AX008651
VERSION     AX008651.1  GI:9996175
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: WO 9966037-A 4 23-DEC-1999;
            RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
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  JOURNAL    Patent: US 6600351-A 79 29-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        891 TGACAGTGGCTGAAGTAC 908
              ||||| ||||||| | ||
Db          3 TGACATTGGCTGATGGAC 20


RESULT 4274
AR370243/c
LOCUS       AR370243                 20 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 64 from patent US 6300132.
ACCESSION   AR370243
VERSION     AR370243.1  GI:34606749
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense inhibition of telomeric repeat binding factor 2
            expression
  JOURNAL   Patent: US 6300132-A 64 09-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        898 GGCTGAAGTACAGAGGCG 915
              ||||| ||| ||| ||||
Db         20 GGCTGGAGTGCAGTGGCG 3


RESULT 4275
AR373462
LOCUS       AR373462                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 32 from patent US 6602713.
ACCESSION   AR373462
VERSION     AR373462.1  GI:40075591
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of protein phosphatase 2 catalytic subunit
            beta expression
  JOURNAL   Patent: US 6602713-A 32 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        468 AGGCCTGGCCCGGCCGCC 485
              || ||  ||||||||||
Db          2 AGCCCCAGCCCGGCCGCC 19


RESULT 4276
AR373710
LOCUS       AR373710                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 102 from patent US 6602857.
ACCESSION   AR373710
VERSION     AR373710.1  GI:40076121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M., Wyatt,J., Monia,B.P., Butler,M.M. and McKay,R.
  TITLE     Antisense modulation of PTP1B expression
  JOURNAL   Patent: US 6602857-A 102 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1133 GCCGAATTTCCTAGTAAA 1150
              | ||||| |||| |||||
Db          2 GTCGAATATCCTGGTAAA 19


RESULT 4277
AR373832/c
LOCUS       AR373832                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 224 from patent US 6602857.
ACCESSION   AR373832
VERSION     AR373832.1  GI:40076243
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M., Wyatt,J., Monia,B.P., Butler,M.M. and McKay,R.
  TITLE     Antisense modulation of PTP1B expression
  JOURNAL   Patent: US 6602857-A 224 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1287 GGACCAGCAGGCTCGCCC 1304
              || | ||||||| |||||
Db         19 GGGCAAGCAGGCCCGCCC 2


RESULT 4278
AR379352/c
LOCUS       AR379352                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 10 from patent US 6607878.
ACCESSION   AR379352
VERSION     AR379352.1  GI:40086986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sorge,J.A.
  TITLE     Collections of uniquely tagged molecules
  JOURNAL   Patent: US 6607878-A 10 19-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
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          Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Watt,A.T.
  TITLE     Antisense modulation of caspase 6 expression
  JOURNAL   Patent: US 6566135-A 51 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1004 GAGAAGTTGGACAAGATC 1021
              ||||||||||||| | |
Db         18 GAGAAGTTGGACACCAAC 1


RESULT 4269
AR337644/c
LOCUS       AR337644                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6566513.
ACCESSION   AR337644
VERSION     AR337644.1  GI:33724177
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Guertler,L.G., Hauser,H.P., Dongmo Deloko,Y.B., Zekeng,L. and
            Kaptue,L.
  TITLE     Lentivirus from the group of immunodeficiency viruses of drill
            monkeys (Mandrillus leucophaeus) and their use
  JOURNAL   Patent: US 6566513-A 1 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2442 GACTTTTTTGAGACATGG 2459
              ||| |||| || ||||||
Db         19 GACATTTTGGACACATGG 2


RESULT 4270
AR362210
LOCUS       AR362210                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 56 from patent US 6600351.
ACCESSION   AR362210
VERSION     AR362210.1  GI:33770420
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bisanti,B., Cipriani,S. and Coppola,F.
  TITLE     Loop filter architecture
  JOURNAL   Patent: US 6600351-A 56 29-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2548 AATTAAGAGGATGCTGGG 2565
              ||| | ||||||||||||
Db          3 AATGTACAGGATGCTGGG 20


RESULT 4271
AR362212
LOCUS       AR362212                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 58 from patent US 6600351.
ACCESSION   AR362212
VERSION     AR362212.1  GI:33770422
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bisanti,B., Cipriani,S. and Coppola,F.
  TITLE     Loop filter architecture
  JOURNAL   Patent: US 6600351-A 58 29-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2548 AATTAAGAGGATGCTGGG 2565
              ||| | ||||||||||||
Db          3 AATGTACAGGATGCTGGG 20


RESULT 4272
AR362213/c
LOCUS       AR362213                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 59 from patent US 6600351.
ACCESSION   AR362213
VERSION     AR362213.1  GI:33770423
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bisanti,B., Cipriani,S. and Coppola,F.
  TITLE     Loop filter architecture
  JOURNAL   Patent: US 6600351-A 59 29-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2548 AATTAAGAGGATGCTGGG 2565
              ||| | ||||||||||||
Db         18 AATGTACAGGATGCTGGG 1


RESULT 4273
AR362233
LOCUS       AR362233                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 79 from patent US 6600351.
ACCESSION   AR362233
VERSION     AR362233.1  GI:33770443
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bisanti,B., Cipriani,S. and Coppola,F.
  TITLE     Loop filter architecture
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VERSION     AR316042.1  GI:31709468
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 6579 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        495 AGGGAGCGGGGCTGCCCT 512
              | || |||||||||| |||
Db         20 ATGGTGCGGGGCTGGCCT 3


RESULT 4264
AR316220/c
LOCUS       AR316220                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6757 from patent US 6559294.
ACCESSION   AR316220
VERSION     AR316220.1  GI:31709646
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 6757 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1068 TCCTGACATCCTTAGTAG 1085
              ||||| ||  ||||||||
Db         20 TCCTGGCAATCTTAGTAG 3


RESULT 4265
AR337010/c
LOCUS       AR337010                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 71 from patent US 6566132.
ACCESSION   AR337010
VERSION     AR337010.1  GI:33722864
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Watt,A.T.
  TITLE     Antisense modulation of Interferon gamma receptor 1 expression
  JOURNAL   Patent: US 6566132-A 71 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1318 GAACATACAGAACTGCTT 1335
              ||||||||||||   |||
Db         19 GAACATACAGAAGAACTT 2


RESULT 4266
AR337070/c
LOCUS       AR337070                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 43 from patent US 6566133.
ACCESSION   AR337070
VERSION     AR337070.1  GI:33722924
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of dual specific phosphatase 9 expression
  JOURNAL   Patent: US 6566133-A 43 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        547 CCTCTCCGGGCTGGAGGC 564
              |||||| ||||||| | |
Db         19 CCTCTCGGGGCTGGGGCC 2


RESULT 4267
AR337073
LOCUS       AR337073                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 46 from patent US 6566133.
ACCESSION   AR337073
VERSION     AR337073.1  GI:33722927
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of dual specific phosphatase 9 expression
  JOURNAL   Patent: US 6566133-A 46 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        256 CCACCTCTCCTCCGCCGG 273
              || | |||||||||| |||
Db          3 CCCCATCTCCTCCGGCGG 20


RESULT 4268
AR337126/c
LOCUS       AR337126                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 51 from patent US 6566135.
ACCESSION   AR337126
VERSION     AR337126.1  GI:33722980
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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ACCESSION   AR313482
VERSION     AR313482.1  GI:31706908
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 4019 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1479 CTAACAAAACCCTGGAGA 1496
              | | ||||| ||||||||
Db          1 CCACCAAAAACCTGGAGA 18


RESULT 4259
AR314502/c
LOCUS       AR314502                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5039 from patent US 6559294.
ACCESSION   AR314502
VERSION     AR314502.1  GI:31707928
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 5039 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2127 ACTTGTAGAAACGAAGCC 2144
              |||| || | ||||||||
Db         18 ACTTCTAAAGACGAAGCC 1


RESULT 4260
AR314593/c
LOCUS       AR314593                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5130 from patent US 6559294.
ACCESSION   AR314593
VERSION     AR314593.1  GI:31708019
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 5130 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        625 ACACGCCCTGGATGCCGC 642
              |||||||||| ||  |||
Db         18 ACACGCCCTGAATATCGC 1


RESULT 4261
AR315581
LOCUS       AR315581                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6118 from patent US 6559294.
ACCESSION   AR315581
VERSION     AR315581.1  GI:31709007
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 6118 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1318 GAACATACAGAACTGCTT 1335
              ||||||| |||||| | |
Db          2 GAACATAGAGAACTCCAT 19


RESULT 4262
AR315755
LOCUS       AR315755                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6292 from patent US 6559294.
ACCESSION   AR315755
VERSION     AR315755.1  GI:31709181
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 6292 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        762 CCATGACCAAGAACCCTC 779
              |||| || |||| |||||
Db          1 CCATCACAAAGACCCCTC 18


RESULT 4263
AR316042/c
LOCUS       AR316042                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6579 from patent US 6559294.
ACCESSION   AR316042
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DEFINITION  Sequence 1828 from patent US 6559294.
ACCESSION   AR311291
VERSION     AR311291.1  GI:31704717
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 1828 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2658 GTGAGTGTGCAGTACAGT 2675
              | ||||||| ||| |||
Db         20 GAGAGTGTGCTGTAAAGT 3


RESULT 4254
AR311500
LOCUS       AR311500                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2037 from patent US 6559294.
ACCESSION   AR311500
VERSION     AR311500.1  GI:31704926
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2037 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        750 AAGGTCCCATTTCCATGA 767
              |||||| ||| |||| ||
Db          3 AAGGTCTCATATCCAGGA 20


RESULT 4255
AR311776
LOCUS       AR311776                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2313 from patent US 6559294.
ACCESSION   AR311776
VERSION     AR311776.1  GI:31705202
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2313 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2046 TCTGCTTAGCAACTAGTT 2063
              ||||||||| |||| | |
Db          3 TCTGCTTAGGAACTTGCT 20


RESULT 4256
AR311993/c
LOCUS       AR311993                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2530 from patent US 6559294.
ACCESSION   AR311993
VERSION     AR311993.1  GI:31705419
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2530 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2551 TAAGAGGATGCTGGGCTC 2568
              || ||||| |||||||| |
Db         20 TATGAGGAGGCTGGGCCC 3


RESULT 4257
AR312044/c
LOCUS       AR312044                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2581 from patent US 6559294.
ACCESSION   AR312044
VERSION     AR312044.1  GI:31705470
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2581 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        686 ATGGACGAGGTGCAGAAT 703
              ||| |||||||||  || |
Db         20 ATGTACGAGGTGCTGACT 3


RESULT 4258
AR313482
LOCUS       AR313482                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4019 from patent US 6559294.
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AR292453/c
LOCUS       AR292453                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4188 from patent US 6537751.
ACCESSION   AR292453
VERSION     AR292453.1  GI:31679737
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4188 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1240 GTGTAAAGAATTCACAGA 1257
              ||||||| || ||| |||
Db         19 GTGTAAAAAACTCAAAGA 2


RESULT 4249
AR293260/c
LOCUS       AR293260                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4995 from patent US 6537751.
ACCESSION   AR293260
VERSION     AR293260.1  GI:31680544
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4995 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        424 CATCAACCCCCTGCACCA 441
              | ||||||||||||  | |
Db         20 CTTCAACCCCCTGCCCAA 3


RESULT 4250
AR295417
LOCUS       AR295417                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 7152 from patent US 6537751.
ACCESSION   AR295417
VERSION     AR295417.1  GI:31682701
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 7152 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        770 AAGAACCCTCTGAACCTC 787
              | |||||| |||||| ||
Db          1 AGGAACCCCCTGAACTTC 18


RESULT 4251
AR298823/c
LOCUS       AR298823                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 10558 from patent US 6537751.
ACCESSION   AR298823
VERSION     AR298823.1  GI:31686107
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 10558 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2688 AATGGAGATTTGGAATTG 2705
              || ||| ||||| |||||
Db         19 AAGGGAAATTTGAAATTG 2


RESULT 4252
AR300837
LOCUS       AR300837                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 65 from patent US 6537973.
ACCESSION   AR300837
VERSION     AR300837.1  GI:31688404
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.F., Dean,N.M., Holmlund,J.T. and Dorr,F.A.
  TITLE     Oligonucleotide inhibition of protein kinase C
  JOURNAL   Patent: US 6537973-A 65 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1660 TCTGCATCACCCGCCCCT 1677
              |||| || || |||||||
Db          2 TCTGGATGACGCGCCCCT 19


RESULT 4253
AR311291/c
LOCUS       AR311291                  20 bp    DNA     linear   PAT 12-JUN-2003
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RESULT 4243
AR264949/c
LOCUS       AR264949                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 33 from patent US 6492121.
ACCESSION   AR264949
VERSION     AR264949.1  GI:29693336
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 33 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2517 GGTTTTATTCATATATAT 2534
              ||||||  |  ||||||||
Db         18 GGTTTTTTATATATATAT 1


RESULT 4244
AR265965/c
LOCUS       AR265965                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 146 from patent US 6492170.
ACCESSION   AR265965
VERSION     AR265965.1  GI:29694811
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Watt,A.T.
  TITLE     Antisense modulation of caspase 9 expression
  JOURNAL   Patent: US 6492170-A 146 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1674 CCCTGGACTTCTTAGTTG 1691
              |||||||||  |||  || |
Db         18 CCCTGGACTGCTTTGTGG 1


RESULT 4245
AR266035/c
LOCUS       AR266035                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 42 from patent US 6492171.
ACCESSION   AR266035
VERSION     AR266035.1  GI:29694881
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Gaarde,W.A., Freier,S.M. and Wancewicz,E.
  TITLE     Antisense modulation of TERT expression
  JOURNAL   Patent: US 6492171-A 42 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        626 CACGCCCTGGATGCCGCG 643
              |||  |||  |||||||||
Db         18 CACCCCCGCGATGCCGCG 1


RESULT 4246
AR279178
LOCUS       AR279178                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 320 from patent US 6514694.
ACCESSION   AR279178
VERSION     AR279178.1  GI:29713821
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Milhausen,M.J.
  TITLE     Methods for the detection of encysted parasites
  JOURNAL   Patent: US 6514694-A 320 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1485 AAACCCTGGAGAAAATGG 1502
              |||| |||| ||||| ||
Db          2 AAACTCTGGGGAAAACGG 19


RESULT 4247
AR292352/c
LOCUS       AR292352                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4087 from patent US 6537751.
ACCESSION   AR292352
VERSION     AR292352.1  GI:31679636
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4087 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1681 CTTCTTAGTTGTTTCTCT 1698
              ||||  ||||||||  |||
Db         20 CTTCCAAGTTGTTTTTCT 3


RESULT 4248
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                  |||| ||||||| | |||
Db          1 GAGCAGGGCTGCACCCGC 18


RESULT 4238
AR232228/c
LOCUS       AR232228                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 18 from patent US 6455307.
ACCESSION   AR232228
VERSION     AR232228.1  GI:27274220
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Freier,S.M. and Wyatt,J.
  TITLE     Antisense modulation of casein kinase 2-alpha prime expression
  JOURNAL   Patent: US 6455307-A 18 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        898 GGCTGAAGTACAGAGGCG 915
              ||||| ||| ||| ||||
Db         18 GGCTGGAGTGCAGTGGCG 1


RESULT 4239
AR232233/c
LOCUS       AR232233                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 23 from patent US 6455307.
ACCESSION   AR232233
VERSION     AR232233.1  GI:27274225
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Freier,S.M. and Wyatt,J.
  TITLE     Antisense modulation of casein kinase 2-alpha prime expression
  JOURNAL   Patent: US 6455307-A 23 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         32 CGGACAGCAAGGCCCGCG 49
              ||| ||||| |||||| |
Db         20 CGGGCAGCAGGGCCCGGG 3


RESULT 4240
AR232385
LOCUS       AR232385                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 80 from patent US 6455308.
ACCESSION   AR232385
VERSION     AR232385.1  GI:27274377
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Freier,S.M.
  TITLE     Antisense modulation of serum amyloid A4 expression
  JOURNAL   Patent: US 6455308-A 80 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1181 CTTGGAGGACGAAATGAG 1198
              | ||| |||| |||||||
Db          3 CCTGGTGGACTAAATGAG 20


RESULT 4241
AR243633/c
LOCUS       AR243633                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 83 from patent US 6475797.
ACCESSION   AR243633
VERSION     AR243633.1  GI:27290998
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of SR-CYP expression
  JOURNAL   Patent: US 6475797-A 83 05-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTT 2178
              |||||||| | || ||||
Db         20 TCTCCTTTATGTTGTTTT 3


RESULT 4242
AR253861/c
LOCUS       AR253861                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 533 from patent US 6479261.
ACCESSION   AR253861
VERSION     AR253861.1  GI:27302289
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,S.C., Abrams,M.A., Braford-Goldberg,S.R., Caparon,M.H.,
            Easton,A.M., Klein,B.K., McKearn,J.P., Olins,P., Paik,K.,
            Polazzi,J. and Thomas,J.W.
  TITLE     Methods of using interleukin-3 (IL-3) mutant polypeptides for
            ex-vivo expansion of hematopoietic stem cells
  JOURNAL   Patent: US 6479261-A 533 12-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1241 TGTAAAGAATTCACAGAA 1258
              ||| |||| || ||||||
Db         18 TGTCAAGAGTTTACAGAA 1
```

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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1257 AACTTCTCAGCCAAGACC 1274
              ||||||||||||  |  ||
Db          1 AACTTCTCAGCCCAAGCC 18


RESULT 4233
AR228184/c
LOCUS       AR228184                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 85 from patent US 6448003.
ACCESSION   AR228184
VERSION     AR228184.1  GI:27266930
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Guida,M. and Kurth,J.
  TITLE     Genotyping the human phenol sulfotransferbase 2 gene STP2
  JOURNAL   Patent: US 6448003-A 85 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2511 TCATAAGGTTTTATTCAT 2528
              |||||  |||  ||  |||||
Db         18 TCATAGGGTCTTCTTCAT 1


RESULT 4234
AR228185/c
LOCUS       AR228185                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 86 from patent US 6448003.
ACCESSION   AR228185
VERSION     AR228185.1  GI:27266931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Guida,M. and Kurth,J.
  TITLE     Genotyping the human phenol sulfotransferbase 2 gene STP2
  JOURNAL   Patent: US 6448003-A 86 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2511 TCATAAGGTTTTATTCAT 2528
              |||||  |||  ||  |||||
Db         18 TCATAGGGTCTTCTTCAT 1


RESULT 4235
AR228758
LOCUS       AR228758                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6448064.
ACCESSION   AR228758
VERSION     AR228758.1  GI:27267872
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Vo-Dinh,T., Wintenberg,A. and Ericson,M.N.
  TITLE     Integrated circuit biochip microsystem
  JOURNAL   Patent: US 6448064-A 1 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        347 CCCCCTCCCTACCAGCAG 364
              || |||||  | |||||||
Db          1 CCTCCTCCTTCCCAGCAG 18


RESULT 4236
AR230837/c
LOCUS       AR230837                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 97 from patent US 6451602.
ACCESSION   AR230837
VERSION     AR230837.1  GI:27271624
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Popoff,I. and Cowsert,L.M.
  TITLE     Antisense modulation of PARP expression
  JOURNAL   Patent: US 6451602-A 97 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        995 TCCTTGCGGGAGAAGTTG 1012
              ||||   ||||||||||
Db         18 TCCTGTTGGGAGAAGTTG 1


RESULT 4237
AR231037
LOCUS       AR231037                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 297 from patent US 6451602.
ACCESSION   AR231037
VERSION     AR231037.1  GI:27271824
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Popoff,I. and Cowsert,L.M.
  TITLE     Antisense modulation of PARP expression
  JOURNAL   Patent: US 6451602-A 297 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        498 GAGCGGGGCTGCCCTCGC 515
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                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        113 GGCTGGGGGGATCCTGGA 130
              ||  |||||| |||||||
Db          2 GGGAGGGGGGGTCCTGGA 19


RESULT 4228
AR210772/c
LOCUS       AR210772                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 16 from patent US 6391543.
ACCESSION   AR210772
VERSION     AR210772.1  GI:21513589
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
            Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
            Roberts-Rapp,L., Russell,J.C. and Stroupe,S.D.
  TITLE     Reagents and methods useful for detecting diseases of the prostate
  JOURNAL   Patent: US 6391543-A 16 21-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        546 ACCTCTCCGGGCTGGAGG 563
              | | || ||||||||||||
Db         18 AACACTGCGGGCTGGAGG 1


RESULT 4229
AR211143/c
LOCUS       AR211143                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 56 from patent US 6399297.
ACCESSION   AR211143
VERSION     AR211143.1  GI:21514387
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 56 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        683 CAGATGGACGAGGTGCAG 700
              |||  | ||||||||||||
Db         20 CAGGAGCACGAGGTGCAG 3


RESULT 4230
AR224714/c
LOCUS       AR224714                  20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 19 from patent US 6440739.
ACCESSION   AR224714
VERSION     AR224714.1  GI:23333554
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.F. and Freier,S.M.
  TITLE     Antisense modulation of glioma-associated oncogene-2 expression
  JOURNAL   Patent: US 6440739-A 19 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        631 CCTGGATGCCGCGGGCCT 648
              |||||| ||||| ||| |
Db         20 CCTGGAGGCCGCTGGCTT 3


RESULT 4231
AR224726/c
LOCUS       AR224726                  20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 31 from patent US 6440739.
ACCESSION   AR224726
VERSION     AR224726.1  GI:23333566
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.F. and Freier,S.M.
  TITLE     Antisense modulation of glioma-associated oncogene-2 expression
  JOURNAL   Patent: US 6440739-A 31 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1567 AAAAATCCTTCTCCACCG 1584
              | ||| |||||||||  ||
Db         18 ACAAAGCCTTCTCCAACG 1


RESULT 4232
AR225136
LOCUS       AR225136                  20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 102 from patent US 6441156.
ACCESSION   AR225136
VERSION     AR225136.1  GI:23334271
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lerman,M.I., Latif,F., Wei,M.-H., Duh,F.-M., Minna,J.D., Sekido,Y.
            and Gao,B.
  TITLE     Calcium channel compositions and methods of use thereof
  JOURNAL   Patent: US 6441156-A 102 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1302 CCCCAGTCTTGGAGACGA 1319
              | |||| ||||| |||||
Db         19 CACCAGACTTGGCGACGA 2


RESULT 4223
I86619
LOCUS       I86619                   20 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 10 from patent US 5702890.
ACCESSION   I86619
VERSION     I86619.1  GI:3206337
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Housman,D.E.
  TITLE     Inhibitors of alternative alleles of genes as a basis for cancer
            therapeutic agents
  JOURNAL   Patent: US 5702890-A 10 30-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1307 GTCTTGGAGACGAACATA 1324
              |||||||||| | || ||
Db          2 GTCTTGGAGAAGCACTTA 19


RESULT 4224
I88643/c
LOCUS       I88643                   20 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 25 from patent US 5719026.
ACCESSION   I88643
VERSION     I88643.1  GI:3408583
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fukui,T., Katsuragi,K., Kinoshita,M. and Shin,S. deceased.
  TITLE     Method for detecting polymorphism of human cytochrome P4501A2 gene
  JOURNAL   Patent: US 5719026-A 25 17-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1521 ATTGGAACGAAGAAAGGT 1538
              |||||  | |||||||||
Db         20 ATTGGTCCCAAGAAAGGT 3


RESULT 4225
AR182757
LOCUS       AR182757                 20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 65 from patent US 6339066.
ACCESSION   AR182757
VERSION     AR182757.1  GI:20225964
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank., Dean,N.M., Cook,P.Dan. and Hoke,G.
  TITLE     Antisense oligonucleotides which have phosphorothioate linkages of
            high chiral purity and which modulate .beta.I, .beta.II, .gamma.,
            .delta., .EPSILON., .zeta. and .eta. isoforms of human protein
            kinase C
  JOURNAL   Patent: US 6339066-A 65 15-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1660 TCTGCATCACCCGCCCCT 1677
              |||| || || |||||||
Db          2 TCTGGATGACGCGCCCCT 19


RESULT 4226
AR202004/c
LOCUS       AR202004                 20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 30 from patent US 6361946.
ACCESSION   AR202004
VERSION     AR202004.1  GI:20256543
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Alitalo,K. and Joukov,V.
  TITLE     Vascular endothelial growth factor C (VEGF-C) protein and gene,
            mutants thereof, and uses thereof
  JOURNAL   Patent: US 6361946-A 30 26-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2593 TTAATTGAAACTCTCTGT 2610
              |||||| | |||| ||||
Db         20 TTAATTCATACTCACTGT 3


RESULT 4227
AR210682
LOCUS       AR210682                 20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 44 from patent US 6391542.
ACCESSION   AR210682
VERSION     AR210682.1  GI:21513475
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Anderson,K.P., Hanecak,R.C., Hoshiko,K., Nozaki,C., Nishihara,T.,
            Nakatake,H., Hamada,F., Eto,T., Furukawa,S., Furasako,S.,
            Bruice,T.W. and Lima,W.F.
  TITLE     Compositions and methods for treatment of Hepatitis C
            virus-associated diseases
  JOURNAL   Patent: US 6391542-A 44 21-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .20
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/mol_type="unassigned DNA"

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1108 TAGGGACTTTGCCTATGT 1125
              |||| || |||| |||||
Db         20 TAGGCACCTTGCATATGT 3
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RESULT 4218
I36563/c
LOCUS I36563 20 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 4 from patent US 5607846.
ACCESSION I36563
VERSION I36563.1 GI:2086388
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murphy,T.F. and Bhushan,R.
TITLE Vaccine for moraxella catarrhalis
JOURNAL Patent: US 5607846-A 4 04-MAR-1997;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        744 TTCGCAAAGGTCCCATTT 761
              |||||| |||| |||| |
Db         20 TTCGCATAGGTACCATCT 3
```

RESULT 4219
I36567/c
LOCUS I36567 20 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 8 from patent US 5607846.
ACCESSION I36567
VERSION I36567.1 GI:2086392
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murphy,T.F. and Bhushan,R.
TITLE Vaccine for moraxella catarrhalis
JOURNAL Patent: US 5607846-A 8 04-MAR-1997;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        744 TTCGCAAAGGTCCCATTT 761
              |||||| |||| |||| |
Db         20 TTCGCATAGGTGCCATCT 3
```

RESULT 4220
I69263/c
LOCUS I69263 20 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 533 from patent US 5677149.
ACCESSION I69263
VERSION I69263.1 GI:2831385
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bauer,S.Christopher., Abrams,M.Allen., Braford-Goldberg,S.Ruth., Caparon,M.Helena., Easton,A.Michael., Klein,B.Kure., McKearn,J.Patrick., Olins,P., Paik,K., Polazzi,J. and Thomas,J.Warren.
TITLE Interleukin-3 (IL-3) mutant polypeptides and their recombinant production
JOURNAL Patent: US 5677149-A 533 14-OCT-1997;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1241 TGTAAAGAATTCACAGAA 1258
              ||| |||| || ||||||
Db         18 TGTCAAGAGTTTACAGAA 1
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RESULT 4221
I72481/c
LOCUS I72481 20 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 65 from patent US 5683987.
ACCESSION I72481
VERSION I72481.1 GI:3008620
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Smith,L.J.
TITLE Therapeutic oligonucleotides targeting the human MDR1 and MRP genes
JOURNAL Patent: US 5683987-A 65 04-NOV-1997;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        415 CGCCGCCGCCATCAACCC 432
              |||||||  ||||| |||
Db         19 CGCCGCCATCATCATCCC 2
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RESULT 4222
I79665/c
LOCUS I79665 20 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 10 from patent US 5707847.
ACCESSION I79665
VERSION I79665.1 GI:3207955
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Christgau,S., Kofod,L.Venke., Andersen,L.Nonboe., Kauppinen,S., Heldt-Hansen,H.Peter., Budolfsen,G. and Dalb.o slashed.ge,H.
TITLE Enzyme exhibiting pectin methylesterase activity
JOURNAL Patent: US 5707847-A 10 13-JAN-1998;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

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     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2568 CTGTTCTTGGCTTGGAAG 2585
              ||||||| || ||||||
Db         19 CTGTTCTCAGCATGGAAG 2


RESULT 4213
I26466/c
LOCUS       I26466                   20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 158 from patent US 5558988.
ACCESSION   I26466
VERSION     I26466.1  GI:1606336
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Prockop,D.J., Ala-Kokko,L. and Ritvaniemi,P.
  TITLE     Primers and methods for detecting mutations in the procollagen II
            gene that indicate a genetic predisposition for osteoarthritis
  JOURNAL   Patent: US 5558988-A 158 24-SEP-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        784 CCTCCCCTGTCAGAAGGA 801
              ||||| ||||||||  ||
Db         18 CCTCCGCTGTCAGACAGA 1


RESULT 4214
I28867
LOCUS       I28867                   20 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 14 from patent US 5574142.
ACCESSION   I28867
VERSION     I28867.1  GI:1819655
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Meyer,R.B. Jr., Gall,A.A. and Reed,M.W.
  TITLE     Peptide linkers for improved oligonucleotide delivery
  JOURNAL   Patent: US 5574142-A 14 12-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1313 GAGACGAACATACAGAAC 1330
              | |||||||||  |||||
Db          1 GTGACGAACATGGAGAAC 18


RESULT 4215
I31143/c
LOCUS       I31143                   20 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 55 from patent US 5582979.
ACCESSION   I31143
VERSION     I31143.1  GI:1821934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Weber,J.L.
  TITLE     Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
            method of using the same
  JOURNAL   Patent: US 5582979-A 55 10-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        298 ACCCCTCTCCCACACTGG 315
              |||| ||||||| | |||
Db         19 ACCCTTCTCCCAGAGTGG 2


RESULT 4216
I31432/c
LOCUS       I31432                   20 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 344 from patent US 5582979.
ACCESSION   I31432
VERSION     I31432.1  GI:1822223
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Weber,J.L.
  TITLE     Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
            method of using the same
  JOURNAL   Patent: US 5582979-A 344 10-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1996 TATCTAGCTTCTTCAGAG 2013
              ||| ||||  ||||||||
Db         20 TATTTAGCCACTTCAGAG 3


RESULT 4217
I31478/c
LOCUS       I31478                   20 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 390 from patent US 5582979.
ACCESSION   I31478
VERSION     I31478.1  GI:1822269
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Weber,J.L.
  TITLE     Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
            method of using the same
  JOURNAL   Patent: US 5582979-A 390 10-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
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     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        632 CTGGATGCCGCGGGCCTG 649
              |||| || |||| |||||
Db          1 CTGGCTGGCGCGCGCCTG 18


RESULT 4208
I24306/c
LOCUS       I24306                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5543294.
ACCESSION   I24306
VERSION     I24306.1  GI:1604176
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Silverstein,S.J., Lungu,O. and Wright,T.C. Jr.
  TITLE     Polymerase chain reaction/restriction fragment length polymorphism
            method for the detection and typing of myobacteria
  JOURNAL   Patent: US 5543294-A 1 06-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1292 AGCAGGCTCGCCCCAGTC 1309
              ||||||| ||| |||| |
Db         20 AGCAGGCGCGCGCCAGCC 3


RESULT 4209
I24668/c
LOCUS       I24668                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 52 from patent US 5545527.
ACCESSION   I24668
VERSION     I24668.1  GI:1604538
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Stevens,J.K. and Dunn,J.M.
  TITLE     Method for testing for mutations in DNA from a patient sample
  JOURNAL   Patent: US 5545527-A 52 13-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        944 TCGTTACTGGGAGGTGTT 961
              | |||| || ||||||||
Db         19 TTGTTAGTGAGAGGTGTT 2


RESULT 4210
I25265/c
LOCUS       I25265                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 52 from patent US 5550020.
ACCESSION   I25265
VERSION     I25265.1  GI:1605135
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Gallie,B.L., Dunn,J.M. and Stevens,J.K.
  TITLE     Method, reagents and kit for diagnosis and targeted screening for
            retinoblastoma
  JOURNAL   Patent: US 5550020-A 52 27-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        944 TCGTTACTGGGAGGTGTT 961
              | |||| || ||||||||
Db         19 TTGTTAGTGAGAGGTGTT 2


RESULT 4211
I25553
LOCUS       I25553                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 37 from patent US 5552273.
ACCESSION   I25553
VERSION     I25553.1  GI:1605423
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cleuziat,P.L., Awade,A., Robert-Baudouy,J. and Gayral,J.-P.
  TITLE     Polypeptides containing sequences characteristic of pyrrolidone
            carboxylyl peptidases, polynucleotides containing a sequence coding
            for such polypeptides, and their use, in particular for diagnostic
            purposes
  JOURNAL   Patent: US 5552273-A 37 03-SEP-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        921 CCCCACCTGAATGCTTAA 938
              ||| | || |||||||||
Db          1 CCCTATCTCAATGCTTAA 18


RESULT 4212
I26387/c
LOCUS       I26387                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 79 from patent US 5558988.
ACCESSION   I26387
VERSION     I26387.1  GI:1606257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Prockop,D.J., Ala-Kokko,L. and Ritvaniemi,P.
  TITLE     Primers and methods for detecting mutations in the procollagen II
            gene that indicate a genetic predisposition for osteoarthritis
  JOURNAL   Patent: US 5558988-A 79 24-SEP-1996;
FEATURES             Location/Qualifiers
```

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  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        113 GGCTGGGGGGATCCTGGA 130
              ||  |||||| |||||||
Db          3 GGGAGGGGGGGTCCTGGA 20


RESULT 4204
E44258
LOCUS       E44258                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Oligo-DNA strongly binding to HCVRNA and process for conveniently
            producing the DNA.
ACCESSION   E44258
VERSION     E44258.1  GI:18629210
KEYWORDS    JP 2000210090-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Taya,T., Ishiguro,T. and Saito,H.
  TITLE     Oligo-DNA strongly binding to HCVRNA and process for conveniently
            producing the DNA
  JOURNAL   Patent: JP 2000210090-A 2 02-AUG-2000;
            TOSOH CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2000210090-A/2
            PD   02-AUG-2000
            PF   19-NOV-1999 JP 1999329333
            PR
            PI   TOSHITAKA TAYA,TAKAHIKO ISHIGURO,HISAKAZU SAITO PC
            C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        113 GGCTGGGGGGATCCTGGA 130
              ||  |||||| |||||||
Db          1 GGGAGGGGGGGTCCTGGA 18


RESULT 4205
E46851
LOCUS       E46851                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Derivative of MGDF stimulating the growth and differentiation of
            megakaryocyte and process for producing it.
ACCESSION   E46851
VERSION     E46851.1  GI:18625189
KEYWORDS    JP 2000103799-A/9.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   D,B.T., M,B.J., A,B.R., Pamera,H., B,K.O. and B,S.B.
  TITLE     Derivative of MGDF stimulating the growth and differentiation of
            megakaryocyte and process for producing it
  JOURNAL   Patent: JP 2000103799-A 9 11-APR-2000;
            AMJEN INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000103799-A/9
            PD   11-APR-2000
            PF   18-AUG-1999 JP 1999231730
            PR   31-MAR-1994 US    08/221768,31-MAY-1994 US    08/252628, PR
            12-OCT-1994 US    08/321488,30-NOV-1994 US    08/347780 PI   BATORE
            TIMOTHY D,BOGENBAGA JACOB M,BOTUSERUMAN ROBERT A, PI   HUNT PAMERA,
            PI   KINSUTORA OAFU B,SAMARU BABURU B
            PC   C07K14/52,A61K38/00,A61K38/22,A61K47/48,A61P7/00,A61P7/06, PC
             C07K17/08//
            PC   C12N15/09,C12P21/02,(C12P21/02,C12R1:19),A61K37/02,A61K37/24,
            PC   C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2301 GTAGGCACGAAGCAATTT 2318
              | || ||||||||| |||
Db          1 GGAGTCACGAAGCAGTTT 18


RESULT 4206
I23916
LOCUS       I23916                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 18 from patent US 5541060.
ACCESSION   I23916
VERSION     I23916.1  GI:1603786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bell,G.I., Stoffel,M., Takeda,J., Vionnet,N., Yasuda,K.,
            Pilkis,S.J., Zouali,H., Velho,G., Cohen,D. and Froguel,P.
  TITLE     Detection of glucokinase-linked early-onset non-insulin-dependent
            diabetes mellitus
  JOURNAL   Patent: US 5541060-A 18 30-JUL-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         66 GCAGACGCCTGGTCACCG 83
              |||||  ||||||| || |
Db          2 GCAGATGCCTGGTGACAG 19


RESULT 4207
I24306
LOCUS       I24306                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5543294.
ACCESSION   I24306
VERSION     I24306.1  GI:1604176
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Silverstein,S.J., Lungu,O. and Wright,T.C. Jr.
  TITLE     Polymerase chain reaction/restriction fragment length polymorphism
            method for the detection and typing of myobacteria
  JOURNAL   Patent: US 5543294-A 1 06-AUG-1996;
FEATURES             Location/Qualifiers
```

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            PN   JP 1999292795-A/98
            PD   26-OCT-1999
            PF   02-APR-1998 JP 1998125452
            PR
            PI   HIROSHI TAKAHISA,NAOKI YAMAMOTO,TORU KIMURA,KAZUYUKI TAKAI, PI
              AKIRA WADA
            PC   A61K48/00,A61K31/70,A61K31/70,C12N15/09,C12N15/00 CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1622 TTGTTACCTACCTTACTA 1639
              ||||| || ||||||||
Db          2 TTGTTGGCTGCCTTACTA 19


RESULT 4201
E40658/c
LOCUS       E40658                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Antihuman Fas humanized antibody-containing antirheumatic.
ACCESSION   E40658
VERSION     E40658.1  GI:18627247
KEYWORDS    JP 2000154149-A/29.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.
  TITLE     Antihuman Fas humanized antibody-containing antirheumatic
  JOURNAL   Patent: JP 2000154149-A 29 06-JUN-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000154149-A/29
            PD   06-JUN-2000
            PF   17-SEP-1999 JP 1999263984
            PR
            PI   NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI   KAORI
            NAKAHARA,
            PI   SHIN YONEHARA
            PC   A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1643 AAAGAGCCTTCACTGGTT 1660
              |||||||||| | ||| |
Db         18 AAAGAGCCTTGAGTGGAT 1


RESULT 4202
E40677/c
LOCUS       E40677                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Antihuman Fas humanized antibody-containing antirheumatic.
ACCESSION   E40677
VERSION     E40677.1  GI:18627266
KEYWORDS    JP 2000154149-A/48.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.
  TITLE     Antihuman Fas humanized antibody-containing antirheumatic
  JOURNAL   Patent: JP 2000154149-A 48 06-JUN-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000154149-A/48
            PD   06-JUN-2000
            PF   17-SEP-1999 JP 1999263984
            PR
            PI   NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI   KAORI
            NAKAHARA,
            PI   SHIN YONEHARA
            PC   A61K39/395,A61P29/00,C12N15/09//C07K16/28,C12P21/02,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        158 CCGGACGCCATGTTGTGG 175
              | |||||||||| |||| |
Db         18 CAGGACGCCATTTTGTCG 1


RESULT 4203
E44257
LOCUS       E44257                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Oligo-DNA strongly binding to HCVRNA and process for conveniently
            producing the DNA.
ACCESSION   E44257
VERSION     E44257.1  GI:18629209
KEYWORDS    JP 2000210090-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Taya,T., Ishiguro,T. and Saito,H.
  TITLE     Oligo-DNA strongly binding to HCVRNA and process for conveniently
            producing the DNA
  JOURNAL   Patent: JP 2000210090-A 1 02-AUG-2000;
            TOSOH CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2000210090-A/1
            PD   02-AUG-2000
            PF   19-NOV-1999 JP 1999329333
            PR
            PI   TOSHITAKA TAYA,TAKAHIKO ISHIGURO,HISAKAZU SAITO PC
            C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
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```
RESULT 4197
E15162/c
LOCUS       E15162                    20 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Phosphorothioate antisence oligo DNA human VEGF mRNA.
ACCESSION   E15162
VERSION     E15162.1  GI:5709845
KEYWORDS    JP 1998052285-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uchida,K.
  TITLE     PREPARATION OF ANTISENSE NUCLEIC ACID
  JOURNAL   Patent: JP 1998052285-A 7 24-FEB-1998;
            TOAGOSEI CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1998052285-A/7
            PD   24-FEB-1998
            PF   20-MAY-1997 JP 1997129767
            PR   23-MAY-1996 JP 96P   128192
            PI   UCHIDA KIYOSHI
            PC   C12N15/09,C07H21/02,C07H21/04;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1545 AGTAGGGAAGGAACAGGA 1562
              || || ||||||| ||||
Db         19 AGAAGAGAAGGAAGAGGA 2


RESULT 4198
E22414
LOCUS       E22414                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Antisense nucleic acid compound.
ACCESSION   E22414
VERSION     E22414.1  GI:13024057
KEYWORDS    JP 1999042091-A/16.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kinya,K., Yoko,M. and Kiyoshi,U.
  TITLE     Antisense nucleic acid compound
  JOURNAL   Patent: JP 1999042091-A 16 16-FEB-1999;
            TOAGOSEI CHEM IND CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999042091-A/16
            PD   16-FEB-1999
            PF   25-JUL-1997 JP 1997213838
            PR
            PI   KINYA KAMIYA,YOKO MATSUDA,KIYOSHI UCHIDA
            PC   C12N15/09,A61K31/70,A61K48/00,C12Q1/68,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
     source          1. .20
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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1545 AGTAGGGAAGGAACAGGA 1562
              || || ||||||| ||||
Db          2 AGAAGAGAAGGAAGAGGA 19


RESULT 4199
E29916/c
LOCUS       E29916                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  HIV cofactor inhibitor.
ACCESSION   E29916
VERSION     E29916.1  GI:13021311
KEYWORDS    JP 1999292795-A/70.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hiroshi,T., Naoki,Y., Toru,K., Kazuyuki,T. and Akira,W.
  TITLE     HIV cofactor inhibitor
  JOURNAL   Patent: JP 1999292795-A 70 26-OCT-1999;
            YAMANOUCHI PHARMACEUT CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999292795-A/70
            PD   26-OCT-1999
            PF   02-APR-1998 JP 1998125452
            PR
            PI   HIROSHI TAKAHISA,NAOKI YAMAMOTO,TORU KIMURA,KAZUYUKI TAKAI, PI
              AKIRA WADA
            PC   A61K48/00,A61K31/70,A61K31/70,C12N15/09,C12N15/00 CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2581 GGAAGATTCTATTTAATT 2598
              |||||||| |||| || |
Db         19 GGAAGATTTTATTGAAAT 2


RESULT 4200
E29944
LOCUS       E29944                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  HIV cofactor inhibitor.
ACCESSION   E29944
VERSION     E29944.1  GI:13021339
KEYWORDS    JP 1999292795-A/98.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hiroshi,T., Naoki,Y., Toru,K., Kazuyuki,T. and Akira,W.
  TITLE     HIV cofactor inhibitor
  JOURNAL   Patent: JP 1999292795-A 98 26-OCT-1999;
            YAMANOUCHI PHARMACEUT CO LTD
COMMENT     OS   Unidentified
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E11007/c
LOCUS       E11007                    20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Primer for detecting human cytochrome P4501A2 polymorphism(one
            member of a couple).
ACCESSION   E11007
VERSION     E11007.1  GI:22024648
KEYWORDS    JP 1996070897-A/25.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fukui,T., Katsuragi,S., Kinoshita,M. and Shin,T.
  TITLE     DETECTION OF POLYMORPHISM OF HUMAN CYTOCHROME P4501A2 GENE
  JOURNAL   Patent: JP 1996070897-A 25 19-MAR-1996;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996070897-A/25
            PD   19-MAR-1996
            PF   06-JUL-1995 JP 1995170693
            PR   06-JUL-1994 JP 94P   154571
            PI   FUKUI TAKASHI, KATSURAGI SHIYUKUTEN, KINOSHITA MORITOSHI, PI
            SHIN TEIKIN
            PC   C12Q1/68,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1521 ATTGGAACGAAGAAAGGT 1538
              |||||  | |||||||||
Db         20 ATTGGTCCCAAGAAAGGT 3


RESULT 4195
E13293/c
LOCUS       E13293                    20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  PCR primer for amplifying ICE (interleukin-1 beta conversion
            enzyme) from human monocyte.
ACCESSION   E13293
VERSION     E13293.1  GI:3252098
KEYWORDS    JP 1997165360-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fukuda,T., Fujisawa,Y. and Watanabe,H.
  TITLE     CYSTEINE PROTEASE INHIBITOR
  JOURNAL   Patent: JP 1997165360-A 1 24-JUN-1997;
            TAKEDA CHEM IND LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997165360-A/1
            PD   24-JUN-1997
            PF   28-MAR-1996 JP 1996073861
            PR   31-MAR-1995 JP 95P    75593, 31-MAR-1995 JP 95P    75594, PR
            13-OCT-1995 JP 95P   265723
            PI   FUKUDA TSUNEHIKO, FUJISAWA YUKIO, WATANABE HIROYUKI PC
            C07C243/12,A61K38/55,A61K38/55,A61K38/55,A61K38/55,A61K38/55, PC
            A61K38/55,
            PC
            C07C243/26,C07C271/12,C07C323/60,C07K5/023,C07K5/027,C07K5/062, PC
            C12N9/99;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2152 TGATTTTTTTCTCCTTTT 2169
              ||  |||| |||||||||
Db         18 TGGCTTTTCTCTCCTTTT 1


RESULT 4196
E13785
LOCUS       E13785                    20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  PCR primer for discriminating genotype 2a of HCV (Hepatitis C
            virus).
ACCESSION   E13785
VERSION     E13785.1  GI:3252553
KEYWORDS    JP 1997234072-A/37.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ono,T., Mukaide,M., Hikichi,K. and Mizogami,M.
  TITLE     NEW OLIGONUCLEOTIDE, PRIMER FOR DISCRIMINATION IN GENOTYPE OF
            HEPATITIS C VIRUS COMPRISING THE SAME AND DISCRIMINATION IN
            GENOTYPE OF HEPATITIS C VIRUS BY USING THE PRIMER
  JOURNAL   Patent: JP 1997234072-A 37 09-SEP-1997;
            S R L:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997234072-A/37
            PD   09-SEP-1997
            PF   01-FEB-1996 JP 1996038875
            PR   01-FEB-1995 JP 95P    35997, 30-DEC-1995 JP 95P   352511 PI
            ONO TOMOYOSHI, MUKAIDE MASAKAZU, HIKICHI KAZUMASA, PI   MIZOGAMI
            MASAFUMI
            PC   C12N15/09,C07H21/04,C12Q1/68,C12Q1/70,(C12N15/09,C12R1:92); CC
              strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        437 CACCAGCCGGCGCCCACA 454
              ||| | ||| ||||||||
Db          2 CACTAACCGTCGCCCACA 19
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        548 CTCTCCGGGCTGGAGGCG 565
              |||| |||||||  ||||
Db         18 CTCTGCGGGCTGTGGGCG 1


RESULT 4191
BD244903/c
LOCUS       BD244903                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Modulation of gene expression by combination therapy.
ACCESSION   BD244903
VERSION     BD244903.1  GI:33054673
KEYWORDS    JP 2002528391-A/31.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Besterman,J.M., Macleod,A.R. and Siders,W.M.
  TITLE     Modulation of gene expression by combination therapy
  JOURNAL   Patent: JP 2002528391-A 31 03-SEP-2002;
            METHYLGENE INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002528391-A/31
            PD   03-SEP-2002
            PF   19-OCT-1999 JP 2000576885
            PR   19-OCT-1998 US    60/104804
            PI   JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
            A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
            706,
            PC
            A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
             09//
            PC   C12N5/10,C12N15/00,C12N5/00
            CC   antisense
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
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                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2661 AGTGTGCAGTACAGTGTG 2678
              | ||||||||||  ||||
Db         19 ATTGTGCAGTACTTTGTG 2


RESULT 4192
BD262872
LOCUS       BD262872                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide modulation of human protein kinase
            C-delta expression.
ACCESSION   BD262872
VERSION     BD262872.1  GI:33072640
KEYWORDS    JP 2002543853-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M.
  TITLE     Antisense oligonucleotide modulation of human protein kinase
            C-delta expression
  JOURNAL   Patent: JP 2002543853-A 4 24-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543853-A/4
            PD   24-DEC-2002
            PF   11-MAY-2000 JP 2000618496
            PR   18-MAY-1999 US    09/313930
            PI   NICHOLAS M DEAN
            PC   C12N15/09,A61K31/7084,A61K31/7088,A61K48/00,A61P1/00,A61P1/16,
            PC   A61P1/18,
            PC   A61P3/10,A61P17/00,A61P17/06,A61P19/02,A61P29/00,A61P29/00, PC
              A61P31/00,
            PC   A61P35/00,A61P35/02,A61P37/00,A61P37/06,C12N15/00 CC
            Synthetic
            FH   Key             Location/Qualifiers
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FEATURES              Location/Qualifiers
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1660 TCTGCATCACCCGCCCCT 1677
              |||| || || |||||||
Db          2 TCTGGATGACGCGCCCCT 19


RESULT 4193
BD276137
LOCUS       BD276137                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel Genes and Expression Products from Hematopoietic Cells.
ACCESSION   BD276137
VERSION     BD276137.1  GI:33085905
KEYWORDS    JP 2002541850-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Liu,X. and Cheng,L.
  TITLE     Novel Genes and Expression Products from Hematopoietic Cells
  JOURNAL   Patent: JP 2002541850-A 9 10-DEC-2002;
            Xuan Liu,Linzhou Cheng
COMMENT     OS   Artificial Sequence
            PN   JP 2002541850-A/9
            PD   10-DEC-2002
            PF   14-APR-2000 JP 2000612461
            PR   15-APR-1999 US    60/129463
            PI   xuan liu,linzhou cheng
            CC   Description of Artificial Sequence:PCR primer based on 5'- CC
                 untranslated
            CC   region of C17 cDNA
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTT 2168
              ||||||||  || |||||
Db          2 TTGATTTTCATCACCTTT 19


RESULT 4194
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            SHANAHAN JR
            PC   C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/
            PC   00,A61P1/16,
            PC   A61P1/18,A61P3/10,A61P17/00,A61P17/04,A61P29/00,A61P31/00, PC
             C07H21/02,
            PC   C07H21/04,C12N15/00
            CC   Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2442 GACTTTTTTGAGACATGG 2459
              ||||| |||||||| ||
Db         18 GACTTCCTTGAGACACGG 1


RESULT 4188
BD230714/c
LOCUS       BD230714                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Total genome radiation hybrid map of canine genome and its use for
            identification of interesting genes.
ACCESSION   BD230714
VERSION     BD230714.1  GI:33040484
KEYWORDS    JP 2002530091-A/583.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Galibert,F. and Andre,C.
  TITLE     Total genome radiation hybrid map of canine genome and its use for
            identification of interesting genes
  JOURNAL   Patent: JP 2002530091-A 583 17-SEP-2002;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
COMMENT     OS   Canis familiaris (dog)
            PN   JP 2002530091-A/583
            PD   17-SEP-2002
            PF   15-NOV-1999 JP 2000582596
            PR   13-NOV-1998 US    60/108193
            PI   FRANCIS GALIBERT,CATHERINE ANDRE
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   ATH1007
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Canis familiaris (dog)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        550 CTCCGGGCTGGAGGCGGG 567
              |||||||| || | ||||
Db         20 CTCCGGGCAGGGGCCGGG 3


RESULT 4189
BD237728
LOCUS       BD237728                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  p53 binding region.
ACCESSION   BD237728
VERSION     BD237728.1  GI:33047498
KEYWORDS    JP 2002527108-A/14.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Krammer,P., Schilling,M.M. and Oren,M.
  TITLE     p53 binding region
  JOURNAL   Patent: JP 2002527108-A 14 27-AUG-2002;
            DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICHEN RECHTS
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002527108-A/14
            PD   27-AUG-2002
            PF   18-OCT-1999 JP 2000577293
            PR   16-OCT-1998 DE 198 47 779.1
            PI   PETER KRAMMER,MARTINA MUELLER SCHILLING,MOSHE OREN PC
            C12N15/09,C12Q1/66,C12Q1/68,G01N33/566,C12N15/00 CC   p53 binding
            region
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1759 TATTCATTAAGCTTTTTT 1776
              | ||  ||||||||||||
Db          3 TGTTGCTTAAGCTTTTTT 20


RESULT 4190
BD241885/c
LOCUS       BD241885                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation.
ACCESSION   BD241885
VERSION     BD241885.1  GI:33051655
KEYWORDS    JP 2002518007-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: JP 2002518007-A 4 25-JUN-2002;
            RECHERCHES EXPERTISES ET DEVELOPPEMENT MEDICAUX PARENZ INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002518007-A/4
            PD   25-JUN-2002
            PF   17-JUN-1999 JP 2000554846
            PR   17-JUN-1998 CA      2235420
            PI   PAOLO RENZI
            PC   C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P11/06,A61P29/00,
            PC   A61P35/00,
            PC   A61P37/08,C12N15/00,A61K37/02
            CC   Antisense oligonucleotide inhibiting the common subunit of IL-
            CC            4 and IL-13
            CC   human receptor
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
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LOCUS       AR176820                 20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 75 from patent US 6312900.
ACCESSION   AR176820
VERSION     AR176820.1  GI:17919175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of activating protein 1
  JOURNAL   Patent: US 6312900-A 75 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         52 CGGCGGGGGCGGCGGCAG 69
              |||||| ||||||  |||
Db         20 CGGCGGCGGCGGCTACAG 3


RESULT 4185
BD227851
LOCUS       BD227851                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha).
ACCESSION   BD227851
VERSION     BD227851.1  GI:33037621
KEYWORDS    JP 2002526125-A/54.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,F.C., Butler,M.M. and Jr,W.J.S.
  TITLE     Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha)
  JOURNAL   Patent: JP 2002526125-A 54 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526125-A/54
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574737
            PR   05-OCT-1998 US    09/166186,18-MAY-1999 US    09/313932 PI
            BRENDA F BAKER,FRANK C BENNETT,MADELINE M BUTLER,WILLIAM J  PI
            SHANAHAN JR
            PC   C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/
            PC   00,A61P1/16,
            PC   A61P1/18,A61P3/10,A61P17/00,A61P17/04,A61P29/00,A61P31/00, PC
             C07H21/02,
            PC   C07H21/04,C12N15/00
            CC   Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTT 2174
              | ||||||| | |||||||
Db          3 TCTTTCTCCATGTTTTTT 20


RESULT 4186
BD228155/c
LOCUS       BD228155                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha).
ACCESSION   BD228155
VERSION     BD228155.1  GI:33037925
KEYWORDS    JP 2002526125-A/358.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,F.C., Butler,M.M. and Jr,W.J.S.
  TITLE     Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha)
  JOURNAL   Patent: JP 2002526125-A 358 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526125-A/358
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574737
            PR   05-OCT-1998 US    09/166186,18-MAY-1999 US    09/313932 PI
            BRENDA F BAKER,FRANK C BENNETT,MADELINE M BUTLER,WILLIAM J  PI
            SHANAHAN JR
            PC   C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/
            PC   00,A61P1/16,
            PC   A61P1/18,A61P3/10,A61P17/00,A61P17/04,A61P29/00,A61P31/00, PC
             C07H21/02,
            PC   C07H21/04,C12N15/00
            CC   Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2099 TCAAACGGGGGCCTTCTG 2116
              |||||| ||||||| | |
Db         20 TCAAACTGGGGCCTCCAG 3


RESULT 4187
BD228172/c
LOCUS       BD228172                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha).
ACCESSION   BD228172
VERSION     BD228172.1  GI:33037942
KEYWORDS    JP 2002526125-A/375.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,F.C., Butler,M.M. and Jr,W.J.S.
  TITLE     Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha)
  JOURNAL   Patent: JP 2002526125-A 375 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526125-A/375
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574737
            PR   05-OCT-1998 US    09/166186,18-MAY-1999 US    09/313932 PI
            BRENDA F BAKER,FRANK C BENNETT,MADELINE M BUTLER,WILLIAM J  PI
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RESULT 4179
AR163800/c
LOCUS       AR163800                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 87 from patent US 6271029.
ACCESSION   AR163800
VERSION     AR163800.1  GI:16234553
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Cowsert,L.M.
  TITLE     Antisense inhibition of cytohesin-2 expression
  JOURNAL   Patent: US 6271029-A 87 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1198 GATGGCAGCTAGGAAGAA 1215
              | ||||||| || ||||||
Db         20 GCTGGCAGCGAGAAAGAA 3


RESULT 4180
AR163845
LOCUS       AR163845                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 43 from patent US 6271030.
ACCESSION   AR163845
VERSION     AR163845.1  GI:16234628
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP beta expression
  JOURNAL   Patent: US 6271030-A 43 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        152 GGGACGCCGGACGCCATG 169
              |||| ||| | |||||||
Db          1 GGGAAGCCCGCCGCCATG 18


RESULT 4181
AR167027
LOCUS       AR167027                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 44 from patent US 6284458.
ACCESSION   AR167027
VERSION     AR167027.1  GI:16243449
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Anderson,K.P., Hanecak,R.C., Hoshiko,K., Nozaki,C., Nishihara,T.,
            Nakatake,H., Hamada,F., Eto,T. and Furukawa,S.
  TITLE     Compositions and methods for treatment of hepatitis C
            virus-associated diseases
  JOURNAL   Patent: US 6284458-A 44 04-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        113 GGCTGGGGGGATCCTGGA 130
              ||  |||||| |||||||
Db          2 GGGAGGGGGGGTCCTGGA 19


RESULT 4182
AR174359/c
LOCUS       AR174359                  20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 19 from patent US 6306655.
ACCESSION   AR174359
VERSION     AR174359.1  GI:17914679
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP alpha expression
  JOURNAL   Patent: US 6306655-A 19 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        555 GGCTGGAGGCGGGCGCGG 572
              |||||||||| | || ||
Db         19 GGCTGGAGGCCGCCGAGG 2


RESULT 4183
AR174400
LOCUS       AR174400                  20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 60 from patent US 6306655.
ACCESSION   AR174400
VERSION     AR174400.1  GI:17914720
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP alpha expression
  JOURNAL   Patent: US 6306655-A 60 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGCCGATGCGTGTCCAGT 27
              | |||  ||||||||||
Db          1 CCCCGCAGCGTGTCCAGT 18


RESULT 4184
AR176820/c
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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1660 TCTGCATCACCCGCCCCT 1677
              |||| || || |||||||
Db          2 TCTGGATGACGCGCCCCT 19


RESULT 4174
AR158938
LOCUS       AR158938                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 560 from patent US 6251588.
ACCESSION   AR158938
VERSION     AR158938.1  GI:16221355
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 560 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTG 2193
              |||| |||||||||  ||
Db          1 TTTTCTTTTTTAACCCTG 18


RESULT 4175
AR162414/c
LOCUS       AR162414                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 94 from patent US 6258600.
ACCESSION   AR162414
VERSION     AR162414.1  GI:16229592
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zhang,H. and Cowsert,L.M.
  TITLE     Antisense modulation of caspase 8 expression
  JOURNAL   Patent: US 6258600-A 94 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        898 GGCTGAAGTACAGAGGCG 915
              ||||| ||| ||| ||||
Db         19 GGCTGGAGTGCAGTGGCG 2


RESULT 4176
AR162752
LOCUS       AR162752                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 75 from patent US 6258790.
ACCESSION   AR162752
VERSION     AR162752.1  GI:16230091
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank., Condon,T.P. and Cowsert,L.M.
  TITLE     Antisense modulation of integrin .alpha.4 expression
  JOURNAL   Patent: US 6258790-A 75 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1900 AGATCAACAGATCAACAA 1917
              ||||||||||   ||||
Db          3 AGATCAACAGAAGTACAA 20


RESULT 4177
AR163069/c
LOCUS       AR163069                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 52 from patent US 6270963.
ACCESSION   AR163069
VERSION     AR163069.1  GI:16233551
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Stevens,J.K., Dunn,J.M., Capatos,D. and Matthews,D.E.
  TITLE     Method for testing for mutations in DNA from a patient sample
  JOURNAL   Patent: US 6270963-A 52 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        944 TCGTTACTGGGAGGTGTT 961
              | |||| || ||||||||
Db         19 TTGTTAGTGAGAGGTGTT 2


RESULT 4178
AR163737/c
LOCUS       AR163737                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 24 from patent US 6271029.
ACCESSION   AR163737
VERSION     AR163737.1  GI:16234435
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Cowsert,L.M.
  TITLE     Antisense inhibition of cytohesin-2 expression
  JOURNAL   Patent: US 6271029-A 24 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        795 AGAAGGAGCTGGTGGGGG 812
              || |||||||| ||| ||
Db         20 AGCAGGAGCTGCTGGTGG 3
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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        440 CAGCCGGCGCCCACAGGC 457
              | |||||| ||||| |||
Db         20 CCGCCGGCTCCCACCGGC 3


RESULT 4169
AR137244
LOCUS       AR137244                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 2 from patent US 6197503.
ACCESSION   AR137244
VERSION     AR137244.1  GI:14478753
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Vo-Dinh,T., Wintenberg,A. and Ericson,M.N.
  TITLE     Integrated circuit biochip microsystem containing lens
  JOURNAL   Patent: US 6197503-A 2 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        347 CCCCCTCCCTACCAGCAG 364
              || |||||  | |||||||
Db          1 CCTCCTCCTTCCCAGCAG 18


RESULT 4170
AR149978
LOCUS       AR149978                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 54 from patent US 6228642.
ACCESSION   AR149978
VERSION     AR149978.1  GI:15114569
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-(.alpha.) (TNF-.alpha.) expression
  JOURNAL   Patent: US 6228642-A 54 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTT 2174
              \ ||||||| | ||||||
Db          3 TCTTTCTCCATGTTTTTT 20


RESULT 4171
AR150282/c
LOCUS       AR150282                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 358 from patent US 6228642.
ACCESSION   AR150282
VERSION     AR150282.1  GI:15114873
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-(.alpha.) (TNF-.alpha.) expression
  JOURNAL   Patent: US 6228642-A 358 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2099 TCAAACGGGGGCCTTCTG 2116
              |||||| ||||||| | |
Db         20 TCAAACTGGGGCCTCCAG 3


RESULT 4172
AR150299/c
LOCUS       AR150299                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 375 from patent US 6228642.
ACCESSION   AR150299
VERSION     AR150299.1  GI:15114890
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-(.alpha.) (TNF-.alpha.) expression
  JOURNAL   Patent: US 6228642-A 375 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2442 GACTTTTTTGAGACATGG 2459
              |||||  |||||||| ||
Db         18 GACTTCCTTGAGACACGG 1


RESULT 4173
AR153557
LOCUS       AR153557                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 5 from patent US 6235723.
ACCESSION   AR153557
VERSION     AR153557.1  GI:15121089
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M.
  TITLE     Antisense oligonucleotide modulation of human protein kinase
            C-.delta. expression
  JOURNAL   Patent: US 6235723-A 5 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
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  JOURNAL    Patent: US 6140125-A 15 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        157 GCCGGACGCCATGTTGTG 174
              ||||||| ||| ||| ||
Db         20 GCCGGACACCAGGTTTTG 3


RESULT 4164
AR117748/c
LOCUS       AR117748                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 56 from patent US 6140126.
ACCESSION   AR117748
VERSION     AR117748.1  GI:14098654
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Cowsert,L.M.
  TITLE     Antisense modulation of Y-box binding protein 1 expression
  JOURNAL   Patent: US 6140126-A 56 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        911 AGGCGACTGTCCCCACCT 928
              |||||| || |||||||
Db         19 AGGCGAAGGTTCCCACCT 2


RESULT 4165
AR118903/c
LOCUS       AR118903                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 29 from patent US 6150092.
ACCESSION   AR118903
VERSION     AR118903.1  GI:14100813
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
  TITLE     Antisense nucleic acid compound targeted to VEGF
  JOURNAL   Patent: US 6150092-A 29 21-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        785 CTCCCCTGTCAGAAGGAG 802
              | ||| || |||||||||
Db         19 CACCCATGGCAGAAGGAG 2


RESULT 4166
AR124508/c
LOCUS       AR124508                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 77 from patent US 6171860.
ACCESSION   AR124508
VERSION     AR124508.1  GI:14109869
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense inhibition of rank expression
  JOURNAL   Patent: US 6171860-A 77 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        461 CAGCAGCAGGCCTGGCCC 478
              |||| |||||||  ||||
Db         18 CAGCTGCAGGCCACGCCC 1


RESULT 4167
AR125583
LOCUS       AR125583                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 84 from patent US 6177273.
ACCESSION   AR125583
VERSION     AR125583.1  GI:14111645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Cowsert,L.M.
  TITLE     Antisense modulation of integrin-linked kinase expression
  JOURNAL   Patent: US 6177273-A 84 23-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1461 ACCAGAGTCCAGCTGATT 1478
              ||||||| || |||| ||
Db          3 ACCAGAGGCCTGCTGCTT 20


RESULT 4168
AR130116/c
LOCUS       AR130116                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 19 from patent US 6187587.
ACCESSION   AR130116
VERSION     AR130116.1  GI:14118013
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Popoff,I., Brown-Driver,V.L. and Cowsert,L.M.
  TITLE     Antisense inhibition of e2f transcription factor 1 expression
  JOURNAL   Patent: US 6187587-A 19 13-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 48 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2144 CTGCTGATTGATTTTTTT 2161
              |||||| || |||| |||
Db          2 CTGCTGTTTTATTTATTT 19


RESULT 4159
AR107609
LOCUS       AR107609                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 49 from patent US 6110664.
ACCESSION   AR107609
VERSION     AR107609.1  GI:12823096
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 49 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2144 CTGCTGATTGATTTTTTT 2161
              |||||| || |||| |||
Db          3 CTGCTGTTTTATTTATTT 20


RESULT 4160
AR107637/c
LOCUS       AR107637                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 77 from patent US 6110664.
ACCESSION   AR107637
VERSION     AR107637.1  GI:12823124
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 77 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2801
              ||||| |||| ||| |||
Db         20 TGAAATAAAAGAAACAAA 3


RESULT 4161
AR112528/c
LOCUS       AR112528                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 30 from patent US 6130071.
ACCESSION   AR112528
VERSION     AR112528.1  GI:14092428
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Alitalo,K. and Joukov,V.
  TITLE     Vascular endothelial growth factor C (VEGF-C) .DELTA.Cys.sub.156
            protein and gene, and uses thereof
  JOURNAL   Patent: US 6130071-A 30 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2593 TTAATTGAAACTCTCTGT 2610
              |||||| | |||| ||||
Db         20 TTAATTCATACTCACTGT 3


RESULT 4162
AR112680/c
LOCUS       AR112680                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 44 from patent US 6130088.
ACCESSION   AR112680
VERSION     AR112680.1  GI:14092580
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of telomeric repeat binding factor 1
            expression
  JOURNAL   Patent: US 6130088-A 44 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1921 CTTTTTTTTCAGTGTTAA 1938
              ||||| || ||||||| |
Db         19 CTTTTGTTCCAGTGTTTA 2


RESULT 4163
AR117618/c
LOCUS       AR117618                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 15 from patent US 6140125.
ACCESSION   AR117618
VERSION     AR117618.1  GI:14098524
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Taylor,J.K. and Cowsert,L.M.
  TITLE     Antisense inhibition of bcl-6 expression
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ACCESSION   AR100057
VERSION     AR100057.1  GI:12810505
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Gaarde,W. and Cowsert,L.M.
  TITLE     Antisense modulation of MEKK5 expression
  JOURNAL   Patent: US 6080546-A 14 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        543 CCCACCTCTCCGGGCTGG 560
              | || |||||||||| ||
Db          1 CTCATCTCTCCGGGCCGG 18


RESULT 4154
AR100058
LOCUS       AR100058                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 15 from patent US 6080546.
ACCESSION   AR100058
VERSION     AR100058.1  GI:12810506
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Gaarde,W. and Cowsert,L.M.
  TITLE     Antisense modulation of MEKK5 expression
  JOURNAL   Patent: US 6080546-A 15 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        543 CCCACCTCTCCGGGCTGG 560
              | || |||||||||| ||
Db          3 CTCATCTCTCCGGGCCGG 20


RESULT 4155
AR100067/c
LOCUS       AR100067                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 24 from patent US 6080546.
ACCESSION   AR100067
VERSION     AR100067.1  GI:12810515
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Gaarde,W. and Cowsert,L.M.
  TITLE     Antisense modulation of MEKK5 expression
  JOURNAL   Patent: US 6080546-A 24 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        265 CTCCGCCGGGCAGCACCT 282
              | |||||||||||| ||
Db         20 CGCCGCCGGGCAGCTTCT 3


RESULT 4156
AR100323
LOCUS       AR100323                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 54 from patent US 6080580.
ACCESSION   AR100323
VERSION     AR100323.1  GI:12810771
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-.alpha. (TNF-.alpha.) expression
  JOURNAL   Patent: US 6080580-A 54 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTT 2174
              | ||||||| | |||||||
Db          3 TCTTTCTCCATGTTTTTT 20


RESULT 4157
AR107574/c
LOCUS       AR107574                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 14 from patent US 6110664.
ACCESSION   AR107574
VERSION     AR107574.1  GI:12823061
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 14 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1329 ACTGCTTGTCTCATTTCA 1346
              ||||||   |||||||||
Db         19 ACTGCTACCCTCATTTCA 2


RESULT 4158
AR107608
LOCUS       AR107608                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 48 from patent US 6110664.
ACCESSION   AR107608
VERSION     AR107608.1  GI:12823095
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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RESULT 4148
AR076700
LOCUS       AR076700                 20 bp    DNA     linear   PAT 30-AUG-2000
DEFINITION  Sequence 65 from patent US 5959096.
ACCESSION   AR076700
VERSION     AR076700.1  GI:10003446
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Dean,N.
  TITLE     Antisense oligonucleotides against human protein kinase C
  JOURNAL   Patent: US 5959096-A 65 28-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1660 TCTGCATCACCCGCCCCT 1677
              |||| || || |||||||
Db          2 TCTGGATGACGCGCCCCT 19


RESULT 4149
AR082034/c
LOCUS       AR082034                 20 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 13 from patent US 5972692.
ACCESSION   AR082034
VERSION     AR082034.1  GI:10008760
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hashimoto,K., Ito,K. and Ishimori,Y.
  TITLE     Gene detection method
  JOURNAL   Patent: US 5972692-A 13 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1597 ACCCCTCCTGGCCTGGGG 1614
              || |||||||||| | ||
Db         19 ACTCCTCCTGGCCGGCGG 2


RESULT 4150
AR086254/c
LOCUS       AR086254                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 75 from patent US 5985558.
ACCESSION   AR086254
VERSION     AR086254.1  GI:10013020
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
  TITLE     Antisense oligonucleotide compositions and methods for the
            inibition of c-Jun and c-Fos
  JOURNAL   Patent: US 5985558-A 75 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         52 CGGCGGGGGCGGCGGCAG 69
              |||||| ||||||  |||
Db         20 CGGCGGCGGCGGCTACAG 3


RESULT 4151
AR092388
LOCUS       AR092388                 20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 59 from patent US 5998148.
ACCESSION   AR092388
VERSION     AR092388.1  GI:10019142
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Ackermann,E.J.
  TITLE     Antisense modulation of microtubule-associated protein 4 expression
  JOURNAL   Patent: US 5998148-A 59 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         55 CGGGGGCGGCGGCAGACG 72
              |||||| | ||| |||||
Db          2 CGGGGGAGACGGAAGACG 19


RESULT 4152
AR092398/c
LOCUS       AR092398                 20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 69 from patent US 5998148.
ACCESSION   AR092398
VERSION     AR092398.1  GI:10019152
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Ackermann,E.J.
  TITLE     Antisense modulation of microtubule-associated protein 4 expression
  JOURNAL   Patent: US 5998148-A 69 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        287 AGCCCCGCGCCACCCCTC 304
              ||||| || |||| ||||
Db         20 AGCCCTGCCCCACACCTC 3


RESULT 4153
AR100057
LOCUS       AR100057                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 14 from patent US 6080546.
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RESULT 4143
AR043098/c
LOCUS       AR043098                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5814448.
ACCESSION   AR043098
VERSION     AR043098.1  GI:5964106
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Silverstein,S.J., Lungu,O. and Wright,T.C. Jr.
  TITLE     Polymerase chain reaction/restriction fragment polymorphism method
            for the detection and typing of human papillomaviruses
  JOURNAL   Patent: US 5814448-A 1 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1292 AGCAGGCTCGCCCCAGTC 1309
              ||||||| ||| |||| |
Db         20 AGCAGGCGCGCGCCAGCC 3


RESULT 4144
AR059098/c
LOCUS       AR059098                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5837854.
ACCESSION   AR059098
VERSION     AR059098.1  GI:5984675
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mulder,C.
  TITLE     Oligonucleotides with anti-Epstein-Barr virus activity
  JOURNAL   Patent: US 5837854-A 16 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        392 TACTCGCATCTGGGGGAA 409
              | ||||||| |||| ||||
Db         19 TGCTCGCAGCTGGAGGAA 2


RESULT 4145
AR070920/c
LOCUS       AR070920                 20 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 8 from patent US 5908971.
ACCESSION   AR070920
VERSION     AR070920.1  GI:7221808
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Van Der Straeten,D., Goodman,H. and Van Montagu,M.
  TITLE     Crucifer ACC synthase and uses thereof
  JOURNAL   Patent: US 5908971-A 8 01-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2106 GGGGCCTTCTGGTTTTAG 2123
              ||| | | ||||||||||
Db         20 GGGACTTCCTGGTTTTAG 3


RESULT 4146
AR072276/c
LOCUS       AR072276                 20 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 79 from patent US 5948611.
ACCESSION   AR072276
VERSION     AR072276.1  GI:9999040
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Prockop,D.J., Ala-Kokko,L., Williams,C.J., Ritvaniemi,P.,
            Baldwin,C., Hopkinson,I. and Ahmad,N.Nina.
  TITLE     Primers and methods for detecting mutations in the procollagen II
            gene (COL2A1) that indicate a genetic predisposition for a
            COL2A1-associated disease
  JOURNAL   Patent: US 5948611-A 79 07-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2568 CTGTTCTTGGCTTGGAAG 2585
              |||||||  || ||||||
Db         19 CTGTTCTCAGCATGGAAG 2


RESULT 4147
AR072355/c
LOCUS       AR072355                 20 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 158 from patent US 5948611.
ACCESSION   AR072355
VERSION     AR072355.1  GI:9999119
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Prockop,D.J., Ala-Kokko,L., Williams,C.J., Ritvaniemi,P.,
            Baldwin,C., Hopkinson,I. and Ahmad,N.Nina.
  TITLE     Primers and methods for detecting mutations in the procollagen II
            gene (COL2A1) that indicate a genetic predisposition for a
            COL2A1-associated disease
  JOURNAL   Patent: US 5948611-A 158 07-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        784 CCTCCCCTGTCAGAAGGA 801
              ||||| ||||||||  ||
Db         18 CCTCCGCTGTCAGACAGA 1
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A90123/c
LOCUS       A90123                    20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 304 from Patent EP0856579.
ACCESSION   A90123
VERSION     A90123.1  GI:6738637
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 304 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        160 GGACGCCATGTTGTGGAA 177
              |||| | || ||||||||
Db         20 GGACACGATTTTGTGGAA 3


RESULT 4139
AR015993/c
LOCUS       AR015993                  20 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 13 from patent US 5776672.
ACCESSION   AR015993
VERSION     AR015993.1  GI:3972270
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hashimoto,K., Ito,K., Ishimori,Y. and Gotoh,M.
  TITLE     Gene detection method
  JOURNAL   Patent: US 5776672-A 13 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1597 ACCCCTCCTGGCCTGGGG 1614
              || |||||||||| | ||
Db         19 ACTCCTCCTGGCCGGCGG 2


RESULT 4140
AR023457
LOCUS       AR023457                  20 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 13 from patent US 5795569.
ACCESSION   AR023457
VERSION     AR023457.1  GI:3976751
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bartley,T.D., Bogenberger,J.M., Bosselman,R.A., Hunt,P.,
            Kinstler,O.B. and Samal,B.B.
  TITLE     Mono-pegylated proteins that stimulate megakaryocyte growth and
            differentiation
  JOURNAL   Patent: US 5795569-A 13 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2301 GTAGGCACGAAGCAATTT 2318
              | || ||||||||| |||
Db          1 GGAGTCACGAAGCAGTTT 18


RESULT 4141
AR032199/c
LOCUS       AR032199                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 28 from patent US 5866777.
ACCESSION   AR032199
VERSION     AR032199.1  GI:5946488
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sijmons,P.Christiaan., Goddijn,O.Johannes.Maria., Van Den
            Elzen,P.Josephus.Maria. and Van Der Lee,F.Marianne.
  TITLE     Method for obtaining plants with reduced susceptibility to
            plant-parasitic nematodes
  JOURNAL   Patent: US 5866777-A 28 02-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        666 TCCACGACATGCCTCACC 683
              | | |||||||| |||||
Db         18 TGCGCGACATGCGTCACC 1


RESULT 4142
AR043098
LOCUS       AR043098                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5814448.
ACCESSION   AR043098
VERSION     AR043098.1  GI:5964106
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Silverstein,S.J., Lungu,O. and Wright,T.C. Jr.
  TITLE     Polymerase chain reaction/restriction fragment polymorphism method
            for the detection and typing of human papillomaviruses
  JOURNAL   Patent: US 5814448-A 1 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        632 CTGGATGCCGCGGGCCTG 649
              |||| || |||| |||||
Db          1 CTGGCTGGCGCGCGCCTG 18
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A24900/c
LOCUS       A24900                    20 bp    RNA     linear   PAT 23-JUN-1995
DEFINITION  oligonucleotide.
ACCESSION   A24900
VERSION     A24900.1  GI:1248045
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  TITLE     A METHOD FOR OBTAINING PLANTS WITH REDUCED SUSCEPTIBILITY TO
            PLANT-PARASITIC NEMATODES
  JOURNAL   Patent: WO 9310251-A 30 27-MAY-1993;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        666 TCCACGACATGCCTCACC 683
              | | ||||||||| |||||
Db         18 TGCGCGACATGCGTCACC 1


RESULT 4134
A25840
LOCUS       A25840                    20 bp    DNA     linear   PAT 02-OCT-1995
DEFINITION  pcp gene PCR primer YU1.
ACCESSION   A25840
VERSION     A25840.1  GI:1248102
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  JOURNAL   Patent: FR 2685334-A 14 25-JUN-1993;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        921 CCCCACCTGAATGCTTAA 938
              ||| | || ||||||||||
Db          1 CCCTATCTCAATGCTTAA 18


RESULT 4135
A28702/c
LOCUS       A28702                    20 bp    RNA     linear   PAT 04-JUN-1995
DEFINITION  Oligonucleotide 26 (comp.).
ACCESSION   A28702
VERSION     A28702.1  GI:1248741
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  TITLE     SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
  JOURNAL   Patent: WO 9014090-A 30 29-NOV-1990;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        106 GCTTGGGGGCTGGGGGGAT 124
              | ||||||| ||||| ||
Db         19 GNTTGGGGGGGGGGGGAAT 1


RESULT 4136
A28704/c
LOCUS       A28704                    20 bp    RNA     linear   PAT 04-JUN-1995
DEFINITION  Oligonucleotide 28 (comp.).
ACCESSION   A28704
VERSION     A28704.1  GI:1248743
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  TITLE     SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
  JOURNAL   Patent: WO 9014090-A 32 29-NOV-1990;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        106 GCTTGGGGGCTGGGGGGAT 124
              | ||||||| ||||| ||
Db         19 GNTTGGGGGGGGGGGGAAT 1


RESULT 4137
A88156/c
LOCUS       A88156                    20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 304 from Patent WO9833904.
ACCESSION   A88156
VERSION     A88156.1  GI:6736726
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 304 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        160 GGACGCCATGTTGTGGAA 177
              |||| | || ||||||||
Db         20 GGACACGATTTTGTGGAA 3


RESULT 4138
```

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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||||||   |||
Db          1 AAAAAAAAAAAAGCGAAA 18


RESULT 4129
AR030970/c
LOCUS       AR030970                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5861501.
ACCESSION   AR030970
VERSION     AR030970.1  GI:5944184
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 2 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         20 GAAAATTAAAAATAAAAA 3


RESULT 4130
AR108815/c
LOCUS       AR108815                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 2 from patent US 6111095.
ACCESSION   AR108815
VERSION     AR108815.1  GI:12824302
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 2 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         20 GAAAATTAAAAATAAAAA 3


RESULT 4131
AR205764/c
LOCUS       AR205764                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 2 from patent US 6369208.
ACCESSION   AR205764
VERSION     AR205764.1  GI:21503429
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 2 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         20 GAAAATTAAAAATAAAAA 3


RESULT 4132
DOGP26302/c
LOCUS       DOGP26302                 20 bp    DNA     linear   MAM 11-JUN-1993
DEFINITION  Dog (Clone: CXX.263) primer for STS 263, 3' end.
ACCESSION   L15677
VERSION     L15677.1  GI:290175
KEYWORDS    PCR identification; PCR primer; STS.
SEGMENT     2 of 2
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ostrander,E.A., Sprague,G.F.Jr. and Rine,J.D.
  TITLE     Identification and characterization of dinucleotide repeat (CA)n
            markers for genetic mapping in dog
  JOURNAL   Genomics (1993) In press
COMMENT     Original source text: Canis familiaris (library: E. Ostrander, in
            pBluescript+) adult spleen DNA.
            Submitted by: Human Genome Center,
            Lawrence Berkeley Laboratory,
            1 Cyclotron Road, Berkeley, CA  94720, USA
            e-mail: EAOstrander@lbl.gov
            PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
            PCR Profile:  Denaturation:    94 degrees C for 1.00 minute
            Annealing:       55 or 59 degrees C for 0.45 minutes
            Polymerization:  74 degrees C for 1.00 minutes
            PCR Cycles:      33
            Final Extension:  74 degrees C for 5.00 minutes.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
                     /tissue_type="spleen"
                     /dev_stage="adult"
                     /tissue_lib="E. Ostrander, in pBluescript+"
     primer_bind     complement(1. .20)
                     /evidence=experimental

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1175 CCTCATCTTGGAGGACGA 1192
              ||  ||||||||||||  ||
Db         20 CCACATCTTGGAGGGTGA 3


RESULT 4133
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SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okano,K. and Kanbara,H.
  TITLE     PRIMER FOR DNA POLYMERASE REACTION AND DETERMINATION OF
            POLYNUCLEOTIDE SEQUENCE USING THE SAME
  JOURNAL   Patent: JP 1996332100-A 1 17-DEC-1996;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996332100-A/1
            PD   17-DEC-1996
            PF   06-JUN-1995 JP 1995139051
            PI   OKANO KAZUNOBU, KANBARA HIDEKI
            PC   C12Q1/68,C07H21/04//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAA 2798
              ||   ||||||||||||
Db         18 AAGCTAAAAAAAAAAAAA 1


RESULT 4125
AR360400
LOCUS       AR360400                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 15 from patent US 6596489.
ACCESSION   AR360400
VERSION     AR360400.1  GI:33767430
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 15 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1514 AAATAAAATTGGAACGAA 1531
              |||  ||||||||||  ||
Db          2 AAAAAAAATTGGAAAAAA 19


RESULT 4126
AR360427
LOCUS       AR360427                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 15 from patent US 6596490.
ACCESSION   AR360427
VERSION     AR360427.1  GI:33767457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 15 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1514 AAATAAAATTGGAACGAA 1531
              |||  ||||||||||  ||
Db          2 AAAAAAAATTGGAAAAAA 19


RESULT 4127
AX441511
LOCUS       AX441511                  20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 15 from Patent WO0206531.
ACCESSION   AX441511
VERSION     AX441511.1  GI:21690472
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 15 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02022"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1514 AAATAAAATTGGAACGAA 1531
              |||  ||||||||||  ||
Db          2 AAAAAAAATTGGAAAAAA 19


RESULT 4128
A40126
LOCUS       A40126                    20 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 2 from Patent WO9423026.
ACCESSION   A40126
VERSION     A40126.1  GI:2296284
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Vasseur,M., Blumenfeld,M., Meguenni,S. and Poddevin,B.
  TITLE     STAPLE AND SEMI-STAPLE OLIGONUCLEOTIDES, METHOD OF PREPARATION AND
            APPLICATIONS
  JOURNAL   Patent: WO 9423026-A 2 13-OCT-1994;
            GENSET (FR)
COMMENT     Other publication AU 6432094 941024
            Other publication FR 2703053 940930.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bougueleret,L.
  TITLE     Nucleic acid encoding retinoblastoma-binding protein (RBP-7) and
            polymorphic marker relating to the nucleic acid
  JOURNAL   Patent: JP 2002519027-A 104 02-JUL-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002519027-A/104
            PD   02-JUL-2002
            PF   30-JUN-1999 JP 2000557360
            PR   30-JUN-1998 US    60/091315,10-DEC-1998 US    60/111909 PI
            LYDIE BOUGUELERET
            PC   C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N5/10,
            PC   C12Q1/68,
            PC   G01N33/53,G01N33/566,C12N15/00,C12N5/00,C12N15/00 CC
            potential microsequencing oligo for 5-129-144.mis1 FH   Key
                Location/Qualifiers
            FT   primer_bind     1. .19.
FEATURES                Location/Qualifiers
     source             1. .19
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAA 2792
              | ||| |||| |||||||
Db          2 TCTTATAATTAAAAAAAA 19


RESULT 4122
BD221990/c
LOCUS       BD221990                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Nucleic acid encoding retinoblastoma-binding protein (RBP-7) and
            polymorphic marker relating to the nucleic acid.
ACCESSION   BD221990
VERSION     BD221990.1  GI:33031760
KEYWORDS    JP 2002519027-A/129.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bougueleret,L.
  TITLE     Nucleic acid encoding retinoblastoma-binding protein (RBP-7) and
            polymorphic marker relating to the nucleic acid
  JOURNAL   Patent: JP 2002519027-A 129 02-JUL-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002519027-A/129
            PD   02-JUL-2002
            PF   30-JUN-1999 JP 2000557360
            PR   30-JUN-1998 US    60/091315,10-DEC-1998 US    60/111909 PI
            LYDIE BOUGUELERET
            PC   C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N5/10,
            PC   C12Q1/68,
            PC   G01N33/53,G01N33/566,C12N15/00,C12N5/00,C12N15/00 CC
            potential microsequencing oligo for 5-140-120.mis2 FH   Key
                Location/Qualifiers
            FT   primer_bind     1. .19.
FEATURES                Location/Qualifiers
     source             1. .19
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTTTGAA 2195
              |||||| ||||| | |||
Db         19 TTTTTTCTTAACCTAGAA 2


RESULT 4123
AJ587912
LOCUS       AJ587912                 19 bp    DNA     linear   PLN 23-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            339D06.
ACCESSION   AJ587912
VERSION     AJ587912.1  GI:37937536
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 19)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES                Location/Qualifiers
     source             1. .19
                        /organism="Arabidopsis thaliana"
                        /mol_type="genomic DNA"
                        /cultivar="Wassillewskija"
                        /db_xref="taxon:3702"
                        /clone="339D06"
                        /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature       1. .19
                        /note="T-DNA flanking sequence
                        left border"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTT 2171
              || ||  ||||||||||||
Db          2 ATCTTAATCTCCTTTTTT 19


RESULT 4124
E12411/c
LOCUS       E12411                   20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide.
ACCESSION   E12411
VERSION     E12411.1  GI:3251244
KEYWORDS    JP 1996332100-A/1.
```

```
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Haseltine,W.A., Ruben,S.M., Wei,Y.F., Adams,M.D., Fleischmann,R.D.,
            Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and Rosen,C.A.
  TITLE     Human DNA mismatch repair proteins
  JOURNAL   Patent: JP 2002325588-A 74 12-NOV-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002325588-A/74
            PD   12-NOV-2002
            PF   25-JAN-2002 JP 2002016830
            PR   27-JAN-1994 US    08/187757,16-MAR-1994 US    08/210143 PR
            23-AUG-1994 US    08/294312
            PI   WILLIAM A HASELTINE,STEVEN M RUBEN,YING FEI WEI,MARK D ADAMS,
            PI   ROBERT D FLEISCHMANN,CLAIRE M FRASER,REBECCA A FULDNER,EWEN F
            PI   KIRKNESS,
            PI   CRAIG A ROSEN
            PC   C12N15/09,C07K14/47,C12P21/02,C12Q1/68//(C12P21/02,C12R1:19),
            PC   C12N15/00
            CC   primer useful for amplifying codons 439 to 472 of hMLH3 FH
            Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        484 CCAGAGCCAGGAGGGAGC 501
              ||||| ||| || |||||
Db          2 CCAGAACCAAGAAGGAGC 19


RESULT 4119
BD195704
LOCUS       BD195704                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  In vivo use of recombinagenic oligonucleobases to correct genetic
            lesions in hepatocytes.
ACCESSION   BD195704
VERSION     BD195704.1  GI:33005474
KEYWORDS    JP 2002511851-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Of,R.O.T.U., Steer,C.J., Kren,B.T. and Opadhyay,P.T.B.
  TITLE     In vivo use of recombinagenic oligonucleobases to correct genetic
            lesions in hepatocytes
  JOURNAL   Patent: JP 2002511851-A 2 16-APR-2002;
            REGENTS OF THE UNIVERSITY OF MINNESOTA,CLIFFORD J STEER, BETSY T
            KREN, PARAMITA T BANDY OPADHYAY
COMMENT     OS   Unidentified
            PN   JP 2002511851-A/2
            PD   16-APR-2002
            PF   30-APR-1998 JP 1998547429
            PR   30-APR-1997 US    60/045288,05-AUG-1997 US    60/054837 PR
            10-NOV-1997 US    60/064996
            PI   REGENTS OF THE UNIVERSITY OF MINNESOTA,CLIFFORD J STEER,BETSY
            PI   T KREN,
            PI   PARAMITA T BANDY OPADHYAY
            PC   C12Q1/68,A61K48/00,C07H21/04
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   In vivo use of recombinagenic oligonucleobases to correct  CC
                 genetic lesions
            CC   in hepatocytes
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        797 AAGGAGCTGGTGGGGGCC 814
              |||||| | ||||||| |
Db          2 AAGGAGATAGTGGGGGAC 19


RESULT 4120
BD196950
LOCUS       BD196950                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Prostatic cancer gene.
ACCESSION   BD196950
VERSION     BD196950.1  GI:33006720
KEYWORDS    JP 2002516657-A/539.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
  TITLE     Prostatic cancer gene
  JOURNAL   Patent: JP 2002516657-A 539 11-JUN-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002516657-A/539
            PD   11-JUN-2002
            PF   22-DEC-1998 JP 2000525562
            PR   22-DEC-1997 US    08/996306,09-SEP-1998 US    60/099658 PI
            DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
            C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
            C12N1/19,
            PC   C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
            ,C12N15/00,C12N5/00,
            PC   C12N5/00,C12N15/00
            CC   potential microsequencing oligo for 99-148-366.mis2 FH   Key
                      Location/Qualifiers
            FT   primer_bind     1. .19.
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        560 GAGGCGGGCGCGGTGAGC 577
              ||||||| || ||||||
Db          1 GAGGCGGCAGCCGTGAGC 18


RESULT 4121
BD221965
LOCUS       BD221965                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Nucleic acid encoding retinoblastoma-binding protein (RBP-7) and
            polymorphic marker relating to the nucleic acid.
ACCESSION   BD221965
VERSION     BD221965.1  GI:33031735
KEYWORDS    JP 2002519027-A/104.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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LOCUS       BD090877                 19 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel protein, process for producing the same, and utilization
            thereof.
ACCESSION   BD090877
VERSION     BD090877.1  GI:22636487
KEYWORDS    JP 2001335598-A/22.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kita,S., Komiyama,T. and Taniyama,Y.
  TITLE     Novel protein, process for producing the same, and utilization
  JOURNAL   Patent: JP 2001335598-A 22 04-DEC-2001;
            TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001335598-A/22
            PD   04-DEC-2001
            PF   23-MAR-2001 JP 2001084088
            PI   SHUNBUN KITA,TOMOKO KOMIYAMA,YOSHIO TANIYAMA
            PC
            C07K14/47,A61K31/711,A61K38/00,A61K39/395,A61K39/395,A61K45/00, PC
             A61K48/00,
            PC
            A61P3/04,A61P3/06,A61P3/10,A61P9/10,A61P25/00,A61P35/00,A61P43/ PC
             00,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/09 PC
            ,C12P21/02,C12Q1/68,
            PC   G01N33/15,G01N33/50//C12P21/08,A61K37/02,C12N5/00,C12N15/00 CC
              Novel protein, process for producing the
            same, and utilization
            CC           thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAGCA 468
              ||| | |||||||||  ||
Db          2 CACGGCCAGCCAGCAACA 19


RESULT 4116
BD101884
LOCUS       BD101884                 19 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel protein, its production and use.
ACCESSION   BD101884
VERSION     BD101884.1  GI:22647458
KEYWORDS    WO 0170974-A/22.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Taniyama,Y., Kita,S. and Komiyama,T.
  TITLE     Novel protein, its production and use
  JOURNAL   Patent: WO 0170974-A 22 27-SEP-2001;
            TAKEDA CHEMICAL INDUSTRIES LTD,YOSHIO TANIYAMA,SHUNBUN KITA,TOMOKO
            KOMIYAMA
COMMENT     OS   Artificial Sequence
            PN   WO 0170974-A/22
            PD   27-SEP-2001
            PF   22-MAR-2001 WO 2001JP002279
            PR   24-MAR-2000 JP 00P   088595
            PI   YOSHIO TANIYAMA,SHUNBUN KITA,TOMOKO KOMIYAMA
            PC   C12N15/12,C07K14/47,C07K16/18,C12Q1/68,A61K38/17,A61K31/711,
            PC   A61K48/00,
            PC
            A61K45/00,A61P3/10,A61P3/04,A61P35/00,A61P9/10,A61P3/06,A61P25/ PC
             00,
            PC   A61P43/00,A61K39/395,G01N33/53,G01N33/50,G01N33/15 CC   Novel
            protein, its production and use
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAGCA 468
              ||| | |||||||||  ||
Db          2 CACGGCCAGCCAGCAACA 19


RESULT 4117
BD132730/c
LOCUS       BD132730                 19 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Regulatory sequences for transgenic plants.
ACCESSION   BD132730
VERSION     BD132730.1  GI:23227675
KEYWORDS    JP 2002504824-A/39.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Ainley,M., Armstrong,K., Belmar,S., Folkerts,O., Hopkins,N.,
            Menke,M.A., Pareddy,D., Petolino,J.F., Smith,K. and Woosley,A.
  TITLE     Regulatory sequences for transgenic plants
  JOURNAL   Patent: JP 2002504824-A 39 12-FEB-2002;
            DOW AGROSCIENCES LLC
COMMENT     PN   JP 2002504824-A/39
            PD   12-FEB-2002
            PF   10-JUN-1998 JP 1999503094
            PR   12-JUN-1997 US    60/049752
            PI   MICHAEL AINLEY,KATHERINE ARMSTRONG,SCOTT BELMAR,OTTO FOLKERTS,
            PI   NICOLE HOPKINS,MICHAEL A MENKE,DAYAKAR PAREDDY,JOSEPH F  PI
            PETOLINO,
            PI   KELLEY SMITH,AARON WOOSLEY
            PC   C12N15/53,C12N15/82,A01H5/00
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2458 GGGATCCAATTTTAATAT 2475
              |||||||||  ||  ||||
Db         19 GGGATCCAAGCTTGATAT 2


RESULT 4118
BD181170
LOCUS       BD181170                 19 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Human DNA mismatch repair proteins.
ACCESSION   BD181170
VERSION     BD181170.1  GI:30792088
KEYWORDS    JP 2002325588-A/74.
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AX806450
LOCUS       AX806450                19 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 26 from Patent WO03054012.
ACCESSION   AX806450
VERSION     AX806450.1  GI:38523057
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fagan,R.J., Gutteridge,A., Phelps,C.B. and Power,C.
  TITLE     Leptin proteins
  JOURNAL   Patent: WO 03054012-A 26 03-JUL-2003;
            ARES TRADING S.A. (CH)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="26841-CP2 primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1076 TCCTTAGTAGAAGGTGAA 1093
              |||| || ||| ||||||
Db          2 TCCTCAGCAGAGGGTGAA 19


RESULT 4112
AX923861/c
LOCUS       AX923861                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 296 from Patent WO03080638.
ACCESSION   AX923861
VERSION     AX923861.1  GI:40216877
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lacasse,E., Mcmanus,D. and Durkin,J.P.
  TITLE     Antisense iap nucleobase oligomers and uses thereof
  JOURNAL   Patent: WO 03080638-A 296 02-OCT-2003;
            Aegera Therapeutics Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="based on Homo sapiens. DNA/RNA hybrid."

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1318 GAACATACAGAACTGCTT 1335
              ||||| | ||||| ||||
Db         19 GAACACATAGAACAGCTT 2


RESULT 4113
BD016786
LOCUS       BD016786                19 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Method for detecting and monitoring leakage of natural gas by
            microorganism.
ACCESSION   BD016786
VERSION     BD016786.1  GI:22557962
KEYWORDS    JP 2001245668-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Hoaki,T. and Suzuki,A.
  TITLE     Method for detecting and monitoring leakage of natural gas by
            microorganism
  JOURNAL   Patent: JP 2001245668-A 5 11-SEP-2001;
            TAISEI CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2001245668-A/5
            PD   11-SEP-2001
            PF   07-MAR-2000 JP 2000062326
            PI   TOSHIHIRO HOAKI,ASAKA SUZUKI
            PC   C12N15/09,C12Q1/06,C12Q1/68,G01N33/00,G01N33/53,G01N33/566//
            PC   (C12Q1/06,C12R1:26),(C12Q1/06,C12R1:00),C12N15/00 CC
            Description of Artificial Sequence:Specifically conserved  CC
                region of 16S
            CC   rRNA among Methylotrophs
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2222 TTGAAATGACATGTTCCC 2239
              |||| ||| |||||| ||
Db          2 TTGACATGGCATGTTACC 19


RESULT 4114
BD082742/c
LOCUS       BD082742                19 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for detecting Helicobacter pylori having clarithromycin
            resistance.
ACCESSION   BD082742
VERSION     BD082742.1  GI:22628352
KEYWORDS    JP 2001321197-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kashimura,H. and Okawa,A.
  TITLE     Method for detecting Helicobacter pylori having clarithromycin
            resistance
  JOURNAL   Patent: JP 2001321197-A 3 20-NOV-2001;
            INSTITUTE OF TSUKUBA LIAISON CO LTD
COMMENT     OS   Helicobacter pylori
            PN   JP 2001321197-A/3
            PD   20-NOV-2001
            PF   12-MAY-2000 JP 2000140221
            PI   HIROMASA KASHIMURA,ATSUSHI OKAWA
            PC   C12Q1/68,C12N15/09,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2337 CAAGTCCCCGTGGAGGTT 2354
              |||| |||||||||  ||
Db         19 CAAGACCCCGTGGACCTT 2


RESULT 4115
BD090877
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            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTT 2168
              ||| ||| |||| |||||
Db         19 TTGCTTTATTTCACCTTT 2

RESULT 4107
AX707719
LOCUS       AX707719                  19 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 486 from Patent WO03013536.
ACCESSION   AX707719
VERSION     AX707719.1  GI:29563892
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Heinrich,G. and Kerb,R.
  TITLE     Methods for treatment of cancer using irinotecan based on UGT1A1
  JOURNAL   Patent: WO 03013536-A 486 20-FEB-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTT 2168
              ||| ||| |||| |||||
Db          1 TTGCTTTATTTCACCTTT 18

RESULT 4108
AX711905/c
LOCUS       AX711905                  19 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 7 from Patent WO02103046.
ACCESSION   AX711905
VERSION     AX711905.1  GI:29787701
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dear,P.H., Thangavelu,M. and Bankier,A.
  TITLE     Happier mapping
  JOURNAL   Patent: WO 02103046-A 7 27-DEC-2002;
            Medical Research Council (GB)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1579 CCACCGCACAGACTGGGA 1596
              ||| || |||||||| ||
Db         19 CCAACGAACAGACTGCGA 2

RESULT 4109
AX769623/c
LOCUS       AX769623                  19 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 17 from Patent WO03020975.
ACCESSION   AX769623
VERSION     AX769623.1  GI:32437331
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Karlsen,F.
  TITLE     Oligonucleotides for use in detection of human papillomavirus L1
            mRNA
  JOURNAL   Patent: WO 03020975-A 17 13-MAR-2003;
            Norchip A/S (NO)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HPV primer"
     modified_base   18
                     /mod_base=i

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        164 GCCATGTTGTGGAAAATAA 182
              | ||||||| |||| || |
Db         19 GNCATGTTGAGGAATATGA 1

RESULT 4110
AX802655/c
LOCUS       AX802655                  19 bp    DNA     linear   PAT 24-NOV-2003
DEFINITION  Sequence 165 from Patent WO03057914.
ACCESSION   AX802655
VERSION     AX802655.1  GI:38501353
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Karlsen,F.
  TITLE     Method for detecting human papillomavirus mRNA
  JOURNAL   Patent: WO 03057914-A 165 17-JUL-2003;
            Norchip A/S (NO)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HPV primer"
     misc_feature    18
                     /note="#n# represents inosine"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        164 GCCATGTTGTGGAAAATAA 182
              | ||||||| |||| || |
Db         19 GNCATGTTGAGGAATATGA 1

RESULT 4111
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              || | || ||||||||||
Db          1 ATGATGTCTTATTCATAT 18


RESULT 4102
AX643405/c
LOCUS       AX643405                 19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 271 from Patent WO02099099.
ACCESSION   AX643405
VERSION     AX643405.1  GI:28551058
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 271 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2513 ATAAGGTTTTATTCATAT 2530
              || | || ||||||||||
Db         19 ATGATGTCTTATTCATAT 2


RESULT 4103
AX645142
LOCUS       AX645142                 19 bp    DNA     linear   PAT 27-FEB-2003
DEFINITION  Sequence 170 from Patent WO02066643.
ACCESSION   AX645142
VERSION     AX645142.1  GI:28610962
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Malyankar,U.M., Shenoy,S.G., Spytek,K.A., Zerhusen,B.D.,
            Patturajan,M., Guo,X., Kekuda,R., Gangolli,E.A., Shimkets,R.A.,
            Taupier,R.J., Li,L. and Padigaru,M.
  TITLE     Proteins, polynucleotides encoding them and methods of using the
            same
  JOURNAL   Patent: WO 02066643-A 170 29-AUG-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR Primer Sequence"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        269 GCCGGGCAGCACCTCTAC 286
              | ||||||| |||| |||
Db          1 GTCGGGCAGGACCTTTAC 18


RESULT 4104
AX706788/c
LOCUS       AX706788                 19 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 485 from Patent WO03013534.
ACCESSION   AX706788
VERSION     AX706788.1  GI:29563211
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Heinrich,G. and Kerb,R.
  TITLE     Methods for the treatment of cancer with irinotecan based on CYP3A5
  JOURNAL   Patent: WO 03013534-A 485 20-FEB-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTT 2168
              ||| ||| |||| |||||
Db         19 TTGCTTTATTTCACCTTT 2


RESULT 4105
AX706789
LOCUS       AX706789                 19 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 486 from Patent WO03013534.
ACCESSION   AX706789
VERSION     AX706789.1  GI:29563212
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Heinrich,G. and Kerb,R.
  TITLE     Methods for the treatment of cancer with irinotecan based on CYP3A5
  JOURNAL   Patent: WO 03013534-A 486 20-FEB-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTT 2168
              ||| ||| |||| |||||
Db          1 TTGCTTTATTTCACCTTT 18


RESULT 4106
AX707718/c
LOCUS       AX707718                 19 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 485 from Patent WO03013536.
ACCESSION   AX707718
VERSION     AX707718.1  GI:29563891
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Heinrich,G. and Kerb,R.
  TITLE     Methods for treatment of cancer using irinotecan based on UGT1A1
  JOURNAL   Patent: WO 03013536-A 485 20-FEB-2003;
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 154 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1917 ATACCTTTTTTTCAGTG 1934
              |||| |||||| | ||||
Db         19 ATACTTTTTTTCTGAGTG 2


RESULT 4098
AX643291
LOCUS       AX643291                19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 157 from Patent WO02099099.
ACCESSION   AX643291
VERSION     AX643291.1  GI:28550913
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 157 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1917 ATACCTTTTTTTCAGTG 1934
              |||| |||||| | ||||
Db          1 ATACTTTTTTTCTGAGTG 18


RESULT 4099
AX643355
LOCUS       AX643355                19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 221 from Patent WO02099099.
ACCESSION   AX643355
VERSION     AX643355.1  GI:28550994
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 221 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="n=t or deleted"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2745 TGTATGATACGTGTATAAT 2763
              |||| |||| || || |||
Db          1 TGTAAGATANGTTTAAAAT 19


RESULT 4100
AX643358/c
LOCUS       AX643358                19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 224 from Patent WO02099099.
ACCESSION   AX643358
VERSION     AX643358.1  GI:28550998
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 224 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="n=a or deleted"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2745 TGTATGATACGTGTATAAT 2763
              |||| |||| || || |||
Db         19 TGTAAGATANGTTTAAAAT 1


RESULT 4101
AX643402
LOCUS       AX643402                19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 268 from Patent WO02099099.
ACCESSION   AX643402
VERSION     AX643402.1  GI:28551055
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Penger,A., Sprenger,R. and Brinkmann,U.
  TITLE     Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
            and their use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 02099099-A 268 12-DEC-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2513 ATAAGGTTTTATTCATAT 2530
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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        346 TCCCCCTCCCTACCAGCA 363
              ||| |||||| ||||| |
Db         18 TCCACCTCCCAACCAGTA 1


RESULT 4093
AX497021
LOCUS       AX497021                 19 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 32 from Patent WO0229031.
ACCESSION   AX497021
VERSION     AX497021.1  GI:23342452
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kloog,Y., Haklai,R., Paz,A., el Ad-Sfadia,G. and Ballan,E.
  TITLE     Isoprenoid-dependent ras anchorage (idra) proteins
  JOURNAL   Patent: WO 0229031-A 32 11-APR-2002;
            RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTR; IAL
            DEVELOPMENT LTD. (IL)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="antisense oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        999 TGCGGGAGAAGTTGGACA 1016
              || ||| || ||||||||
Db          1 TGTGGGGGACGTTGGACA 18


RESULT 4094
AX505292/c
LOCUS       AX505292                 19 bp    RNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 20 from Patent WO0250261.
ACCESSION   AX505292
VERSION     AX505292.1  GI:23386530
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Legrain,P., Benarous,R., Blot,G. and Lassot,I.
  TITLE     Proteins that interact with _g(b)trcp
  JOURNAL   Patent: WO 0250261-A 20 27-JUN-2002;
            Hybrigenics (FR) ; Institut National de la Sante et de la Recherche
            Medicale (FR)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"
                     /note="RasSF1dsRNA185, Sense strand
                     sequence~RasSF1dsRNA185, Sense strand sequence (dTdT in
                     3')"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        834 TCTTCTGCTCAGTCCCTG 851
              |||||||||| || | |
Db         19 TCTTCTGCTCAATCTCAG 2


RESULT 4095
AX553752
LOCUS       AX553752                 19 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 86 from Patent WO02075507.
ACCESSION   AX553752
VERSION     AX553752.1  GI:25897750
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lowery,D.E., Fuller,T.E. and Kennedy,M.J.
  TITLE     Anti-bacterial vaccine compositions
  JOURNAL   Patent: WO 02075507-A 86 26-SEP-2002;
            Pharmacia & Upjohn Company (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PRIMER"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        468 AGGCCTGGCCCGGCCGCC 485
              ||||| |  |||||||||
Db          1 AGGCCGGTACCGGCCGCC 18


RESULT 4096
AX554343/c
LOCUS       AX554343                 19 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 30 from Patent WO0244403.
ACCESSION   AX554343
VERSION     AX554343.1  GI:25898159
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   White,J.H.
  TITLE     Markers for testing analogs of vitamin d and therapeutical uses
  JOURNAL   Patent: WO 0244403-A 30 06-JUN-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2555 AGGATGCTGGGCTCTGTT 2572
              |||||| ||| |||| ||
Db         19 AGGATGATGGCCTCTCTT 2


RESULT 4097
AX643288/c
LOCUS       AX643288                 19 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 154 from Patent WO02099099.
ACCESSION   AX643288
VERSION     AX643288.1  GI:28550910
KEYWORDS    .
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AX352996
LOCUS       AX352996                19 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 202 from Patent EP1174518.
ACCESSION   AX352996
VERSION     AX352996.1  GI:18618078
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Loukachov,V.V., van Gemen,B. and Goudsmit,J.
  TITLE     Collection of binding molecules
  JOURNAL   Patent: EP 1174518-A 202 23-JAN-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="position 70"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 CTGGAGAAAATGGAGAAA 1507
              | | || ||||||||||
Db          2 CAGTAGTAAATGGAGAAA 19


RESULT 4089
AX362717
LOCUS       AX362717                19 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 78 from Patent WO0208463.
ACCESSION   AX362717
VERSION     AX362717.1  GI:18694857
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Loukachov,V.V., Goudsmit,J. and van Gemen,B.
  TITLE     Collection of binding molecules
  JOURNAL   Patent: WO 0208463-A 78 31-JAN-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="position 62"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1966 AATATTTACCTTGAAAAA 1983
              ||||||| || | |||||
Db          2 AATATTTGCCATAAAAAA 19


RESULT 4090
AX362841
LOCUS       AX362841                19 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 202 from Patent WO0208463.
ACCESSION   AX362841
VERSION     AX362841.1  GI:18694981
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Loukachov,V.V., Goudsmit,J. and van Gemen,B.
  TITLE     Collection of binding molecules
  JOURNAL   Patent: WO 0208463-A 202 31-JAN-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="position 70"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1490 CTGGAGAAAATGGAGAAA 1507
              | | || ||||||||||
Db          2 CAGTAGTAAATGGAGAAA 19


RESULT 4091
AX443261
LOCUS       AX443261                19 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 43 from Patent WO0210382.
ACCESSION   AX443261
VERSION     AX443261.1  GI:21690656
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wissenbach,U.
  TITLE     Trp8, trp9 and trp10, markers for cancer
  JOURNAL   Patent: WO 0210382-A 43 07-FEB-2002;
            Wissenbach, Ulrich (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        359 CAGCAGCTGGCCTACTCC 376
              |||| ||||| ||| |||
Db          2 CAGCTGCTGGTCTATTCC 19


RESULT 4092
AX472056/c
LOCUS       AX472056                19 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 47 from Patent WO02053775.
ACCESSION   AX472056
VERSION     AX472056.1  GI:22207097
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hustert,E., Haberl,M. and Wojnowski,L.
  TITLE     Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
  JOURNAL   Patent: WO 02053775-A 47 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1315 GACGAACATACAGAACTG 1332
              || |||||  ||||||||
Db         19 GATGAACAGGCAGAACTG 2


RESULT 4084
AX252279
LOCUS       AX252279                 19 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 5 from Patent WO0168147.
ACCESSION   AX252279
VERSION     AX252279.1  GI:15985621
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bianchi,N., Feriotto,G., Gambari,R. and Mischiati,C.
  TITLE     Synthetic oligonucleotides as inducers of erythroid differentiation
  JOURNAL   Patent: WO 0168147-A 5 20-SEP-2001;
            Universita' Degli Studi di Ferrara (IT) ; ASSOCIAZIONE VENETA PER
            LA LOTTA ALLA TALASSEMIA (IT) ; ASSOCIAZIONE PER LA LOTTA ALLA
            TALASSEMIA DI FERRARA (IT) ; CHIESI FARMACEUTICI S.p.A. (IT)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||| ||| ||| ||||||
Db          2 TTTCTTTCTTTCTTTTT 19


RESULT 4085
AX252279/c
LOCUS       AX252279                 19 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 5 from Patent WO0168147.
ACCESSION   AX252279
VERSION     AX252279.1  GI:15985621
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bianchi,N., Feriotto,G., Gambari,R. and Mischiati,C.
  TITLE     Synthetic oligonucleotides as inducers of erythroid differentiation
  JOURNAL   Patent: WO 0168147-A 5 20-SEP-2001;
            Universita' Degli Studi di Ferrara (IT) ; ASSOCIAZIONE VENETA PER
            LA LOTTA ALLA TALASSEMIA (IT) ; ASSOCIAZIONE PER LA LOTTA ALLA
            TALASSEMIA DI FERRARA (IT) ; CHIESI FARMACEUTICI S.p.A. (IT)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||| ||| ||| |||
Db         19 AAAAAAGAAAGAAAGAAA 2


RESULT 4086
AX348014/c
LOCUS       AX348014                 19 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 47 from Patent EP1172444.
ACCESSION   AX348014
VERSION     AX348014.1  GI:18614124
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schreiber,S., Hampe,J. and Mascheretti,S.
  TITLE     Diagnostic use of polymorphisms in the gene coding for the tnf
            receptor II and method for detecting non-responders to anti-tnf
            therapy
  JOURNAL   Patent: EP 1172444-A 47 16-JAN-2002;
            Conaris Research Institute GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Forward Primer"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2566 CTCTGTTCTTGGCTTGGA 2583
              ||||| ||||||| || |
Db         19 CTCTGCTCTTGGCCTGCA 2


RESULT 4087
AX352872
LOCUS       AX352872                 19 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 78 from Patent EP1174518.
ACCESSION   AX352872
VERSION     AX352872.1  GI:18617954
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Loukachov,V.V., van Gemen,B. and Goudsmit,J.
  TITLE     Collection of binding molecules
  JOURNAL   Patent: EP 1174518-A 78 23-JAN-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="position 62"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1966 AATATTTACCTTGAAAAA 1983
              ||||||| || | |||||
Db          2 AATATTTGCCATAAAAAA 19


RESULT 4088
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LOCUS       AX132095                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3313 from Patent WO0130362.
ACCESSION   AX132095
VERSION     AX132095.1  GI:14138400
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3313 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin B1 ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1410 ACATCAAAGAAGCCCTGA 1427
              |||||| ||||  |||||
Db         19 ACATCAGAGAAAGCCTGA 2


RESULT 4080
AX132835/c
LOCUS       AX132835                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 4053 from Patent WO0130362.
ACCESSION   AX132835
VERSION     AX132835.1  GI:14139145
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 4053 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="PCNA HH ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              |||| || |||||||| |
Db         19 GAATAGAGAAAAAAAATA 2


RESULT 4081
AX148872/c
LOCUS       AX148872                 19 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 74 from Patent WO0136625.
ACCESSION   AX148872
VERSION     AX148872.1  GI:14347396
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 74 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              ||| ||||| | ||||||
Db         19 GAAATGAAAGAGAAAAAA 2


RESULT 4082
AX149169/c
LOCUS       AX149169                 19 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 371 from Patent WO0136625.
ACCESSION   AX149169
VERSION     AX149169.1  GI:14347693
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 371 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              ||||||| |||||  |||
Db         19 TTGAAAATAAAAATGAAA 2


RESULT 4083
AX224438/c
LOCUS       AX224438                 19 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 16 from Patent WO0160857.
ACCESSION   AX224438
VERSION     AX224438.1  GI:15554676
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Koutnikova,H., Brice,A., Fournier,A., Pradier,L., Prades,C.,
            Arnould-Reguigne,I., Rosier-Montus,M.F. and Corti,O.
  TITLE     Compositions useful for regulating parkin gene activity
  JOURNAL   Patent: WO 0160857-A 16 23-AUG-2001;
            Aventis Pharma S.A. (FR) ; INSTITUT NATIONAL DE LA SANTE ET DE LA
            RECHERCHE MEDICALE (INSERM) (FR)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /note="Cyclin E ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1571 ATCCTTCTCCACCGCACA 1588
              ||||||||||||  | |
Db          2 ATCCTTCTCCACCAAAGA 19


RESULT 4075
AX131607
LOCUS       AX131607                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2825 from Patent WO0130362.
ACCESSION   AX131607
VERSION     AX131607.1  GI:14137912
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 2825 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin H ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2265 TATTTATTTCAGATGTTT 2282
              ||| ||||||| | ||||
Db          2 TATGTATTTCAAACGTTT 19


RESULT 4076
AX131608
LOCUS       AX131608                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2826 from Patent WO0130362.
ACCESSION   AX131608
VERSION     AX131608.1  GI:14137913
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 2826 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin H ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2265 TATTTATTTCAGATGTTT 2282
              ||| ||||||| | ||||
Db          1 TATGTATTTCAAACGTTT 18


RESULT 4077
AX131849/c
LOCUS       AX131849                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3067 from Patent WO0130362.
ACCESSION   AX131849
VERSION     AX131849.1  GI:14138154
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3067 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin A1 ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2234 GTTCCCTTAAGGTACTGA 2251
              | | || ||||||||||||
Db         18 GCTTCCCTAAGGTACTGA 1


RESULT 4078
AX132037
LOCUS       AX132037                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3255 from Patent WO0130362.
ACCESSION   AX132037
VERSION     AX132037.1  GI:14138342
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3255 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin A1 ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1329 ACTGCTTGTCTCATTTCA 1346
              ||||||||||| ||  ||
Db          1 ACTGCTTGTCTTATGACA 18


RESULT 4079
AX132095/c
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1656 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin C ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2264 ATATTTATTTCAGATGTT 2281
              |||||| || || |||||
Db          2 ATATTTTTTACAAATGTT 19


RESULT 4071
AX130439
LOCUS       AX130439                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1657 from Patent WO0130362.
ACCESSION   AX130439
VERSION     AX130439.1  GI:14136744
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1657 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin C ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2264 ATATTTATTTCAGATGTT 2281
              |||||| || || |||||
Db          1 ATATTTTTTACAAATGTT 18


RESULT 4072
AX130672
LOCUS       AX130672                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1890 from Patent WO0130362.
ACCESSION   AX130672
VERSION     AX130672.1  GI:14136977
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1890 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin D2 ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         28 GACCCGGACAGCAAGGCC 45
              ||||||| | ||| ||||
Db          2 GACCCGGTCCGCAGGGCC 19


RESULT 4073
AX130690/c
LOCUS       AX130690                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1908 from Patent WO0130362.
ACCESSION   AX130690
VERSION     AX130690.1  GI:14136995
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1908 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin D2 ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1602 TCCTGGCCTGGGGGAAGA 1619
              || ||||| | |||||||
Db         19 TCATGGCCAGAGGGAAGA 2


RESULT 4074
AX131033
LOCUS       AX131033                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2251 from Patent WO0130362.
ACCESSION   AX131033
VERSION     AX131033.1  GI:14137338
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 2251 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTT 2168
              ||| ||| |||| |||||
Db          1 TTGCTTTATTTCACCTTT 18


RESULT 4066
AX128817
LOCUS       AX128817                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 35 from Patent WO0130362.
ACCESSION   AX128817
VERSION     AX128817.1  GI:14135122
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 35 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk1 ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1130 GAAGCCGAATTTCCTAGT 1147
              ||||  || |||||||||
Db          1 GAAGAAGATTTTCCTAGT 18


RESULT 4067
AX129062
LOCUS       AX129062                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 280 from Patent WO0130362.
ACCESSION   AX129062
VERSION     AX129062.1  GI:14135367
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 280 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk2 ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2116 GGTTTTAGGAAACTTGTA 2133
              | |||||| ||| |||||
Db          1 GATTTTAGTAAAGTTGTA 18


RESULT 4068
AX130221
LOCUS       AX130221                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1439 from Patent WO0130362.
ACCESSION   AX130221
VERSION     AX130221.1  GI:14136526
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1439 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin A2 ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1470 CAGCTGATTCTAACAAAA 1487
              ||||||| ||| | ||||
Db          1 CAGCTGAATCTCAAAAAA 18


RESULT 4069
AX130260/c
LOCUS       AX130260                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1478 from Patent WO0130362.
ACCESSION   AX130260
VERSION     AX130260.1  GI:14136565
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1478 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin A2 ribozyme binding site"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2651 CCCTAAGGTGAGTGTGCA 2668
              ||||||||| ||||| |
Db         18 CCCTAAGGTATGTGTGAA 1


RESULT 4070
AX130438
LOCUS       AX130438                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1656 from Patent WO0130362.
ACCESSION   AX130438
VERSION     AX130438.1  GI:14136743
KEYWORDS    .
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RESULT 4061
AR298519/c
LOCUS       AR298519                  19 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 10254 from patent US 6537751.
ACCESSION   AR298519
VERSION     AR298519.1  GI:31685803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 10254 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2735 AATTGTTGTGTGTATGAT 2752
              ||||| ||||||||  ||
Db         18 AATTGGTGTGTGTAGAAT 1


RESULT 4062
AR342579
LOCUS       AR342579                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 19 from patent US 6576441.
ACCESSION   AR342579
VERSION     AR342579.1  GI:33737750
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kimura,T. and Kikuchi,K.
  TITLE     Semaphorin Z and gene encoding the same
  JOURNAL   Patent: US 6576441-A 19 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1724 GACCTATTATCAGAAGGT 1741
              || |||||||||| | ||
Db          2 GAACTATTATCAGGACGT 19


RESULT 4063
AR382095
LOCUS       AR382095                  19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 77 from patent US 6610477.
ACCESSION   AR382095
VERSION     AR382095.1  GI:40090500
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Haseltine,W.A., Ruben,S.M., Wei,Y.-F., Adams,M.D.,
            Fleischmann,R.D., Fraser,C.M., Fuldner,R.A., Kirkness,E.F.,
            Rosen,C.A., Vogelstein,B., Kinzler,K.W., Nicolaides,N.C. and
            Papadopoulos,N.
  TITLE     Human DNA mismatch repair proteins
  JOURNAL   Patent: US 6610477-A 77 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        484 CCAGAGCCAGGAGGGAGC 501
              ||||| ||| || |||||
Db          2 CCAGAACCAAGAAGGAGC 19


RESULT 4064
AX081958/c
LOCUS       AX081958                  19 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 202 from Patent WO0109183.
ACCESSION   AX081958
VERSION     AX081958.1  GI:13170765
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S., Eichelbaum,M. and Roots,I.
  TITLE     Polymorphisms in the human mdr-1 gene and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 0109183-A 202 08-FEB-2001;
            EPIDAUROS AG Biotechnologie Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTT 2168
              ||| ||| |||| |||||
Db         19 TTGCTTTATTTCACCTTT 2


RESULT 4065
AX081959
LOCUS       AX081959                  19 bp    DNA     linear   PAT 27-FEB-2001
DEFINITION  Sequence 203 from Patent WO0109183.
ACCESSION   AX081959
VERSION     AX081959.1  GI:13170766
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S., Eichelbaum,M. and Roots,I.
  TITLE     Polymorphisms in the human mdr-1 gene and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 0109183-A 203 08-FEB-2001;
            EPIDAUROS AG Biotechnologie Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
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Db          1 TAAATAAAAGATGCCCTG 18


RESULT 4056
AR267614/c
LOCUS       AR267614                  19 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 4 from patent US 6497872.
ACCESSION   AR267614
VERSION     AR267614.1  GI:29697716
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S., Reynolds,B., Hammang,J.P. and Baetge,E.E.
  TITLE     Neural transplantation using proliferated multipotent neural stem
            cells and their progeny
  JOURNAL   Patent: US 6497872-A 4 24-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="mRNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db         19 TAAATAAAAGATGCCCTG 2


RESULT 4057
AR282797
LOCUS       AR282797                  19 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 28 from patent US 6524613.
ACCESSION   AR282797
VERSION     AR282797.1  GI:29719581
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Steer,C.J., Kren,B.T., Bandyopadhyay,P. and Roy-Chowdhury,J.
  TITLE     Hepatocellular chimeraplasty
  JOURNAL   Patent: US 6524613-A 28 25-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        797 AAGGAGCTGGTGGGGGCC 814
              |||||| | ||||||| |
Db          2 AAGGAGATAGTGGGGGAC 19


RESULT 4058
AR292807
LOCUS       AR292807                  19 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4542 from patent US 6537751.
ACCESSION   AR292807
VERSION     AR292807.1  GI:31680091
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4542 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1967 ATATTTACCTTGAAAAAA 1984
              |||||||||| || | ||
Db          1 ATATTTACCTGGAGAGAA 18


RESULT 4059
AR295171
LOCUS       AR295171                  19 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6906 from patent US 6537751.
ACCESSION   AR295171
VERSION     AR295171.1  GI:31682455
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 6906 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2661 AGTGTGCAGTACAGTGTG 2678
              || ||||||||||  |||
Db          1 AGAGTGCAGTACATGGTG 18


RESULT 4060
AR298367
LOCUS       AR298367                  19 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 10102 from patent US 6537751.
ACCESSION   AR298367
VERSION     AR298367.1  GI:31685651
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 10102 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2377 TTGAGTGTACAGATTTTA 2394
              | ||||||| |||| ||||
Db          1 TGGAGTGTTCAGAATTTA 18
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                || ||  |||||  ||||||
Db         19 TAAATAAAAGATGCCCTG 2


RESULT 4051
AR211895
LOCUS       AR211895                  19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 105 from patent US 6399373.
ACCESSION   AR211895
VERSION     AR211895.1  GI:21515338
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bougueleret,L.
  TITLE     Nucleic acid encoding a retinoblastoma binding protein (RBP-7) and
            polymorphic markers associated with said nucleic acid
  JCURNAL   Patent: US 6399373-A 105 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAA 2792
              | |||  ||||  |||||||
Db          2 TCTTATAATTAAAAAAAA 19


RESULT 4052
AR211920/c
LOCUS       AR211920                  19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 130 from patent US 6399373.
ACCESSION   AR211920
VERSION     AR211920.1  GI:21515369
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bougueleret,L.
  TITLE     Nucleic acid encoding a retinoblastoma binding protein (RBP-7) and
            polymorphic markers associated with said nucleic acid
  JOURNAL   Patent: US 6399373-A 130 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTTTGAA 2195
              ||||||  |||||  | |||
Db         19 TTTTTTCTTAACCTAGAA 2


RESULT 4053
AR217737
LOCUS       AR217737                  19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 77 from patent US 6416984.
ACCESSION   AR217737
VERSION     AR217737.1  GI:23317608
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Haseltine,W.A., Ruben,S.M., Wei,Y.-F., Adams,M.D.,
            Fleischmann,R.D., Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and
            Rosen,C.A.
  TITLE     Human DNA mismatch repair proteins
  JOURNAL   Patent: US 6416984-A 77 09-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        484 CCAGAGCCAGGAGGGAGC 501
              |||||  |||  ||  |||||
Db          2 CCAGAACCAAGAAGGAGC 19


RESULT 4054
AR241724/c
LOCUS       AR241724                  19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 12 from patent US 6472154.
ACCESSION   AR241724
VERSION     AR241724.1  GI:27287536
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 12 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||  |||  |||  |||
Db         18 GAAAAAGAAAGAAAGAAA 1


RESULT 4055
AR267613
LOCUS       AR267613                  19 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 3 from patent US 6497872.
ACCESSION   AR267613
VERSION     AR267613.1  GI:29697715
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S., Reynolds,B., Hammang,J.P. and Baetge,E.E.
  TITLE     Neural transplantation using proliferated multipotent neural stem
            cells and their progeny
  JOURNAL   Patent: US 6497872-A 3 24-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="mRNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              ||  ||  |||||  ||||||
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          artificial sequences.
REFERENCE 1  (bases 1 to 19)
  AUTHORS   Austrup,F. and Giesing,M.
  TITLE     Cancer cells from cell-containing body fluids, the isolation and
            use thereof, and compositions containing said cancer cells
  JOURNAL   Patent: JP 2002523017-A 5 30-JUL-2002;
            MICHAEL GIESING
COMMENT     OS   Artificial Sequence
            PN   JP 2002523017-A/5
            PD   30-JUL-2002
            PF   27-JUL-1999 JP 2000562484
            PR   27-JUL-1998 DE 198 33 738.8
            PI   FRANK AUSTRUP,MICHAEL GIESING
            PC   C12N15/09,A61K35/12,C12M1/00,C12M1/12,C12N5/06,C12Q1/02 PC
            ,C12Q1/68,C12N15/00,
            PC   C12N5/00
            CC   Cancer cells from cell-containing body fluids, the isolation
            CC             and use
            CC   thereof, and compositions containing said cancer cells FH
            Key              Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2227 ATGACATGTTCCCTTAAG 2244
              ||||||| ||||||  ||
Db          2 ATGACATTTTCCCTCTAG 19


RESULT 4047
I73729
LOCUS       I73729                   19 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 7 from patent US 5686598.
ACCESSION   I73729
VERSION     I73729.1  GI:3009870
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   North,M., Nishina,P. and Naggert,J.
  TITLE     Genes associated with retinal dystrophies
  JOURNAL   Patent: US 5686598-A 7 11-NOV-1997;
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1495 GAAAATGGAGAAACACAG 1512
              ||||| |||| || ||||
Db          2 GAAAACGGAGCAAGACAG 19


RESULT 4048
AR209033/c
LOCUS       AR209033                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 40 from patent US 6384207.
ACCESSION   AR209033
VERSION     AR209033.1  GI:21510344
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Ainley,M., Armstrong,K., Belmar,S., Folkerts,O., Hopkins,N.,
            Menke,M.A., Pareddy,D., Petolino,J.F., Smith,K. and Woosley,A.
  TITLE     Regulatory sequences for transgenic plants
  JOURNAL   Patent: US 6384207-A 40 07-MAY-2002;
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2458 GGGATCCAATTTTAATAT 2475
              |||||||||  || ||||
Db         19 GGGATCCAAGCTTGATAT 2


RESULT 4049
AR211759
LOCUS       AR211759                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 3 from patent US 6399369.
ACCESSION   AR211759
VERSION     AR211759.1  GI:21515167
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S. and Reynolds,B.
  TITLE     Multipotent neural stem cell cDNA libraries
  JOURNAL   Patent: US 6399369-A 3 04-JUN-2002;
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db          1 TAAATAAAAGATGCCCTG 18


RESULT 4050
AR211760/c
LOCUS       AR211760                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 4 from patent US 6399369.
ACCESSION   AR211760
VERSION     AR211760.1  GI:21515168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S. and Reynolds,B.
  TITLE     Multipotent neural stem cell cDNA libraries
  JOURNAL   Patent: US 6399369-A 4 04-JUN-2002;
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
```

```
Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db         19 TAAATAAAAGATGCCCTG 2


RESULT 4042
AR110289
LOCUS       AR110289                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 41 from patent US 6114502.
ACCESSION   AR110289
VERSION     AR110289.1  GI:12826565
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   North,M., Nishina,P., Naggert,J. and Noben-Trauth,K.
  TITLE     Gene family associated with neurosensory defects
  JOURNAL   Patent: US 6114502-A 41 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1495 GAAAATGGAGAAACACAG 1512
              ||||| |||| || ||||
Db          2 GAAAACGGAGCAAGACAG 19


RESULT 4043
AR139000
LOCUS       AR139000                 19 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 3 from patent US 6200801.
ACCESSION   AR139000
VERSION     AR139000.1  GI:14481345
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Ferkol,T.W. Jr., Davis,P.B. and Ziady,A.-G.
  TITLE     Serpin enzyme complex receptor-mediated gene transfer
  JOURNAL   Patent: US 6200801-A 3 13-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTT 2174
              || |||| ||| ||||||
Db          2 TTCTTCTTCTTCTTTTTT 19


RESULT 4044
AR162033/c
LOCUS       AR162033                 19 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 15 from patent US 6258547.
ACCESSION   AR162033
VERSION     AR162033.1  GI:16229085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Beri,R.Kumar., Carling,D. and Forder,R.Anthony.
  TITLE     Nucleic acid encoding amp-activated protein kinase
  JOURNAL   Patent: US 6258547-A 15 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1259 CTTCTCAGCCAAGACCGG 1276
              |||||||||| |  |||
Db         19 CTTCTCAGCCATGTTCGG 2


RESULT 4045
BD252160
LOCUS       BD252160                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Anti-bacterial vaccine compositions.
ACCESSION   BD252160
VERSION     BD252160.1  GI:33061930
KEYWORDS    JP 2002541790-A/44.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lowery,D.E., Fuller,T.E. and Kennedy,M.J.
  TITLE     Anti-bacterial vaccine compositions
  JOURNAL   Patent: JP 2002541790-A 44 10-DEC-2002;
            PHARMACIA AND UPJOHN CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002541790-A/44
            PD   10-DEC-2002
            PF   06-APR-2000 JP 2000611649
            PR   09-APR-1999 US    60/128689,10-SEP-1999 US    60/153453 PI
            DAVID E LOWERY,TROY E FULLER,MICHAEL J KENNEDY PC
            C12N15/09,A61K39/02,A61K39/102,A61K39/395,A61P31/04,C07K14/285, PC
             C07K16/12,
            PC   C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/01,C12P21/02 PC
            ,C12P21/08,C12Q1/18,
            PC   G01N33/15,G01N33/50,G01N33/53,G01N33/569,G01N33/577,C12N15/00,
            PC   C12N15/00,
            PC   C12N5/00
            CC   Description of Artificial Sequence: PRIMER
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        468 AGGCCTGGCCCGGCCGCC 485
              ||||| |  |||||||||
Db          1 AGGCCGGTACCGGCCGCC 18


RESULT 4046
BD262907
LOCUS       BD262907                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Cancer cells from cell-containing body fluids, the isolation and
            use thereof, and compositions containing said cancer cells.
ACCESSION   BD262907
VERSION     BD262907.1  GI:33072675
KEYWORDS    JP 2002523017-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
```

```
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1206 CTAGGAAGAACATGCTAT 1223
              ||| ||| || |||||||
Db         18 CTAAGAACAAGATGCTAT 1


RESULT 4037
AR082444
LOCUS       AR082444                  19 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 3 from patent US 5972901.
ACCESSION   AR082444
VERSION     AR082444.1  GI:10009170
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Ferkol,T.W. Jr., Davis,P.B. and Ziady,A.-G.
  TITLE     Serpin enzyme complex receptor--mediated gene transfer
  JOURNAL   Patent: US 5972901-A 3 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTT 2174
              || |||| ||| ||||||
Db          2 TTCTTCTTCTTCTTTTT 19


RESULT 4038
AR084247
LOCUS       AR084247                  19 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 3 from patent US 5980885.
ACCESSION   AR084247
VERSION     AR084247.1  GI:10011018
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S. and Reynolds,B.
  TITLE     Growth factor-induced proliferation of neural precursor cells in
            vivo
  JOURNAL   Patent: US 5980885-A 3 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db          1 TAAATAAAAGATGCCCTG 18


RESULT 4039
AR084248/c
LOCUS       AR084248                  19 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 4 from patent US 5980885.
ACCESSION   AR084248
VERSION     AR084248.1  GI:10011019
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S. and Reynolds,B.
  TITLE     Growth factor-induced proliferation of neural precursor cells in
            vivo
  JOURNAL   Patent: US 5980885-A 4 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db         19 TAAATAAAAGATGCCCTG 2


RESULT 4040
AR097619
LOCUS       AR097619                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 3 from patent US 6071889.
ACCESSION   AR097619
VERSION     AR097619.1  GI:12806349
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S., Reynolds,B., Hammang,J.P. and Baetge,E.Edward.
  TITLE     In vivo genetic modification of growth factor-responsive neural
            precursor cells
  JOURNAL   Patent: US 6071889-A 3 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db          1 TAAATAAAAGATGCCCTG 18


RESULT 4041
AR097620/c
LOCUS       AR097620                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6071889.
ACCESSION   AR097620
VERSION     AR097620.1  GI:12806350
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S., Reynolds,B., Hammang,J.P. and Baetge,E.Edward.
  TITLE     In vivo genetic modification of growth factor-responsive neural
            precursor cells
  JOURNAL   Patent: US 6071889-A 4 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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                    /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db         19 TAAATAAAAGATGCCCTG 2


RESULT 4032
AR019659/c
LOCUS       AR019659                  19 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 7 from patent US 5783681.
ACCESSION   AR019659
VERSION     AR019659.1  GI:3974773
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Matusik,R.J.
  TITLE     Androgen regulation with DNA sequences of rat probasin gene
  JOURNAL   Patent: US 5783681-A 7 21-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1206 CTAGGAAGAACATGCTAT 1223
              ||| ||| || |||||||
Db         18 CTAAGAACAAGATGCTAT 1


RESULT 4033
AR067985
LOCUS       AR067985                  19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5851832.
ACCESSION   AR067985
VERSION     AR067985.1  GI:5999207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S., Reynolds,B., Hammang,J.P. and Baetge,E.Edward.
  TITLE     In vitro growth and proliferation of multipotent neural stem cells
            and their progeny
  JOURNAL   Patent: US 5851832-A 3 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db          1 TAAATAAAAGATGCCCTG 18


RESULT 4034
AR067986/c
LOCUS       AR067986                  19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5851832.
ACCESSION   AR067986
VERSION     AR067986.1  GI:5999208
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S., Reynolds,B., Hammang,J.P. and Baetge,E.Edward.
  TITLE     In vitro growth and proliferation of multipotent neural stem cells
            and their progeny
  JOURNAL   Patent: US 5851832-A 4 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db         19 TAAATAAAAGATGCCCTG 2


RESULT 4035
AR069633
LOCUS       AR069633                  19 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 10 from patent US 5891679.
ACCESSION   AR069633
VERSION     AR069633.1  GI:7220521
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lucas,R., De Baetselier,P., Fransen,L. and Sablon,E.
  TITLE     TNF-alpha muteins and a process for preparing them
  JOURNAL   Patent: US 5891679-A 10 06-APR-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        575 AGCGCCCGCAGGGATGCC 592
              |||||| |||||| || |
Db          2 AGCGCCTGCAGGGGTGTC 19


RESULT 4036
AR074187/c
LOCUS       AR074187                  19 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 7 from patent US 5952488.
ACCESSION   AR074187
VERSION     AR074187.1  GI:10000943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Matusik,R.J.
  TITLE     Androgen regulation with DNA sequences of rat probasin gene
  JOURNAL   Patent: US 5952488-A 7 14-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        575 AGCGCCCGCAGGGATGCC 592
              |||||| |||||| || |
Db          2 AGCGCCTGCAGGGGTGTC 19


RESULT 4027
A41231/c
LOCUS       A41231                   19 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 15 from Patent WO9428116.
ACCESSION   A41231
VERSION     A41231.1  GI:2297046
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Beri,R.K., Carling,D. and Forder,R.A.
  TITLE     NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
  JOURNAL   Patent: WO 9428116-A 15 08-DEC-1994;
            ZENECA LTD (GB)
COMMENT     Other publication AU 6727394 941220
            Other publication GB 2279956 950118.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1259 CTTCTCAGCCAAGACCGG 1276
              |||||||||||  |  |||
Db         19 CTTCTCAGCCATGTTCGG 2


RESULT 4028
A91188/c
LOCUS       A91188                   19 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 1 from Patent WO9826092.
ACCESSION   A91188
VERSION     A91188.1  GI:6740213
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Grant,P.J.
  TITLE     ATHEROTHROMBOTIC DISORDERS: MUTATION IN THE FACTOR XIII GENE
  JOURNAL   Patent: WO 9826092-A 1 18-JUN-1998;
            UNIV LEEDS (GB); GRANT PETER JOHN (GB)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        539 CTGCCCCACCTCTCCGGG 556
              || ||||||| ||| |||
Db         19 CTTCCCCACCACTCTGGG 2


RESULT 4029
AR002990/c
LOCUS       AR002990                 19 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 20 from patent US 5743477.
ACCESSION   AR002990
VERSION     AR002990.1  GI:3964249
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Walsh,T.A., Houtchens,R.A., Strickland,J.A., Orr,G.L. and
            Merlo,D.J.
  TITLE     Insecticidal proteins and method for plant protection
  JOURNAL   Patent: US 5743477-A 20 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2458 GGGATCCAATTTTAATAT 2475
              |||||||||  || ||||
Db         19 GGGATCCAAGCTTGATAT 2


RESULT 4030
AR007260
LOCUS       AR007260                 19 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5750376.
ACCESSION   AR007260
VERSION     AR007260.1  GI:3966744
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S., Reynolds,B., Hammang,J.P. and Baetge,E.Edward.
  TITLE     In vitro growth and proliferation of genetically modified
            multipotent neural stem cells and their progeny
  JOURNAL   Patent: US 5750376-A 3 12-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTG 1426
              || || ||||| ||||||
Db          1 TAAATAAAAGATGCCCTG 18


RESULT 4031
AR007261/c
LOCUS       AR007261                 19 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 4 from patent US 5750376.
ACCESSION   AR007261
VERSION     AR007261.1  GI:3966745
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weiss,S., Reynolds,B., Hammang,J.P. and Baetge,E.Edward.
  TITLE     In vitro growth and proliferation of genetically modified
            multipotent neural stem cells and their progeny
  JOURNAL   Patent: US 5750376-A 4 12-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
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              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4022
AR205776/c
LOCUS       AR205776                  19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 14 from patent US 6369208.
ACCESSION   AR205776
VERSION     AR205776.1  GI:21503444
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 14 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4023
AR205777/c
LOCUS       AR205777                  19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 15 from patent US 6369208.
ACCESSION   AR205777
VERSION     AR205777.1  GI:21503445
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 15 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4024
AR205778/c
LOCUS       AR205778                  19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 16 from patent US 6369208.
ACCESSION   AR205778
VERSION     AR205778.1  GI:21503447
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 16 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4025
A37094/c
LOCUS       A37094                    19 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 7 from Patent WO9403594.
ACCESSION   A37094
VERSION     A37094.1  GI:2294267
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Matusik,R.J.
  TITLE     ANDROGEN REGULATION WITH DNA SEQUENCES OF RAT PROBASIN GENE
  JOURNAL   Patent: WO 9403594-A 7 17-FEB-1994;
            UNIV MANITOBA (CA)
COMMENT     Other publication CA 2142181 940217
            Other publication AU 4694793 940303
            Other publication JP 7509608T 951026.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1206 CTAGGAAGAACATGCTAT 1223
              ||| ||| || |||||||
Db         18 CTAAGAACAAGATGCTAT 1


RESULT 4026
A39742
LOCUS       A39742                    19 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 10 from Patent WO9418325.
ACCESSION   A39742
VERSION     A39742.1  GI:2295995
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Lucas,R., De,B.P., Fransen,L. and Sablon,E.
  TITLE     TNF-ALPHA MUTEINS AND A PROCESS FOR PREPARING THEM
  JOURNAL   Patent: WO 9418325-A 10 18-AUG-1994;
            INNOGENETICS NV (BE)
COMMENT     Other publication AU 6001094 940829
            Other publication CA 2155103 940818.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  |||||  |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4017
AR205769/c
LOCUS       AR205769                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 7 from patent US 6369208.
ACCESSION   AR205769
VERSION     AR205769.1  GI:21503435
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 7 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  |||||  |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4018
AR205770/c
LOCUS       AR205770                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 8 from patent US 6369208.
ACCESSION   AR205770
VERSION     AR205770.1  GI:21503437
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 8 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  |||||  |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4019
AR205771/c
LOCUS       AR205771                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 9 from patent US 6369208.
ACCESSION   AR205771
VERSION     AR205771.1  GI:21503438
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 9 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  |||||  |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4020
AR205772/c
LOCUS       AR205772                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 10 from patent US 6369208.
ACCESSION   AR205772
VERSION     AR205772.1  GI:21503439
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 10 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  |||||  |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4021
AR205775/c
LOCUS       AR205775                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 13 from patent US 6369208.
ACCESSION   AR205775
VERSION     AR205775.1  GI:21503443
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 13 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
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  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 15 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4012
AR108829/c
LOCUS       AR108829                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 16 from patent US 6111095.
ACCESSION   AR108829
VERSION     AR108829.1  GI:12824316
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 16 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4013
I62823/c
LOCUS       I62823                  19 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5660989.
ACCESSION   I62823
VERSION     I62823.1  GI:2480531
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C. and Olsen,D.B.
  TITLE     DNA polymerase extension assay for influenza virus endonuclease
  JOURNAL   Patent: US 5660989-A 1 26-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4014
AR205763/c
LOCUS       AR205763                19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 1 from patent US 6369208.
ACCESSION   AR205763
VERSION     AR205763.1  GI:21503428
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 1 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4015
AR205766/c
LOCUS       AR205766                19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 4 from patent US 6369208.
ACCESSION   AR205766
VERSION     AR205766.1  GI:21503432
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 4 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4016
AR205768/c
LOCUS       AR205768                19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6369208.
ACCESSION   AR205768
VERSION     AR205768.1  GI:21503434
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 6 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 8 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4007
AR108822/c
LOCUS       AR108822                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 9 from patent US 6111095.
ACCESSION   AR108822
VERSION     AR108822.1  GI:12824309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 9 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4008
AR108823/c
LOCUS       AR108823                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 10 from patent US 6111095.
ACCESSION   AR108823
VERSION     AR108823.1  GI:12824310
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 10 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4009
AR108826/c
LOCUS       AR108826                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 13 from patent US 6111095.
ACCESSION   AR108826
VERSION     AR108826.1  GI:12824313
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 13 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4010
AR108827/c
LOCUS       AR108827                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 14 from patent US 6111095.
ACCESSION   AR108827
VERSION     AR108827.1  GI:12824314
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 14 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4011
AR108828/c
LOCUS       AR108828                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 15 from patent US 6111095.
ACCESSION   AR108828
VERSION     AR108828.1  GI:12824315
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
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RESULT 4001
AR030984/c
LOCUS       AR030984                19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5861501.
ACCESSION   AR030984
VERSION     AR030984.1  GI:5944198
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 16 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4002
AR108814/c
LOCUS       AR108814                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 1 from patent US 6111095.
ACCESSION   AR108814
VERSION     AR108814.1  GI:12824301
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 1 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4003
AR108817/c
LOCUS       AR108817                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6111095.
ACCESSION   AR108817
VERSION     AR108817.1  GI:12824304
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 4 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4004
AR108819/c
LOCUS       AR108819                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 6 from patent US 6111095.
ACCESSION   AR108819
VERSION     AR108819.1  GI:12824306
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 6 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4005
AR108820/c
LOCUS       AR108820                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 7 from patent US 6111095.
ACCESSION   AR108820
VERSION     AR108820.1  GI:12824307
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 7 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4006
AR108821/c
LOCUS       AR108821                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 8 from patent US 6111095.
ACCESSION   AR108821
VERSION     AR108821.1  GI:12824308
```

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Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 3996
AR030977/c
LOCUS       AR030977                  19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 9 from patent US 5861501.
ACCESSION   AR030977
VERSION     AR030977.1  GI:5944191
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 9 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 3997
AR030978/c
LOCUS       AR030978                  19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 10 from patent US 5861501.
ACCESSION   AR030978
VERSION     AR030978.1  GI:5944192
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 10 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 3998
AR030981/c
LOCUS       AR030981                  19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 13 from patent US 5861501.
ACCESSION   AR030981
VERSION     AR030981.1  GI:5944195
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 13 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 3999
AR030982/c
LOCUS       AR030982                  19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5861501.
ACCESSION   AR030982
VERSION     AR030982.1  GI:5944196
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 14 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 4000
AR030983/c
LOCUS       AR030983                  19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5861501.
ACCESSION   AR030983
VERSION     AR030983.1  GI:5944197
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 15 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||| ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2
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                    /note="T-DNA flanking sequence
                    right border"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAA 2795
              ||  ||||| ||||||||
Db          1 TAATATTGACAAAAAAAA 18


RESULT 3991
AR030969/c
LOCUS       AR030969                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5861501.
ACCESSION   AR030969
VERSION     AR030969.1  GI:5944183
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 1 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 3992
AR030972/c
LOCUS       AR030972                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5861501.
ACCESSION   AR030972
VERSION     AR030972.1  GI:5944186
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 4 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 3993
AR030974/c
LOCUS       AR030974                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5861501.
ACCESSION   AR030974
VERSION     AR030974.1  GI:5944188
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 6 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 3994
AR030975/c
LOCUS       AR030975                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 7 from patent US 5861501.
ACCESSION   AR030975
VERSION     AR030975.1  GI:5944189
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 7 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||  ||||| |||||
Db         19 GAAAATTAAAAATAAAAA 2


RESULT 3995
AR030976/c
LOCUS       AR030976                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5861501.
ACCESSION   AR030976
VERSION     AR030976.1  GI:5944190
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 8 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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RESULT 3988
BD166064/c
LOCUS       BD166064                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166064
VERSION     BD166064.1  GI:27871876
KEYWORDS    JP 2002191372-A/44.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 44 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/44
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              ||||||||||||   ||||
Db         18 TTTTTTTTTTTTCCCCCC 1


RESULT 3989
BD225045
LOCUS       BD225045                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD225045
VERSION     BD225045.1  GI:33034815
KEYWORDS    JP 2002526095-A/180.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 180 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/180
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1565 GCAAAAATCCTTCTCCAC 1582
              |||||| ||| |||| ||
Db          1 GCAAAACTCCGTCTCTAC 18


RESULT 3990
AJ589110
LOCUS       AJ589110                 18 bp    DNA     linear   PLN 23-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, right border, clone
            544G01.
ACCESSION   AJ589110
VERSION     AJ589110.1  GI:37938734
KEYWORDS    right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 18)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Arabidopsis thaliana"
                      /mol_type="genomic DNA"
                      /cultivar="Wassillewskija"
                      /db_xref="taxon:3702"
                      /clone="544G01"
                      /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature     1. .18
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KEYWORDS    WO 0192572-A/1065.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1065 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1065
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
           MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
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FEATURES            Location/Qualifiers
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                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        633 TGGATGCCGCGGGCCTGG 650
              ||||||||  ||  ||  |||
Db          1 TGGATGCCACGTGCGTGG 18


RESULT 3986
BD107532/c
LOCUS       BD107532                 18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107532
VERSION     BD107532.1  GI:23202350
KEYWORDS    JP 2002000275-A/41.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 41 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/41
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC                   nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .18
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              ||||||||||   ||||
Db         18 TTTTTTTTTTTCCCCCC 1


RESULT 3987
BD145064/c
LOCUS       BD145064                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145064
VERSION     BD145064.1  GI:27850822
KEYWORDS    JP 2002119291-A/45.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 45 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/45
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
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                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              ||||||||||   ||||
Db         18 TTTTTTTTTTTCCCCCC 1
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RESULT 3982
BD081036
LOCUS       BD081036                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Coding sequence haplotypes of the human BRCA2 gene.
ACCESSION   BD081036
VERSION     BD081036.1  GI:22626639
KEYWORDS    JP 2001514887-A/44.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Murphy,P.D., White,M.B., Rabin,M.B., Olson,S.J., Yoshikawa,M.,
            Jackson,G.M., Eskandari,T., Schryer,B. and Park,M.
  TITLE     Coding sequence haplotypes of the human BRCA2 gene
  JOURNAL   Patent: JP 2001514887-A 44 18-SEP-2001;
            ONCORMED INC
COMMENT     OS   Unidentified
            PN   JP 2001514887-A/44
            PD   18-SEP-2001
            PF   14-AUG-1998 JP 2000509828
            PR   15-AUG-1997 US    60/055784,07-NOV-1997 US    60/064926 PR
            12-NOV-1997 US    60/065367,01-MAY-1998 US    09/071715 PR
            22-MAY-1998 US    09/084471
            PI   PATRICIA D MURPHY,MARGA B WHITE,MARK B RABIN,SHERI J OLSON, PI
              MATTHEW YOSHIKAWA,GEOFFREY M JACKSON,TARA ESKANDARI,BRENDA  PI
            SCHRYER,
            PI   MICHAEL PARK
            PC   C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00,C07K14/47,
            PC   C07K16/18,
            PC
            C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68//C12P21/02,C12P21/ PC
             08,
            PC   C12N15/00,A61K37/02,C12N5/00
            CC   11HF primer
            FH   Key             Location/Qualifiers
            FT   source          1. .18
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FEATURES             Location/Qualifiers
     source          1. .18
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                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        454 AGGCAGCCAGCAGCAGGC 471
              ||| || |||||||| ||
Db          1 AGGTAGACAGCAGCAAGC 18


RESULT 3983
BD089313/c
LOCUS       BD089313                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089313
VERSION     BD089313.1  GI:22634923
KEYWORDS    JP 2001321190-A/1557.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 1557 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/1557
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
              Location/Qualifiers
            FT   source          1. .18
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FEATURES             Location/Qualifiers
     source          1. .18
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                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        503 GGGCTGCCCTCGCACCAC 520
              ||||| |  |||||||||
Db         18 GGGCTACAATCGCACCAC 1


RESULT 3984
BD089762/c
LOCUS       BD089762                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089762
VERSION     BD089762.1  GI:22635372
KEYWORDS    JP 2001321190-A/2006.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 2006 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/2006
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
              Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2625 CTTTGTCTCGTTCCTGTT 2642
              || |||||||  ||||||
Db         18 CTGTGTCTCGCCCCTGTT 1


RESULT 3985
BD104961
LOCUS       BD104961                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104961
VERSION     BD104961.1  GI:22650535
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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        480 GCCGCCAGAGCCAGGAGG 497
              ||| || |||||||| ||
Db         18 GCCCCCCGAGCCAGGGGG 1


RESULT 3979
BD065377/c
LOCUS       BD065377                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065377
VERSION     BD065377.1  GI:22610980
KEYWORDS    JP 2001511000-A/12.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 12 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/12
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
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            FT                   /organism='Unknown'.
FEATURES              Location/Qualifiers
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        527 CCGGCCGGCCTACTGCCC 544
              ||| ||||||  ||||||
Db         18 CCGCCCGGCCCGCTGCCC 1


RESULT 3980
BD065506
LOCUS       BD065506                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065506
VERSION     BD065506.1  GI:22611109
KEYWORDS    JP 2001511000-A/141.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 141 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/141
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
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            FT                   /organism='Unknown'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGG 504
              | |||||||||| || ||
Db          1 GGGCCAGGAGGGGGCTGG 18


RESULT 3981
BD072905/c
LOCUS       BD072905                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072905
VERSION     BD072905.1  GI:22618508
KEYWORDS    JP 2001286300-A/43.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 43 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/43
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,  PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTGAACCCC 1788
              ||||||||||   ||||
Db         18 TTTTTTTTTTTCCCCCC 1
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FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ESR1"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2347 TGGAGGTTCTGTATTTTA 2364
              ||||||||| | | ||||
Db          1 TGGAGGTTCGGGAGTTTA 18


RESULT 3975
AX825818
LOCUS       AX825818                 18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 70 from Patent WO03072821.
ACCESSION   AX825818
VERSION     AX825818.1  GI:39751332
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferactive disorder
  JOURNAL   Patent: WO 03072821-A 70 04-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        240 GGAATCCGCGGGTCCCCC 257
              ||| |||||||| ||| |
Db          1 GGAGTCCGCGGGACCCTC 18


RESULT 3976
AX826638
LOCUS       AX826638                 18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 890 from Patent WO03072821.
ACCESSION   AX826638
VERSION     AX826638.1  GI:39752152
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferactive disorder
  JOURNAL   Patent: WO 03072821-A 890 04-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for MSH5"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2733 ATAATTGTTGTGTGTATG 2750
              ||| ||||||  ||||||
Db          1 ATAGTTGTTGAATGTATG 18


RESULT 3977
AX826717
LOCUS       AX826717                 18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 969 from Patent WO03072821.
ACCESSION   AX826717
VERSION     AX826717.1  GI:39752231
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferactive disorder
  JOURNAL   Patent: WO 03072821-A 969 04-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
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                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ESR1"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2347 TGGAGGTTCTGTATTTTA 2364
              ||||||||| | | ||||
Db          1 TGGAGGTTCGGGAGTTTA 18


RESULT 3978
BD065375/c
LOCUS       BD065375                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065375
VERSION     BD065375.1  GI:22610978
KEYWORDS    JP 2001511000-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 10 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/10
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
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DEFINITION  Sequence 856 from Patent WO03052135.
ACCESSION   AX796513
VERSION     AX796513.1  GI:37517179
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
            and Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lung cell
            proliferative disorder
  JOURNAL   Patent: WO 03052135-A 856 26-JUN-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ESR1"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2347 TGGAGGTTCTGTATTTTA 2364
              ||||||||| | | ||||
Db          1 TGGAGGTTCGGGAGTTTA 18


RESULT 3971
AX796532
LOCUS       AX796532                 18 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 875 from Patent WO03052135.
ACCESSION   AX796532
VERSION     AX796532.1  GI:37517198
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
            and Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lung cell
            proliferative disorder
  JOURNAL   Patent: WO 03052135-A 875 26-JUN-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for HOXA5"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2748 ATGATACGTGTATAATAA 2765
              |||||| |||| || |||
Db          1 ATGATAGGTGTTTATTAA 18


RESULT 3972
AX822178
LOCUS       AX822178                 18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 70 from Patent EP1340818.
ACCESSION   AX822178
VERSION     AX822178.1  GI:39748806
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferative disorder
  JOURNAL   Patent: EP 1340818-A 70 03-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        240 GGAATCCGCGGGTCCCCC 257
              ||| |||||||| ||| |
Db          1 GGAGTCCGCGGGACCCTC 18


RESULT 3973
AX822998
LOCUS       AX822998                 18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 890 from Patent EP1340818.
ACCESSION   AX822998
VERSION     AX822998.1  GI:39749634
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferative disorder
  JOURNAL   Patent: EP 1340818-A 890 03-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for MSH5"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2733 ATAATTGTTGTGTGTATG 2750
              ||| ||||||  ||||||
Db          1 ATAGTTGTTGAATGTATG 18


RESULT 3974
AX823077
LOCUS       AX823077                 18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 969 from Patent EP1340818.
ACCESSION   AX823077
VERSION     AX823077.1  GI:39749713
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferative disorder
  JOURNAL   Patent: EP 1340818-A 969 03-SEP-2003;
            Epigenomics AG (DE)
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           RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1453 CCCTGGAGACCAGAGTCC 1470
              |||||| || ||||| ||
Db         18 CCCTGGGGAGCAGAGGCC 1


RESULT 3966
AX705457
LOCUS       AX705457                  18 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 126 from Patent WO03014388.
ACCESSION   AX705457
VERSION     AX705457.1  GI:29562122
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Distler,J., Model,F. and Taubert,H.
  TITLE     Method and nucleic acids for the analysis of colon cancer
  JOURNAL   Patent: WO 03014388-A 126 20-FEB-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ESR1"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2347 TGGAGGTTCTGTATTTTA 2364
              ||||||||| | | ||||
Db          1 TGGAGGTTCGGGAGTTTA 18


RESULT 3967
AX705459/c
LOCUS       AX705459                  18 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 128 from Patent WO03014388.
ACCESSION   AX705459
VERSION     AX705459.1  GI:29562124
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Distler,J., Model,F. and Taubert,H.
  TITLE     Method and nucleic acids for the analysis of colon cancer
  JOURNAL   Patent: WO 03014388-A 128 20-FEB-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ESR1"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2347 TGGAGGTTCTGTATTTTA 2364
              ||||||||| | | ||||
Db         18 TGGAGGTTCGGGAGTTTA 1


RESULT 3968
AX708192
LOCUS       AX708192                  18 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 17 from Patent WO02059248.
ACCESSION   AX708192
VERSION     AX708192.1  GI:29564116
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Reue,K. and Peterfy,M.
  TITLE     A novel gene associated with regulation of adiposity and insulin
            response
  JOURNAL   Patent: WO 02059248-A 17 01-AUG-2002;
            The Regents of the University of California (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       113 GGCTGGGGGGATCCTGGA 130
             || || ||||| ||||||
Db         1 GGTTGTGGGGACCCTGGA 18


RESULT 3969
AX767877
LOCUS       AX767877                  18 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 525 from Patent WO03044226.
ACCESSION   AX767877
VERSION     AX767877.1  GI:32436563
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
            Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lymphoid cell
            proliferative disorder
  JOURNAL   Patent: WO 03044226-A 525 30-MAY-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for ESR1"

  Query Match              0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2347 TGGAGGTTCTGTATTTTA 2364
              ||||||||| | | ||||
Db          1 TGGAGGTTCGGGAGTTTA 18


RESULT 3970
AX796513
LOCUS       AX796513                  18 bp    DNA     linear   PAT 04-OCT-2003
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Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.
REFERENCE 1
AUTHORS de Smet,K. and Stuyver,L.
TITLE Method for detection of drug-induced mutations in the hiv reverse transcriptase gene
JOURNAL Patent: WO 02055741-A 875 18-JUL-2002; INNOGENETICS N.V. (BE)
FEATURES Location/Qualifiers
source 1. .18
/organism="Human immunodeficiency virus"
/mol_type="unassigned DNA"
/db_xref="taxon:12721"

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 679 TCACCAGATGGACGAGGT 696
||| | ||||||||||
Db 1 TCAATACATGGACGAGGT 18

RESULT 3962
AX599553
LOCUS AX599553 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 893 from Patent WO02077272.
ACCESSION AX599553
VERSION AX599553.1 GI:28399699
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J., Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E., Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T., Pelet,C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders
JOURNAL Patent: WO 02077272-A 893 03-OCT-2002; Epigenomics AG (DE)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for ESR1"

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2347 TGGAGGTTCTGTATTTTA 2364
|||||||||| | | ||||
Db 1 TGGAGGTTCGGGAGTTTA 18

RESULT 3963
AX599628
LOCUS AX599628 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 968 from Patent WO02077272.
ACCESSION AX599628
VERSION AX599628.1 GI:28399774
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J., Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E., Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T., Pelet,C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders
JOURNAL Patent: WO 02077272-A 968 03-OCT-2002; Epigenomics AG (DE)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for HOXA5"

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2748 ATGATACGTGTATAATAA 2765
|||||| |||| || |||
Db 1 ATGATAGGTGTTTATTAA 18

RESULT 3964
AX600742/c
LOCUS AX600742 18 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 49 from Patent EP1260520.
ACCESSION AX600742
VERSION AX600742.1 GI:28400696
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Tavtigian,S.V., Kamb,A., Simard,J., Couch,F., Rommens,J.M. and Weber,B.L.
TITLE Chromosome 13-linked breast cancer susceptibility gene
JOURNAL Patent: EP 1260520-A 49 27-NOV-2002; MYRIAD GENETICS, INC. (US) ; Endo Recherche Inc. (CA) ; THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA (US) ; HSC Research and Development Limited Partnership (CA)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 453 CAGGCAGCCAGCAGCAGG 470
|||| || |||||||| |
Db 18 CAGGTAGACAGCAGCAAG 1

RESULT 3965
AX637756/c
LOCUS AX637756 18 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 4895 from Patent EP1260586.
ACCESSION AX637756
VERSION AX637756.1 GI:28473370
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 4895 27-NOV-2002;

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                    ||||||  |  ||  ||||||
Db          18 ACAGGCCGGCACCAGCAG 1


RESULT 3957
AX137004/c
LOCUS       AX137004                  18 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 78 from Patent EP1088900.
ACCESSION   AX137004
VERSION     AX137004.1  GI:14273351
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hustert,E., Wojnowski,L. and Eiselt,R.
  TITLE     Polymorphisms in the human cyp3a4, cyp3a7 and hpxr genes and their
            use in diagnostic and therapeutic applications
  JOURNAL   Patent: EP 1088900-A 78 04-APR-2001;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        452 ACAGGCAGCCAGCAGCAG 469
                ||||||  |  ||  ||||||
Db         18 ACAGGCCGGCACCAGCAG 1


RESULT 3958
AX191970
LOCUS       AX191970                  18 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 122 from Patent WO0149833.
ACCESSION   AX191970
VERSION     AX191970.1  GI:15210119
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Ford,J.D. and Sarkanen,S.
  TITLE     Recombinant pinoresinol/lariciresinol reductase, recombinant
            dirigent protein, and methods of use
  JOURNAL   Patent: WO 0149833-A 122 12-JUL-2001;
            Washington State University Research Foundation (US) ; REGENTS OF
            THE UNIVERSITY OF MINNESOTA (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
     misc_feature    1. .18
                     /note="Linker primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTT 2179
                |||   ||||||||||||
Db          1 CTCGAGTTTTTTTTTTTT 18


RESULT 3959
AX469443/c
LOCUS       AX469443                  18 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 9 from Patent WO0222877.
ACCESSION   AX469443
VERSION     AX469443.1  GI:21901729
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hill,J.A., Wang,Z.C., Anderson,D.J. and Yunis,E.J.
  TITLE     Variants of il-1 beta gene and cd46 gene for diagnosing unexplained
            recurrent pregnancy loss
  JOURNAL   Patent: WO 0222877-A 9 21-MAR-2002;
            THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; DANA-FARBER CANCER
            INSTITUTE, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1751 TGGCTCTTTATTCATTAA 1768
                ||||  ||  |  ||||||||
Db         18 TGGCCCTGTCTTCATTAA 1


RESULT 3960
AX473186
LOCUS       AX473186                  18 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 19 from Patent WO0238727.
ACCESSION   AX473186
VERSION     AX473186.1  GI:22207894
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Enckevort,L.J., Jacobsen,E., Stiekema,W.J. and Pereira,A.
  TITLE     Dna sequences encoding proteins conferring phytophthora infestans
            resistance on plants
  JOURNAL   Patent: WO 0238727-A 19 16-MAY-2002;
            Plant Research International B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1913 AACAATACCTTTTTTTTC 1930
                ||||||  |||||  ||  ||
Db          1 AACAATGCCTTTCTTCTC 18


RESULT 3961
AX572835
LOCUS       AX572835                  18 bp    DNA     linear   PAT 29-NOV-2002
DEFINITION  Sequence 875 from Patent WO02055741.
ACCESSION   AX572835
VERSION     AX572835.1  GI:26004925
KEYWORDS    .
SOURCE      Human immunodeficiency virus
  ORGANISM  Human immunodeficiency virus
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                  ||||||||||  || ||
Db         18 TTGTTAGAATTCTAACAA 1


RESULT 3952
AR351522
LOCUS       AR351522                  18 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 14 from patent US 6586581.
ACCESSION   AR351522
VERSION     AR351522.1  GI:33753299
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bancroft,F.C., Fliss,M. and Clelland,C.L.
  TITLE     Prolactin regulatory element binding protein and uses thereof
  JOURNAL   Patent: US 6586581-A 14 01-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        627 ACGCCCTGGATGCCGCGG 644
              | | ||||| ||||||||
Db          1 ATGTCCTGGGTGCCGCGG 18


RESULT 3953
AR351534
LOCUS       AR351534                  18 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 27 from patent US 6586581.
ACCESSION   AR351534
VERSION     AR351534.1  GI:33753311
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bancroft,F.C., Fliss,M. and Clelland,C.L.
  TITLE     Prolactin regulatory element binding protein and uses thereof
  JOURNAL   Patent: US 6586581-A 27 01-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        627 ACGCCCTGGATGCCGCGG 644
              | | ||||| ||||||||
Db          1 ATGTCCTGGGTGCCGCGG 18


RESULT 3954
AR410329
LOCUS       AR410329                  18 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 122 from patent US 6635459.
ACCESSION   AR410329
VERSION     AR410329.1  GI:40161608
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Sarkanen,S. and Ford,J.D.
  TITLE     Nucleotide sequences encoding pinoresinol/lariciresinol reductase
            proteins and their methods of use
  JOURNAL   Patent: US 6635459-A 122 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTT 2179
              |||   ||||||||||||
Db          1 CTCGAGTTTTTTTTTTTT 18


RESULT 3955
AR437532
LOCUS       AR437532                  18 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 16 from patent US 6660483.
ACCESSION   AR437532
VERSION     AR437532.1  GI:40202620
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kask,K., Melcher,T. and Chin,D.J.
  TITLE     Diagnostic marker for neurological conditions
  JOURNAL   Patent: US 6660483-A 16 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1493 GAGAAAATGGAGAAACAC 1510
              ||||| |||||| ||| |
Db          1 GAGAACATGGAGCAACCC 18


RESULT 3956
AX098985/c
LOCUS       AX098985                  18 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 48 from Patent WO0120026.
ACCESSION   AX098985
VERSION     AX098985.1  GI:13538195
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wojnowski,L. and Hustert,E.
  TITLE     Polymorphisms in the human hpxr gene and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 0120026-A 48 22-MAR-2001;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        452 ACAGGCAGCCAGCAGCAG 469
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  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              ||||||||||||    ||||
Db          1 TTTTTTTTTTTTCCCCCC 18


RESULT 3947
AR268663/c
LOCUS       AR268663                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 13 from patent US 6500614.
ACCESSION   AR268663
VERSION     AR268663.1  GI:29699278
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Arguello,R., Avakian,H. and Madrigal,A.
  TITLE     Method for identifying an unknown allele
  JOURNAL   Patent: US 6500614-A 13 31-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1381 CTGTGCCGCGGTGTCTGC 1398
              ||| ||||| ||||| ||
Db         18 CTGAGCCGCCGTGTCCGC 1


RESULT 3948
AR294187/c
LOCUS       AR294187                 18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5922 from patent US 6537751.
ACCESSION   AR294187
VERSION     AR294187.1  GI:31681471
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 5922 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        343 CTTTCCCCCTCCCTACCA 360
              ||||  ||||||||  |||
Db         18 CTTTATCCCTCCCTTCCA 1


RESULT 3949
AR295456
LOCUS       AR295456                 18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 7191 from patent US 6537751.
ACCESSION   AR295456
VERSION     AR295456.1  GI:31682740
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 7191 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        773 AACCCTCTGAACCTCCCC 790
              ||| |||| |||||||  |
Db          1 AACACTCTCAACCTCCTC 18


RESULT 3950
AR305637
LOCUS       AR305637                 18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 40 from patent US 6548021.
ACCESSION   AR305637
VERSION     AR305637.1  GI:31695076
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Church,G.M. and Bulyk,M.L.
  TITLE     Surface-bound, double-stranded DNA protein arrays
  JOURNAL   Patent: US 6548021-A 40 15-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAA 2791
              ||||||||||||  || ||
Db          1 TTGTTAGAATTCTAACAA 18


RESULT 3951
AR305637/c
LOCUS       AR305637                 18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 40 from patent US 6548021.
ACCESSION   AR305637
VERSION     AR305637.1  GI:31695076
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Church,G.M. and Bulyk,M.L.
  TITLE     Surface-bound, double-stranded DNA protein arrays
  JOURNAL   Patent: US 6548021-A 40 15-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAA 2791
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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        442 GCCGGCGCCCACAGGCAG 459
              ||||||||||||   |||
Db         18 GCCGGCGCCCACCACCAG 1


RESULT 3942
I83492
LOCUS       I83492                   18 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 28 from patent US 5714329.
ACCESSION   I83492
VERSION     I83492.1  GI:3407022
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Dracopoli,N., Tucker,M. and Goldstein,A.
  TITLE     Methods for the diagnosis of a genetic predisposition to cancer
            associated with variant CDK4 allele
  JOURNAL   Patent: US 5714329-A 28 03-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1840 CATTCCCTGGGCCAACAG 1857
              | ||||||| ||| ||||
Db          1 CTTTCCCTGTGCCCACAG 18


RESULT 3943
AR196142/c
LOCUS       AR196142                 18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 607 from patent US 6350934.
ACCESSION   AR196142
VERSION     AR196142.1  GI:20245579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 607 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        152 GGGACGCCGGACGCCATG 169
              |||| | ||| |||||||
Db         18 GGGATGGCGGCCGCCATG 1


RESULT 3944
AR196694/c
LOCUS       AR196694                 18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1159 from patent US 6350934.
ACCESSION   AR196694
VERSION     AR196694.1  GI:20246131
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 1159 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         42 GGCCCGCGCGCGGCGGGG 59
              || | ||| |||||||||
Db         18 GGGCGGCGAGCGGCGGGG 1


RESULT 3945
AR211267
LOCUS       AR211267                 18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 180 from patent US 6399297.
ACCESSION   AR211267
VERSION     AR211267.1  GI:21514544
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 180 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1565 GCAAAAATCCTTCTCCAC 1582
              |||||| ||| |||| ||
Db          1 GCAAAACTCCGTCTCTAC 18


RESULT 3946
AR264964
LOCUS       AR264964                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 48 from patent US 6492121.
ACCESSION   AR264964
VERSION     AR264964.1  GI:29693351
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 48 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
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RESULT 3938
AR160886/c
LOCUS       AR160886                 18 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 90 from patent US 6255111.
ACCESSION   AR160886
VERSION     AR160886.1  GI:16225883
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,C.Frank. and Cowsert,L.M.
  TITLE     Antisense modulation of Her-4 expression
  JOURNAL   Patent: US 6255111-A 90 03-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCT 1793
              |||| ||||| ||||| |
Db         18 TTTTCTGAACTCCATTTT 1


RESULT 3939
BD234557/c
LOCUS       BD234557                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of cellular inhibitor of
            apoptosis-2.
ACCESSION   BD234557
VERSION     BD234557.1  GI:33044327
KEYWORDS    JP 2002531102-A/39.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,F.C., Ackermann,E.J. and Cowsert,L.M.
  TITLE     Antisense modulation of expression of cellular inhibitor of
  JOURNAL   Patent: JP 2002531102-A 39 24-SEP-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002531102-A/39
            PD   24-SEP-2002
            PF   23-SEP-1999 JP 2000585449
            PR   03-DEC-1998 US    09/205144
            PI   FRANK C BENNETT,ELIZABETH J ACKERMANN,LEX M COWSERT PC
            C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K31/713,A61K48/ PC
             00,
            PC   A61P35/00,A61P37/00,C12N15/00
            CC   Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1150 ACCAGTGGCAGAATATTT 1167
              |||||||| |||| | ||
Db         18 ACCAGTGGAAGAACAATT 1


RESULT 3940
BD250635/c
LOCUS       BD250635                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Identification of genetic targets for modulation by
            oligonucleotides and generation of oligonucleotides for gene
            modulation.
ACCESSION   BD250635
VERSION     BD250635.1  GI:33060405
KEYWORDS    JP 2002511276-A/189.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cowsert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasmor,H.M.,
            Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
  TITLE     Identification of genetic targets for modulation by
            oligonucleotides and generation of oligonucleotides for gene
            modulation
  JOURNAL   Patent: JP 2002511276-A 189 16-APR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002511276-A/189
            PD   16-APR-2002
            PF   13-APR-1999 JP 2000543647
            PR   13-APR-1998 US    60/081483,28-APR-1998 US    09/067638 PI
            LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI  PI
            M SASMOR,
            PI   DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H  PI
              BORCHERS,
            PI   TIMOTHY A VIKKARS
            PC   C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
              C12N15/00
            CC   Antisense Oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1150 ACCAGTGGCAGAATATTT 1167
              |||||||| |||| | ||
Db         18 ACCAGTGGAAGAACAATT 1


RESULT 3941
I12014/c
LOCUS       I12014                   18 bp    DNA     linear   PAT 26-JUL-1995
DEFINITION  Sequence 6 from Patent US 5418150.
ACCESSION   I12014
VERSION     I12014.1  GI:909455
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Topal,M.D. and Conrad,M.J.
  TITLE     Method of cleaving DNA
  JOURNAL   Patent: US 5418150-A 6 23-MAY-1995;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
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Qy       1446 ACATGAACCCTGGAGACC 1463
              ||| ||||||| ||| ||
Db          1 ACAAGAACCCTTGAGCCC 18


RESULT 3933
AR098789
LOCUS       AR098789                 18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 44 from patent US 6077672.
ACCESSION   AR098789
VERSION     AR098789.1  GI:12808555
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of TRADD expression
  JOURNAL   Patent: US 6077672-A 44 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCA 68
              ||||||| ||||||  ||
Db          1 GCGGCGGCGGCGGCTTCA 18


RESULT 3934
AR098791/c
LOCUS       AR098791                 18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 46 from patent US 6077672.
ACCESSION   AR098791
VERSION     AR098791.1  GI:12808557
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of TRADD expression
  JOURNAL   Patent: US 6077672-A 46 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         415 CGCCGCCGCCATCAACCC 432
               |||||||||||  |  |||
Db          18 CGCCGCCGCCACCTGCCC 1


RESULT 3935
AR101834
LOCUS       AR101834                 18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 25 from patent US 6083713.
ACCESSION   AR101834
VERSION     AR101834.1  GI:12812632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Manly,S.P., Kozlowski,M.R. and Neve,R.L.
  TITLE     Cloning and expression of .beta.APP-C100 receptor (C100-R)
  JOURNAL   Patent: US 6083713-A 25 04-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||||| |||  ||||
Db          1 AAAAAAAAGAAAGCAAAA 18


RESULT 3936
AR101834/c
LOCUS       AR101834                 18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 25 from patent US 6083713.
ACCESSION   AR101834
VERSION     AR101834.1  GI:12812632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Manly,S.P., Kozlowski,M.R. and Neve,R.L.
  TITLE     Cloning and expression of .beta.APP-C100 receptor (C100-R)
  JOURNAL   Patent: US 6083713-A 25 04-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2160 TTCTCCTTTTTTTTTTTT 2177
              || | |||| ||||||||
Db         18 TTTTGCTTTCTTTTTTTT 1


RESULT 3937
AR144877
LOCUS       AR144877                 18 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 122 from patent US 6210942.
ACCESSION   AR144877
VERSION     AR144877.1  GI:15106744
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Sarkanen,S. and Ford,J.D.
  TITLE     Recombinant pinoresinol/lariciresinol reductase, recombinant
            dirigent protein, and methods of use
  JOURNAL   Patent: US 6210942-A 122 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTT 2179
              |||   ||||||||||||
Db          1 CTCGAGTTTTTTTTTTTT 18
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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        324 AATATCAGCCGCCACCCT 341
              ||| |||||| ||||| |
Db         18 AATGTCAGCCTCCACCTT 1


RESULT 3928
AR042299/c
LOCUS       AR042299                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1089 from patent US 5811300.
ACCESSION   AR042299
VERSION     AR042299.1  GI:5962795
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
  TITLE     TNF-.alpha. ribozymes
  JOURNAL   Patent: US 5811300-A 1089 22-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1453 CCCTGGAGACCAGAGTCC 1470
              |||||| || ||||| ||
Db         18 CCCTGGGGAGCAGAGGCC 1


RESULT 3929
AR055425/c
LOCUS       AR055425                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 49 from patent US 5837492.
ACCESSION   AR055425
VERSION     AR055425.1  GI:5981002
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Tavtigian,S.V., Kamb,A., Simard,J., Couch,F., Rommens,J.M. and
            Weber,B.L.
  TITLE     Chromosome 13-linked breast cancer susceptibility gene
  JOURNAL   Patent: US 5837492-A 49 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        453 CAGGCAGCCAGCAGCAGG 470
              |||| || |||||||| |
Db         18 CAGGTAGACAGCAGCAAG 1


RESULT 3930
AR076325/c
LOCUS       AR076325                 18 bp    DNA     linear   PAT 30-AUG-2000
DEFINITION  Sequence 39 from patent US 5958771.
ACCESSION   AR076325
VERSION     AR076325.1  GI:10003071
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,C.Frank., Ackermann,E.J. and Cowsert,L.M.
  TITLE     Antisense modulation of cellular inhibitor of Apoptosis-2
            expression
  JOURNAL   Patent: US 5958771-A 39 28-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1150 ACCAGTGGCAGAATATTT 1167
              |||||||| |||| | ||
Db         18 ACCAGTGGAAGAACAATT 1


RESULT 3931
AR092808/c
LOCUS       AR092808                 18 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 23 from patent US 5998206.
ACCESSION   AR092808
VERSION     AR092808.1  GI:10019560
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibiton of human G-alpha-12 expression
  JOURNAL   Patent: US 5998206-A 23 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        794 CAGAAGGAGCTGGTGGGG 811
              ||||||| |||| ||| |
Db         18 CAGAAGGCGCTGCTGGAG 1


RESULT 3932
AR092813
LOCUS       AR092813                 18 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 28 from patent US 5998206.
ACCESSION   AR092813
VERSION     AR092813.1  GI:10019565
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibiton of human G-alpha-12 expression
  JOURNAL   Patent: US 5998206-A 28 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGG 504
              | |||||||||| || ||
Db          1 GGGCCAGGAGGGGGCTGG 18


RESULT 3923
A89829/c
LOCUS       A89829                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 10 from Patent EP0856579.
ACCESSION   A89829
VERSION     A89829.1  GI:6738343
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 10 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        480 GCCGCCAGAGCCAGGAGG 497
              ||| || ||||||||| ||
Db         18 GCCCCCCGAGCCAGGGGG 1


RESULT 3924
A89831/c
LOCUS       A89831                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 12 from Patent EP0856579.
ACCESSION   A89831
VERSION     A89831.1  GI:6738345
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 12 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        527 CCGGCCGGCCTACTGCCC 544
              ||| |||||| ||||||
Db         18 CCGCCCGGCCCGCTGCCC 1


RESULT 3925
A89960
LOCUS       A89960                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 141 from Patent EP0856579.
ACCESSION   A89960
VERSION     A89960.1  GI:6738474
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 141 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGG 504
              | |||||||||| || ||
Db          1 GGGCCAGGAGGGGGCTGG 18


RESULT 3926
AR019212/c
LOCUS       AR019212                 18 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 6 from patent US 5783393.
ACCESSION   AR019212
VERSION     AR019212.1  GI:3974326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kellogg,J.Anne. and Bestwick,R.Keith.
  TITLE     Plant tissue/stage specific promoters for regulated expression of
            transgenes in plants
  JOURNAL   Patent: US 5783393-A 6 21-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        324 AATATCAGCCGCCACCCT 341
              ||| |||||| ||||| |
Db         18 AATGTCAGCCTCCACCTT 1


RESULT 3927
AR019245/c
LOCUS       AR019245                 18 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 17 from patent US 5783394.
ACCESSION   AR019245
VERSION     AR019245.1  GI:3974359
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bestwick,R.K. and Kellogg,J.Anne.
  TITLE     Raspberry promoters for expression of transgenes in plants
  JOURNAL   Patent: US 5783394-A 17 21 JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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RESULT 3918
AX662307
LOCUS       AX662307                  18 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 46 from Patent WO02059293.
ACCESSION   AX662307
VERSION     AX662307.1  GI:29163190
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Forster,A.C. and Blacklow,S.C.
  TITLE     Process and compositions for peptide, protein and peptidomimetic
            synthesis
  JOURNAL   Patent: WO 02059293-A 46 01-AUG-2002;
            Forster, Anthony C. (US) ; Blacklow, Stephen C. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="FROM SYNTHETIC DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAAC 2189
              ||||||||||  || |||
Db          1 TTTTTTTTTTAATTCAAC 18


RESULT 3919
A63086/c
LOCUS       A63086                    18 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 13 from Patent WO9720197.
ACCESSION   A63086
VERSION     A63086.1  GI:3716950
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Arguello,R., Avakian,H. and Madrigal,A.
  TITLE     METHOD FOR IDENTIFYING AN UNKNOWN ALLELE
  JOURNAL   Patent: WO 9720197-A 13 05-JUN-1997;
            ANTHONY NOLAN BONE MARROW TRUS (GB)
COMMENT     Other publication AU 7703796 19970619.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1381 CTGTGCCGCGGTGTCTGC 1398
              ||| ||||| ||||| ||
Db         18 CTGAGCCGCCGTGTCCGC 1


RESULT 3920
A87862/c
LOCUS       A87862                    18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 10 from Patent WO9833904.
ACCESSION   A87862
VERSION     A87862.1  GI:6736432
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 10 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        480 GCCGCCAGAGCCAGGAGG 497
              ||| || |||||||| ||
Db         18 GCCCCCCGAGCCAGGGGG 1


RESULT 3921
A87864/c
LOCUS       A87864                    18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 12 from Patent WO9833904.
ACCESSION   A87864
VERSION     A87864.1  GI:6736434
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 12 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        527 CCGGCCGGCCTACTGCCC 544
              ||| ||||||  ||||||
Db         18 CCGCCCGGCCCGCTGCCC 1


RESULT 3922
A87993
LOCUS       A87993                    18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 141 from Patent WO9833904.
ACCESSION   A87993
VERSION     A87993.1  GI:6736563
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 141 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
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  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||| | |||||||| |
Db         18 AAAAAGAGAAAAAAAAGA 1


RESULT 3913
AR008471
LOCUS       AR008471                  18 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5753489.
ACCESSION   AR008471
VERSION     AR008471.1  GI:3967580
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kistner,O., Barrett,N., Mundt,W. and Dorner,F.
  TITLE     Method for producing viruses and vaccines in serum-free culture
  JOURNAL   Patent: US 5753489-A 6 19-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||| | |||||||| |
Db          1 AAAAAGAGAAAAAAAAGA 18


RESULT 3914
AR009718/c
LOCUS       AR009718                  18 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5756341.
ACCESSION   AR009718
VERSION     AR009718.1  GI:3968523
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kistner,O., Barrett,N., Mundt,W. and Dorner,F.
  TITLE     Method for controlling the infectivity of viruses
  JOURNAL   Patent: US 5756341-A 5 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||| | |||||||| |
Db         18 AAAAAGAGAAAAAAAAGA 1


RESULT 3915
AR009719
LOCUS       AR009719                  18 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5756341.
ACCESSION   AR009719
VERSION     AR009719.1  GI:3968524
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kistner,O., Barrett,N., Mundt,W. and Dorner,F.
  TITLE     Method for controlling the infectivity of viruses
  JOURNAL   Patent: US 5756341-A 6 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||| | |||||||| |
Db          1 AAAAAGAGAAAAAAAAGA 18


RESULT 3916
AR063241
LOCUS       AR063241                  18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5844110.
ACCESSION   AR063241
VERSION     AR063241.1  GI:5990932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Gold,B.I.
  TITLE     Synthetic triple helix-forming compound precursors
  JOURNAL   Patent: US 5844110-A 2 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              |||| |||||| |||| |
Db          1 TTTTCTTTTTTCTTTTCT 18


RESULT 3917
AR063243/c
LOCUS       AR063243                  18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5844110.
ACCESSION   AR063243
VERSION     AR063243.1  GI:5990934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Gold,B.I.
  TITLE     Synthetic triple helix-forming compound precursors
  JOURNAL   Patent: US 5844110-A 4 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||| |||||||| ||| |
Db         18 AAAGAAAAAAAAGAAAGA 1
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```
  Query Match             0.5%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              |:||||||||||||
Db         14 TBAAAAAAAAAAAA 1


RESULT 3908
AR266627
LOCUS       AR266627                  14 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 65 from patent US 6495319.
ACCESSION   AR266627
VERSION     AR266627.1  GI:29695691
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 65 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTA 2187
              |||||||||||||:
Db          1 TTTTTTTTTTTTV 14


RESULT 3909
AR266627/c
LOCUS       AR266627                  14 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 65 from patent US 6495319.
ACCESSION   AR266627
VERSION     AR266627.1  GI:29695691
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 65 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              :||||||||||||||
Db         14 BAAAAAAAAAAAAA 1


RESULT 3910
AR084213
LOCUS       AR084213                  16 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 4 from patent US 5977440.
ACCESSION   AR084213
VERSION     AR084213.1  GI:10010984
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Luthe,D.S., Williams,W.P., Jiang,B. and Pechan,T.
  TITLE     DNA molecule encoding a 33kD cysteine proteinase and its use in
            transforming plants to provide insect resistance
  JOURNAL   Patent: US 5977440-A 4 02-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 16;
  Best Local Similarity   75.0%;  Pred. No. 2.5e+03;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        704 GTCGACGACCAGCACC 719
              ||:||||||||:|: |
Db          1 GTSGACGACCARCRGC 16


RESULT 3911
AR264960/c
LOCUS       AR264960                  18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 44 from patent US 6492121.
ACCESSION   AR264960
VERSION     AR264960.1  GI:29693347
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 44 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCC 1788
              ||||||||||||   ||||
Db         18 TTTTTTTTTTTTTCCCCC 1


RESULT 3912
AR008470/c
LOCUS       AR008470                  18 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5753489.
ACCESSION   AR008470
VERSION     AR008470.1  GI:3967579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kistner,O., Barrett,N., Mundt,W. and Dorner,F.
  TITLE     Method for producing viruses and vaccines in serum-free culture
  JOURNAL   Patent: US 5753489-A 5 19-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 18;
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            PI   SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
            PC   C12N15/09,C12N9/02,(C12N9/02,C12R1:91);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .14
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAA 2188
              ||||||||||||:|
Db          1 TTTTTTTTTTTTVA 14


RESULT 3905
E13665/c
LOCUS       E13665                    14 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Primer.
ACCESSION   E13665
VERSION     E13665.1  GI:3252442
KEYWORDS    JP 1997224671-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Shibata,D., Kato,T. and Ota,H.
  TITLE     DNA CODING NEW CYTOCHROME P450
  JOURNAL   Patent: JP 1997224671-A 3 02-SEP-1997;
            MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997224671-A/3
            PD   02-SEP-1997
            PF   19-FEB-1996 JP 1996031075
            PI   SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
            PC   C12N15/09,C12N9/02,(C12N9/02,C12R1:91);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .14
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              |:||||||||||||
Db         14 TBAAAAAAAAAAAA 1


RESULT 3906
E13670
LOCUS       E13670                    14 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Primer.
ACCESSION   E13670
VERSION     E13670.1  GI:3252447
KEYWORDS    JP 1997224672-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Shibata,D., Kato,T. and Ota,H.
  TITLE     DNA CODING NEW DNA-CONNECTED PROTEIN
  JOURNAL   Patent: JP 1997224672-A 3 02-SEP-1997;
            MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997224672-A/3
            PD   02-SEP-1997
            PF   21-FEB-1996 JP 1996033973
            PI   SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
            PC   C12N15/09,A01H5/00,C07H21/04,C07K14/415//C12N5/10,C12Q1/68; CC
              strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .14
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAA 2188
              ||||||||||||:|
Db          1 TTTTTTTTTTTTVA 14


RESULT 3907
E13670/c
LOCUS       E13670                    14 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Primer.
ACCESSION   E13670
VERSION     E13670.1  GI:3252447
KEYWORDS    JP 1997224672-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Shibata,D., Kato,T. and Ota,H.
  TITLE     DNA CODING NEW DNA-CONNECTED PROTEIN
  JOURNAL   Patent: JP 1997224672-A 3 02-SEP-1997;
            MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997224672-A/3
            PD   02-SEP-1997
            PF   21-FEB-1996 JP 1996033973
            PI   SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
            PC   C12N15/09,A01H5/00,C07H21/04,C07K14/415//C12N5/10,C12Q1/68; CC
              strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .14
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
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AR434873
LOCUS       AR434873                 25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1296 from patent US 6656700.
ACCESSION   AR434873
VERSION     AR434873.1  GI:40197716
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1296 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 25;
  Best Local Similarity   73.9%;  Pred. No. 4.6e+03;
  Matches   17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
              ||||  |   ||||||||| |||
Db          2 AGAAGGGGGGAAAAAAAAAGAAA 24


RESULT 3901
AX043060/c
LOCUS       AX043060                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 626 from Patent WO0065088.
ACCESSION   AX043060
VERSION     AX043060.1  GI:11341668
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 626 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 25;
  Best Local Similarity   93.3%;  Pred. No. 4.6e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAA 2797
              | ||||||||||||||
Db         15 TCGAAAAAAAAAAAA 1


RESULT 3902
A52265
LOCUS       A52265                   14 bp    DNA     linear   PAT 12-DEC-1997
DEFINITION  Sequence 55 from Patent EP0705842.
ACCESSION   A52265
VERSION     A52265.1  GI:2852047
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Bartnik,E.D. and Margerie,D.D.
  TITLE     Regulated genes by stimulation of chondrocytes with 1L-1beta
  JOURNAL   Patent: EP 0705842-A 55 10-APR-1996;
            HOECHST AG (DE)
COMMENT     Other publication ZA 9508381 960424
            Other publication JP 8191693 960730
            Other publication CA 2159957 960407
            Other publication AU 3308695 960418.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAA 2188
              |||||||||||||:|
Db          1 TTTTTTTTTTTTVA 14


RESULT 3903
A52265/c
LOCUS       A52265                   14 bp    DNA     linear   PAT 12-DEC-1997
DEFINITION  Sequence 55 from Patent EP0705842.
ACCESSION   A52265
VERSION     A52265.1  GI:2852047
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Bartnik,E.D. and Margerie,D.D.
  TITLE     Regulated genes by stimulation of chondrocytes with 1L-1beta
  JOURNAL   Patent: EP 0705842-A 55 10-APR-1996;
            HOECHST AG (DE)
COMMENT     Other publication ZA 9508381 960424
            Other publication JP 8191693 960730
            Other publication CA 2159957 960407
            Other publication AU 3308695 960418.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.2;  DB 1;  Length 14;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+03;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              |:|||||||||||||
Db         14 TBAAAAAAAAAAAA 1


RESULT 3904
E13665
LOCUS       E13665                   14 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Primer.
ACCESSION   E13665
VERSION     E13665.1  GI:3252442
KEYWORDS    JP 1997224671-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Shibata,D., Kato,T. and Ota,H.
  TITLE     DNA CODING NEW CYTOCHROME P450
  JOURNAL   Patent: JP 1997224671-A 3 02-SEP-1997;
            MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997224671-A/3
            PD   02-SEP-1997
            PF   19-FEB-1996 JP 1996031075
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  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .20
                     /note="forward primer for human STS sts-STGDB:578894 at
                     1p36
                     sts-STGDB:578894 obtained from clones B252K20, B362I4,
                     Human BAC library RPCI-11"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2117 GTTTTAGGAAACTTG 2131
              ||||| |||||||||
Db         20 GTTTTTGGAAACTTG 6


RESULT 3896
AR138736
LOCUS       AR138736                  21 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 34 from patent US 6200754.
ACCESSION   AR138736
VERSION     AR138736.1  GI:14481081
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Housman,D.E., Ledley,F.D. and Stanton,V.P. Jr.
  TITLE     Inhibitors of alternative alleles of genes encoding products that
            mediate cell response to environmental changes
  JOURNAL   Patent: US 6200754-A 34 13-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 4e+03;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              || | ||:|||||||||
Db          5 AACATAARAAAAAAAAA 21


RESULT 3897
AX498248/c
LOCUS       AX498248                  21 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 4 from Patent WO0218951.
ACCESSION   AX498248
VERSION     AX498248.1  GI:23343167
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 4 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 21;
  Best Local Similarity   93.3%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||| |||||||
Db         16 TTTTTTGTTTTTTT 2


RESULT 3898
I24714
LOCUS       I24714                    21 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 18 from patent US 5545545.
ACCESSION   I24714
VERSION     I24714.1  GI:1604584
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Gengenbach,B.G., Somers,D.A., Bittel,D.C., Shaver,J.M. and
            Sellner,J.M. deceased.
  TITLE     Lysine-insensitive maize dihydrodipicolinic acid synthase
  JOURNAL   Patent: US 5545545-A 18 13-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 21;
  Best Local Similarity   93.3%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        654 AGAACCTGGGGCTCC 668
              ||||||||||  ||||
Db          2 AGAACCTGGGCCTCC 16


RESULT 3899
AR364668/c
LOCUS       AR364668                  24 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 1 from patent US 5399676.
ACCESSION   AR364668
VERSION     AR364668.1  GI:34427592
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Froehler,B.
  TITLE     Oligonucleotides with inverted polarity
  JOURNAL   Patent: US 5399676-A 1 21-MAR-1995;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 24;
  Best Local Similarity   73.9%;  Pred. No. 4.5e+03;
  Matches   17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2803
              ||  ||| |||| |||| ||| |
Db         23 AAAAGAAGAAAAGAAAAGAAAGA 1


RESULT 3900
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```
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kawakami,H. and Rosenberg,S.A.
  TITLE     Human malignant melanoma antigen
  JOURNAL   Patent: JP 2002065276-A 13 05-MAR-2002;
            KEIO UNIVERSITY,UNITED STATES OF AMERICA
COMMENT     OS   Artificial Sequence
            PN   JP 2002065276-A/13
            PD   05-MAR-2002
            PF   31-AUG-2000 JP 2000263725
            PI   HIROSHI KAWAKAMI,STEVEN A ROSENBERG
            PC   C12N15/09,A01K67/027,A61K38/00,A61K45/00,A61P35/00,A61P37/04,
            PC   C07K14/82,
            PC   C07K16/32,C07K19/00,C12N5/10,C12P21/08,C12Q1/68,G01N33/15, PC
             G01N33/50,
            PC   G01N33/566,C12N15/00,A61K37/02,C12N5/00
            CC   Description of Artificial Sequence:Primer 2
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1417 AGAAGCCCTGATTGT 1431
              || |||||||||||||
Db         16 AGTAGCCCTGATTGT 2


RESULT 3893
BD138288/c
LOCUS       BD138288                 20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Antisense modulation of human MDM2 expression.
ACCESSION   BD138288
VERSION     BD138288.1  GI:23233233
KEYWORDS    JP 2002508944-A/214.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of human MDM2 expression
  JOURNAL   Patent: JP 2002508944-A 214 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002508944-A/214
            PD   26-MAR-2002
            PF   26-MAR-1999 JP 2000538025
            PR   26-MAR-1998 US    09/048810
            PI   LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

            PI   COWSERT
            PC   C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
            PC   C12Q1/68,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense modulation of human MDM2 expression FH   Key
                Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2520 TTTATTCATATATAT 2534
              ||||||| ||||||
Db         15 TTTATTCACATATAT 1


RESULT 3894
BD182266
LOCUS       BD182266                 20 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Stem cell and separating method thereof.
ACCESSION   BD182266
VERSION     BD182266.1  GI:30793184
KEYWORDS    WO 02088335-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Taniguchi,H. and Suzuki,A.
  TITLE     Stem cell and separating method thereof
  JOURNAL   Patent: WO 02088335-A 3 07-NOV-2002;
            AJINOMOTO CO INC,HIDEKI TANIGUCHI,ATSUSHI SUZUKI
COMMENT     OS   Artificial Sequence
            PN   WO 02088335-A/3
            PD   07-NOV-2002
            PF   24-APR-2002 WO 2002JP004084
            PR   24-APR-2001 JP 01P   126315
            PI   HIDEKI TANIGUCHI,ATSUSHI SUZUKI
            PC   C12N5/08,C12N15/09,G01N33/50,G01N33/15,A61K35/39,A61P1/18, PC
             C12Q1/68,
            PC   C12Q1/02
            CC   Oligonucleotide designed to act as PCR primer for detection of
            CC   preproinsulin I (beta cell specific marker) gene FH   Key
                   Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2427 TGGTGCACTTCTTAC 2441
              |||||||||||| |||
Db          5 TGGTGCACTTCCTAC 19


RESULT 3895
AB069398/c
LOCUS       AB069398                 20 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, forward primer for human STS
            sts-STGDB:578894 at 1p36.
ACCESSION   AB069398
VERSION     AB069398.1  GI:15130202
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
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LOCUS       BD088505                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD088505
VERSION     BD088505.1  GI:22634115
KEYWORDS    JP 2001321190-A/749.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 749 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/749
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2117 GTTTTAGGAAACTTG 2131
              ||||| |||||||||
Db         20 GTTTTTGGAAACTTG 6


RESULT 3890
BD106121/c
LOCUS       BD106121                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel LDL-receptor.
ACCESSION   BD106121
VERSION     BD106121.1  GI:23200939
KEYWORDS    JP 2002501376-A/136.
SOURCE      Chlamydia sp.
  ORGANISM  Chlamydia sp.
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H.
            and Hey,P.
  TITLE     Novel LDL-receptor
  JOURNAL   Patent: JP 2002501376-A 136 15-JAN-2002;
            THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO
            INC
COMMENT     PN   JP 2002501376-A/136
            PD   15-JAN-2002
            PF   15-APR-1998 JP 1998543635
            PR   15-APR-1997 US    60/043553,05-JUN-1997 US    60/048740 PI
            JOHN ANDREW TODD,JOHN WILFRED HESS,CHARLES
            THOMAS CASKEY,ROGER
            PI   DAVID COX,
            PI   DAVID GERHOLD,HOLLY HAMMOND,PATRICIA HEY
            PC   C12N15/12,C12N15/11,C12Q1/68,C07K14/705,C07K16/28,A61K38/17,
            PC   A61K39/395,
            PC   A61K48/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Chlamydia sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:35827"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        914 CGACTGTCCCCACCT 928
              | ||||||||||||||
Db         20 CAACTGTCCCCACCT 6


RESULT 3891
BD128192
LOCUS       BD128192                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD128192
VERSION     BD128192.1  GI:23223137
KEYWORDS    JP 2002017375-A/3623.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
            Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
            Koga,H.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002017375-A 3623 22-JAN-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2002017375-A/3623
            PD   22-JAN-2002
            PF   07-JUL-2000 JP 2000253172
            PI   TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
            PI   ISHII,
            PI   YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
            SHINICHI KOJIMA,
            PI   TETSUJI OTSUKI,HISASHI KOGA
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Description of Artificial Sequence: an artificially  CC
            synthesized primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1482 ACAAAACCCTGGAGA 1496
              ||||||||||||| |
Db          5 ACAAAACCCTGGAAA 19


RESULT 3892
BD134696/c
LOCUS       BD134696                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Human malignant melanoma antigen.
ACCESSION   BD134696
VERSION     BD134696.1  GI:23229641
KEYWORDS    JP 2002065276-A/13.
SOURCE      synthetic construct
```

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RESULT 3885
AX697401/c
LOCUS       AX697401                  20 bp    DNA     linear   PAT 02-APR-2003
DEFINITION  Sequence 469 from Patent WO0078961.
ACCESSION   AX697401
VERSION     AX697401.1  GI:29498532
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
            Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
            Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
            Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0078961-A 469 28-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide probe"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              ||||||| |||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3886
AX753521
LOCUS       AX753521                  20 bp    DNA     linear   PAT 23-JUN-2003
DEFINITION  Sequence 26 from Patent WO03035684.
ACCESSION   AX753521
VERSION     AX753521.1  GI:32166267
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schneider,A., Maurer,M., Kuschinsky,W., Gruenewald,S. and
            Gassler,N.
  TITLE     Ee3-protein family and corresponding dna sequences
  JOURNAL   Patent: WO 03035684-A 26 01-MAY-2003;
            BASF-LYNX Bioscience AG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Vorwarts-Primer zur Identifizierung von ee3_1_m (S.
                     105 der Beschreibung) und der Messung von Ratten ee3_1 (S.
                     125 der Beschreibung)"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        2678 GTGTGGGTGAAATGG 2692
               ||||||| |||||||
Db           2 GTGTGGGAGAAATGG 16


RESULT 3887
AX753625
LOCUS       AX753625                  20 bp    DNA     linear   PAT 23-JUN-2003
DEFINITION  Sequence 130 from Patent WO03035684.
ACCESSION   AX753625
VERSION     AX753625.1  GI:32166346
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schneider,A., Maurer,M., Kuschinsky,W., Gruenewald,S. and
            Gassler,N.
  TITLE     Ee3-protein family and corresponding dna sequences
  JOURNAL   Patent: WO 03035684-A 130 01-MAY-2003;
            BASF-LYNX Bioscience AG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Vorwarts-Primer f. Ratten ee3_1 (S. 125, Z. 28 der
                     Beschreibung) /Primer ee3_plus (S. 140, Z. 2)"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        2678 GTGTGGGTGAAATGG 2692
               ||||||| |||||||
Db           2 GTGTGGGAGAAATGG 16


RESULT 3888
BD023379/c
LOCUS       BD023379                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for detecting abnormality in chromosome.
ACCESSION   BD023379
VERSION     BD023379.1  GI:22564602
KEYWORDS    JP 2001505428-A/124.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Parisgard,N. and Hokurando,P.
  TITLE     Method for detecting abnormality in chromosome
  JOURNAL   Patent: JP 2001505428-A 124 24-APR-2001;
            NEILLS PARISGARD
COMMENT     PN   JP 2001505428-A/124
            PD   24-APR-2001
            PF   08-DEC-1997 JP 1998525090
            PI   NEILLS PARISGARD,PATER HOKURANDO
            PC   C12N15/09,C12Q1/68,G01N33/50,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   /desc = 'DNA (synthetic)'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         681 ACCAGATGGACGAGG 695
               ||||| |||||||||
Db          16 ACCAGCTGGACGAGG 2


RESULT 3889
BD088505/c
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  AUTHORS   Cowsert,L.M., Wyatt,J., Freier,S.M., Monia,B.P., Butler,M.M. and
            Mckay,R.
  TITLE     Antisense modulation of ptp1b expression
  JOURNAL   Patent: WO 0210378-A 210 07-FEB-2002;
            ISIS PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense Oligonucleotide"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        479 GGCCGCCAGAGCCAG 493
              ||||||||||||| ||
Db         18 GGCCGCCAGAGCGAG 4


RESULT 3881
AX462751/c
LOCUS       AX462751                 20 bp    DNA     linear   PAT 15-JUL-2002
DEFINITION  Sequence 495 from Patent EP1217079.
ACCESSION   AX462751
VERSION     AX462751.1  GI:21885977
KEYWORDS    .
SOURCE      Aegilops tauschii
  ORGANISM  Aegilops tauschii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Aegilops.
REFERENCE   1
  AUTHORS   Bernard,M., Sourdille,P. and Guyomarch,H.
  TITLE     Microsatellite markers from Triticum tauschii
  JOURNAL   Patent: EP 1217079-A 495 26-JUN-2002;
            INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Aegilops tauschii"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:37682"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2242 AAGGTACTGAAGCTT 2256
              |||| ||||||||||
Db         15 AAGGCACTGAAGCTT 1


RESULT 3882
AX477137
LOCUS       AX477137                 20 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 228 from Patent WO0220848.
ACCESSION   AX477137
VERSION     AX477137.1  GI:22216390
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,
            Lusis,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
  TITLE     Gene and sequence variation associated with cancer
  JOURNAL   Patent: WO 0220848-A 228 14-MAR-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Primer"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2427 TGGTGCACTTCTTAC 2441
              ||||||||||||| |
Db          1 TGGTGCACTTCTTCC 15


RESULT 3883
AX526513
LOCUS       AX526513                 20 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 228 from Patent WO0220847.
ACCESSION   AX526513
VERSION     AX526513.1  GI:25171320
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,
            Lusis,A.J., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.
  TITLE     Gene and sequence variation associated with lipid disorder
  JOURNAL   Patent: WO 0220847-A 228 14-MAR-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Primer"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2427 TGGTGCACTTCTTAC 2441
              ||||||||||||| |
Db          1 TGGTGCACTTCTTCC 15


RESULT 3884
AX613548
LOCUS       AX613548                 20 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 4573 from Patent WO02072882.
ACCESSION   AX613548
VERSION     AX613548.1  GI:28408977
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 4573 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1614 GGAAGAGTTTGTTAC 1628
              ||||||||||||| |
Db          1 GGAAGAGTTTGTTTC 15
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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1912 CAACAATACCTTTTT 1926
              ||||||||||||| ||
Db          2 CAACAATACCTTCTT 16


RESULT 3876
AX149191
LOCUS       AX149191                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 393 from Patent WO0136625.
ACCESSION   AX149191
VERSION     AX149191.1  GI:14347715
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 393 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1912 CAACAATACCTTTTT 1926
              ||||||||||||| ||
Db          2 CAACAATACCTTCTT 16


RESULT 3877
AX201485/c
LOCUS       AX201485                  20 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 164 from Patent WO0153486.
ACCESSION   AX201485
VERSION     AX201485.1  GI:15391311
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
            Stone,D.M., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of tumour
  JOURNAL   Patent: WO 0153486-A 164 26-JUL-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide Probe."

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        203 GAGGACTGCGAGGAT 217
              |||||| ||||||||
Db         19 GAGGACGGCGAGGAT 5


RESULT 3878
AX338230/c
LOCUS       AX338230                  20 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 12 from Patent WO0181576.
ACCESSION   AX338230
VERSION     AX338230.1  GI:18128765
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lind,P. and Berthold,M.
  TITLE     G protein-coupled receptor con-218
  JOURNAL   Patent: WO 0181576-A 12 01-NOV-2001;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2674 GTGTGTGTGGGTGAA 2688
              | ||||||||||||||
Db         15 GGGTGTGTGGGTGAA 1


RESULT 3879
AX418735
LOCUS       AX418735                  20 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 130 from Patent WO0210378.
ACCESSION   AX418735
VERSION     AX418735.1  GI:21523598
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Cowsert,L.M., Wyatt,J., Freier,S.M., Monia,B.P., Butler,M.M. and
            Mckay,R.
  TITLE     Antisense modulation of ptp1b expression
  JOURNAL   Patent: WO 0210378-A 130 07-FEB-2002;
            ISIS PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense Oligonucleotide"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2003 CTTCTTCAGAGATCA 2017
              | ||||||||||||||
Db          6 CATCTTCAGAGATCA 20


RESULT 3880
AX418815/c
LOCUS       AX418815                  20 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 210 from Patent WO0210378.
ACCESSION   AX418815
VERSION     AX418815.1  GI:21523678
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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RESULT 3871
AR373818/c
LOCUS       AR373818                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 210 from patent US 6602857.
ACCESSION   AR373818
VERSION     AR373818.1  GI:40076229
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M., Wyatt,J., Monia,B.P., Butler,M.M. and McKay,R.
  TITLE     Antisense modulation of PTP1B expression
  JOURNAL   Patent: US 6602857-A 210 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        479 GGCCGCCAGAGCCAG 493
              ||||||||||||| ||
Db         18 GGCCGCCAGAGCGAG 4


RESULT 3872
AR432278
LOCUS       AR432278                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 78 from patent US 6653133.
ACCESSION   AR432278
VERSION     AR432278.1  GI:40194551
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M., Marcusson,E.G. and Wyatt,J.
  TITLE     Antisense modulation of Fas mediated signaling
  JOURNAL   Patent: US 6653133-A 78 25-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2441 CGACTTTTTTGAGAC 2455
              || ||||||||||||
Db          1 CGGCTTTTTTGAGAC 15


RESULT 3873
AX099164
LOCUS       AX099164                  20 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 13 from Patent WO0120337.
ACCESSION   AX099164
VERSION     AX099164.1  GI:13538364
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Thakker,N., Dixon,M. and James,J.
  TITLE     Genetic testing for periodontitis based on cathepsin c
  JOURNAL   Patent: WO 0120337-A 13 22-MAR-2001;
            The Victoria University of Manchester (GB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .20
                     /note="Primer for PCR"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1414 CAAAGAAGCCCTGAT 1428
              ||| ||||||||||
Db          1 CAATGAAGCCCTGAT 15


RESULT 3874
AX148814
LOCUS       AX148814                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 16 from Patent WO0136625.
ACCESSION   AX148814
VERSION     AX148814.1  GI:14347338
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 16 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              |||||| ||||||||
Db          5 GAAAAAGAAAAAAAA 19


RESULT 3875
AX149017
LOCUS       AX149017                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 219 from Patent WO0136625.
ACCESSION   AX149017
VERSION     AX149017.1  GI:14347541
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 219 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
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Db          5 CAGAAGGACCTGGTG 19


RESULT 3866
AR313616/c
LOCUS       AR313616                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4153 from patent US 6559294.
ACCESSION   AR313616
VERSION     AR313616.1  GI:31707042
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 4153 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1706 AGCTATCTCCTAACT 1720
              ||||||||||| |||
Db         18 AGCTATCTCCTTACT 4


RESULT 3867
AR314827
LOCUS       AR314827                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5364 from patent US 6559294.
ACCESSION   AR314827
VERSION     AR314827.1  GI:31708253
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 5364 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2626 TTTGTCTCGTTCCTG 2640
              |||| ||||||||||
Db          1 TTTGGCTCGTTCCTG 15


RESULT 3868
AR315171/c
LOCUS       AR315171                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5708 from patent US 6559294.
ACCESSION   AR315171
VERSION     AR315171.1  GI:31708597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 5708 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        275 CAGCACCTCTACAGC 289
              ||||| |||||||||
Db         15 CAGCAGCTCTACAGC 1


RESULT 3869
AR315937/c
LOCUS       AR315937                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6474 from patent US 6559294.
ACCESSION   AR315937
VERSION     AR315937.1  GI:31709363
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 6474 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        744 TTCGCAAAGGTCCCA 758
              ||||||||| |||||
Db         20 TTCGCAAAGATCCCA 6


RESULT 3870
AR373738
LOCUS       AR373738                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 130 from patent US 6602857.
ACCESSION   AR373738
VERSION     AR373738.1  GI:40076149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M., Wyatt,J., Monia,B.P., Butler,M.M. and McKay,R.
  TITLE     Antisense modulation of PTP1B expression
  JOURNAL   Patent: US 6602857-A 130 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2003 CTTCTTCAGAGATCA 2017
              | ||||||||||||||
Db          6 CATCTTCAGAGATCA 20
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```
Db         20 CAACTGTCCCCACCT 6


RESULT 3861
AR309314/c
LOCUS       AR309314                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 164 from patent US 6555654.
ACCESSION   AR309314
VERSION     AR309314.1  GI:31701319
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
            Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
            Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
  TITLE     LDL-receptor
  JOURNAL   Patent: US 6555654-A 164 29-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        914 CGACTGTCCCCACCT 928
              | ||||||||||||||
Db         20 CAACTGTCCCCACCT 6


RESULT 3862
AR311840
LOCUS       AR311840                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2377 from patent US 6559294.
ACCESSION   AR311840
VERSION     AR311840.1  GI:31705266
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2377 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2361 TTTAAGAAACAGTGC 2375
              |||||||||| ||||
Db          6 TTTAAGAAACGGTGC 20


RESULT 3863
AR312330/c
LOCUS       AR312330                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2867 from patent US 6559294.
ACCESSION   AR312330
VERSION     AR312330.1  GI:31705756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2867 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2626 TTTGTCTCGTTCCTG 2640
              |||| ||||||||||
Db         15 TTTGGCTCGTTCCTG 1


RESULT 3864
AR312943
LOCUS       AR312943                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3480 from patent US 6559294.
ACCESSION   AR312943
VERSION     AR312943.1  GI:31706369
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 3480 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1548 AGGGAAGGAACAGGA 1562
              ||||||||||||| |
Db          6 AGGGAAGGAACAGAA 20


RESULT 3865
AR312983
LOCUS       AR312983                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3520 from patent US 6559294.
ACCESSION   AR312983
VERSION     AR312983.1  GI:31706409
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 3520 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        794 CAGAAGGAGCTGGTG 808
              |||||||| ||||||
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```
Qy         51 GCGGCGGGGGCGGCG 65
              ||||||||||| |||
Db         19 GCGGCGGGGGCAGCG 5


RESULT 3856
I78382/c
LOCUS       I78382                   20 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 180 from patent US 5693535.
ACCESSION   I78382
VERSION     I78382.1  GI:3014536
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and
            Thompson,J.D.
  TITLE     HIV targeted ribozymes
  JOURNAL   Patent: US 5693535-A 180 02-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GAAAATGGAGAAACA 1509
              ||||||||| |||||
Db         19 GAAAATGGATAAACA 5


RESULT 3857
AR220978/c
LOCUS       AR220978                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 31 from patent US 6426188.
ACCESSION   AR220978
VERSION     AR220978.1  GI:23327863
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of phosphorylase kinase alpha 1 expression
  JOURNAL   Patent: US 6426188-A 31 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        725 CTGCACGATCAGACA 739
              ||||| |||||||||
Db         15 CTGCATGATCAGACA 1


RESULT 3858
AR229050
LOCUS       AR229050                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 60 from patent US 6448081.
ACCESSION   AR229050
VERSION     AR229050.1  GI:27268192
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F. and Freier,S.M.
  TITLE     Antisense modulation of interleukin 12 p40 subunit expression
  JOURNAL   Patent: US 6448081-A 60 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1423 CCTGATTGTCATAGA 1437
              ||||||||||||| |
Db          6 CCTGATTGTCATAAA 20


RESULT 3859
AR234664/c
LOCUS       AR234664                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 105 from patent US 6458591.
ACCESSION   AR234664
VERSION     AR234664.1  GI:27277371
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of phosphorylase kinase Alpha 2 expression
  JOURNAL   Patent: US 6458591-A 105 01-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1146 GTAAACCAGTGGCAG 1160
              |||| ||||||||||
Db         15 GTAACCCAGTGGCAG 1


RESULT 3860
AR305210/c
LOCUS       AR305210                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 164 from patent US 6545137.
ACCESSION   AR305210
VERSION     AR305210.1  GI:31694520
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
            Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
            Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
  TITLE     Receptor
  JOURNAL   Patent: US 6545137-A 164 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        914 CGACTGTCCCCACCT 928
              | ||||||||||||||
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            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        848 CCTGGAAGATTGTCG 862
              ||||||||||||| |
Db          6 CCTGGAAGATTGTGG 20


RESULT 3852
E35764
LOCUS       E35764                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Plant-origin asparagine residue-specific endoprotease cDNA and
            gene.
ACCESSION   E35764
VERSION     E35764.1  GI:18624599
KEYWORDS    JP 2000139472-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Arahira,M. and Fukasawa,N.
  TITLE     Plant-origin asparagine residue-specific endoprotease cDNA and gene
  JOURNAL   Patent: JP 2000139472-A 3 23-MAY-2000;
            NATL FOOD RES INST
COMMENT     OS   Artificial Sequence
            PN   JP 2000139472-A/3
            PD   23-MAY-2000
            PF   04-NOV-1998 JP 1998327537
            PR
            PI   MASAOMI ARAHIRA,NORIFUSA FUKASAWA
            PC   C12N15/09,C12N9/50//(C12N15/09,C12R1:91),C12N15/00,(C12N15/00,
            PC   C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   63.2%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1135 CGAATTTCCTAGTAAACCA 1153
              | ||:||: |:|| ||:||
Db          2 CNAAYTTYATHGTNAAYCA 20


RESULT 3853
I51693
LOCUS       I51693                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 14 from patent US 5645985.
ACCESSION   I51693
VERSION     I51693.1  GI:2472894
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Froehler,B., Wagner,R., Matteucci,M., Jones,R.J., Gutierrez,A.J.
            and Pudlo,J.
  TITLE     Enhanced triple-helix and double-helix formation with oligomers
            containing modified pyrimidines
  JOURNAL   Patent: US 5645985-A 14 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||| ||  |||||| ||
Db          2 TTTTNTTNATTTTTTNTT 19


RESULT 3854
I51693/c
LOCUS       I51693                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 14 from patent US 5645985.
ACCESSION   I51693
VERSION     I51693.1  GI:2472894
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Froehler,B., Wagner,R., Matteucci,M., Jones,R.J., Gutierrez,A.J.
            and Pudlo,J.
  TITLE     Enhanced triple-helix and double-helix formation with oligomers
            containing modified pyrimidines
  JOURNAL   Patent: US 5645985-A 14 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              || ||||||  || ||||
Db         19 AANAAAAAAATNAANAAAA 2


RESULT 3855
I77271/c
LOCUS       I77271                    20 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 35 from patent US 5693518.
ACCESSION   I77271
VERSION     I77271.1  GI:3013425
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kofod,L.Venke., Kauppinen,M.Sakari., Christgau,S.,
            Heldt-Hansen,H.Peter., Dalb.o slashed.ge,H., Andersen,L.Nonboe.,
            Si,J.Qi., Jacobsen,T.Sejersgangrd., Munk,N. and Mullertz,A.
  TITLE     Enzymes with xylanase activity from Aspergillus aculeatus
  JOURNAL   Patent: US 5693518-A 35 02-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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COMMENT     OS   Artificial Sequence
            PN   JP 2002540812-A/74
            PD   03-DEC-2002
            PF   10-APR-2000 JP 2000610483
            PR   12-APR-1999 US    09/290640
            PI   NICHOLAS M DEAN,ERIC G MARCUSSON
            PC   C12N15/09,A61K31/7088,A61K31/7115,A61K31/712,A61K31/7125, PC
           A61K48/00,
            PC   A61P1/16,A61P29/00,A61P35/00,A61P37/00,A61P43/00//C12N5/06, PC
             C12N15/00,
            PC   C12N5/00
            CC   Synthetic Sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2441 CGACTTTTTTGAGAC 2455
              || |||||||||||||
Db          1 CGGCTTTTTTGAGAC 15


RESULT 3849
BD272700/c
LOCUS       BD272700                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide modulation of STAT3 expression.
ACCESSION   BD272700
VERSION     BD272700.1  GI:33082468
KEYWORDS    JP 2002541784-A/100.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Karras,J.G.
  TITLE     Antisense oligonucleotide modulation of STAT3 expression
  JOURNAL   Patent: JP 2002541784-A 100 10-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002541784-A/100
            PD   10-DEC-2002
            PF   06-APR-2000 JP 2000611544
            PR   08-APR-1999 US    09/288461
            PI   JAMES G KARRAS
            PC   C12N15/09,A61K31/711,A61K48/00,A61P29/00,A61P29/00,A61P35/00,
            PC   A61P37/02,
            PC   A61P43/00,C12N5/06,C12Q1/02,C12N15/00,C12N5/00 CC   Antisense
           oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2673 AGTGTGTGTGGGTGA 2687
              |||| ||||||||||
Db         16 AGTGAGTGTGGGTGA 2


RESULT 3850
E11827/c
LOCUS       E11827                   20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Primer.
ACCESSION   E11827
VERSION     E11827.1  GI:22025449
KEYWORDS    JP 1996205898-A/12.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Matsumoto,H., Iwasaki,T., Shimazu,M., Osumi,K. and Yamamori,T.
  TITLE     DNA FRAGMENT CONTAINING GENE PARTICIPATING IN SEX-LINKED
            AGAMMAGLOBULINEMIA AND METHOD FOR ANALYZING THE SAME
  JOURNAL   Patent: JP 1996205898-A 12 13-AUG-1996;
            MITSUBISHI KAGAKU B C L:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996205898-A/12
            PD   13-AUG-1996
            PF   01-FEB-1995 JP 1995034715
            PI   MATSUMOTO HIROSHI, IWASAKI TATSU, SHIMAZU MITSUNOBU, PI
            OSUMI KAZUOKI,
            PI   YAMAMORI TOSHIHARU
            PC   C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1492 GGAGAAAATGGAGAA 1506
              | |||||||||||||
Db         15 GAAGAAAATGGAGAA 1


RESULT 3851
E11838
LOCUS       E11838                   20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Primer.
ACCESSION   E11838
VERSION     E11838.1  GI:22025460
KEYWORDS    JP 1996205898-A/23.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Matsumoto,H., Iwasaki,T., Shimazu,M., Osumi,K. and Yamamori,T.
  TITLE     DNA FRAGMENT CONTAINING GENE PARTICIPATING IN SEX-LINKED
            AGAMMAGLOBULINEMIA AND METHOD FOR ANALYZING THE SAME
  JOURNAL   Patent: JP 1996205898-A 23 13-AUG-1996;
            MITSUBISHI KAGAKU B C L:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996205898-A/23
            PD   13-AUG-1996
            PF   01-FEB-1995 JP 1995034715
            PI   MATSUMOTO HIROSHI, IWASAKI TATSU, SHIMAZU MITSUNOBU, PI
            OSUMI KAZUOKI,
            PI   YAMAMORI TOSHIHARU
            PC   C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              ||||||  ||||||||
Db          6 TTTTTTCTTTTTTAA 20


RESULT 3845
AR163732
LOCUS       AR163732                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 19 from patent US 6271029.
ACCESSION   AR163732
VERSION     AR163732.1  GI:16234427
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Cowsert,L.M.
  TITLE     Antisense inhibition of cytohesin-2 expression
  JOURNAL   Patent: US 6271029-A 19 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1199 ATGGCAGCTAGGAAG 1213
              |||||  |||||||||
Db          2 ATGGCGGCTAGGAAG 16


RESULT 3846
BD228264/c
LOCUS       BD228264                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha).
ACCESSION   BD228264
VERSION     BD228264.1  GI:33038034
KEYWORDS    JP 2002526125-A/467.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,F.C., Butler,M.M. and Jr,W.J.S.
  TITLE     Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha)
  JOURNAL   Patent: JP 2002526125-A 467 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526125-A/467
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574737
            PR   05-OCT-1998 US    09/166186,18-MAY-1999 US    09/313932 PI
            BRENDA F BAKER,FRANK C BENNETT,MADELINE M BUTLER,WILLIAM J  PI
            SHANAHAN JR
            PC   C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/
            PC   00,A61P1/16,
            PC   A61P1/18,A61P3/10,A61P17/00,A61P17/04,A61P29/00,A61P31/00, PC
             C07H21/02,
            PC   C07H21/04,C12N15/00
            CC   Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2098 TTCAAACGGGGGCCT 2112
              |||||||  |||||||
Db         16 TTCAAACTGGGGCCT 2


RESULT 3847
BD243056/c
LOCUS       BD243056                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of bcl-x expression.
ACCESSION   BD243056
VERSION     BD243056.1  GI:33052826
KEYWORDS    JP 2002526093-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,F.C., Dean,N.M., Monia,B.P., Nickoloff,B.J. and Zhang,Q.
  TITLE     Antisense modulation of bcl-x expression
  JOURNAL   Patent: JP 2002526093-A 15 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526093-A/15
            PD   20-AUG-2002
            PF   28-SEP-1999 JP 2000574543
            PR   07-OCT-1998 US    09/167921,26-MAR-1999 US    09/277020 PR
            02-JUN-1999 US    09/323743
            PI   FRANK C BENNETT,NICHOLAS M DEAN,BRETT P MONIA,BRIAN J  PI
            NICKOLOFF,
            PI   QINGQING ZHANG
            PC   C12N15/09,A61K9/10,A61K31/337,A61K31/711,A61K31/7115,A61K31/
            PC   712,
            PC   A61K31/7125,A61K33/24,A61K48/00,A61P35/00,A61P43/00,C07H21/04,
            PC   C12N5/10//
            PC   (C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC
             Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2104 CGGGGGCCTTCTGGT 2118
              |||||  |||||||||
Db         20 CGGGGTCCTTCTGGT 6


RESULT 3848
BD249359
LOCUS       BD249359                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of FAS mediated signaling.
ACCESSION   BD249359
VERSION     BD249359.1  GI:33059129
KEYWORDS    JP 2002540812-A/74.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of FAS mediated signaling
  JOURNAL   Patent: JP 2002540812-A 74 03-DEC-2002;
            ISIS PHARMACEUTICALS INC
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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2441 CGACTTTTTTGAGAC 2455
              || ||||||||||||
Db          1 CGGCTTTTTTGAGAC 15


RESULT 3840
AR149869/c
LOCUS       AR149869                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 35 from patent US 6228630.
ACCESSION   AR149869
VERSION     AR149869.1  GI:15114460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kofod,L.Venke., Kauppinen,M.Sakari., Christgau,S.,
            Heldt-Hansen,H.Peter., Dalb.o slashed.ge,H., Andersen,L.Nonboe.,
            Si,J.Qi., Jacobsen,T.Sejersgangard., Munk,N. and Mullertz,A.
  TITLE     Enzymes with xylanase activity from aspergillus aculeatus
  JOURNAL   Patent: US 6228630-A 35 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCG 65
              ||||||||||| |||
Db         19 GCGGCGGGGGCAGCG 5


RESULT 3841
AR150391/c
LOCUS       AR150391                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 467 from patent US 6228642.
ACCESSION   AR150391
VERSION     AR150391.1  GI:15114982
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-(.alpha.) (TNF-.alpha.) expression
  JOURNAL   Patent: US 6228642-A 467 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2098 TTCAAACGGGGGCCT 2112
              ||||||| |||||||
Db         16 TTCAAACTGGGGCCT 2


RESULT 3842
AR153754
LOCUS       AR153754                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 15 from patent US 6235887.
ACCESSION   AR153754
VERSION     AR153754.1  GI:15121286
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Froehler,B. and Jones,R.J.
  TITLE     Enhanced triple-helix and double-helix formation directed by
            oligonucleotides containing modified pyrimidines
  JOURNAL   Patent: US 6235887-A 15 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              |||| ||  |||||| ||
Db          2 TTTTNTTNATTTTTTNTT 19


RESULT 3843
AR153754/c
LOCUS       AR153754                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 15 from patent US 6235887.
ACCESSION   AR153754
VERSION     AR153754.1  GI:15121286
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Froehler,B. and Jones,R.J.
  TITLE     Enhanced triple-helix and double-helix formation directed by
            oligonucleotides containing modified pyrimidines
  JOURNAL   Patent: US 6235887-A 15 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              || |||||| || ||||
Db         19 AANAAAAAATNAANAAAA 2


RESULT 3844
AR158931
LOCUS       AR158931                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 553 from patent US 6251588.
ACCESSION   AR158931
VERSION     AR158931.1  GI:16221341
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 553 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
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  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GAAAATGGAGAAACA 1509
              ||||||||| |||||
Db         19 GAAAATGGATAAACA 5


RESULT 3835
AR121079/c
LOCUS       AR121079                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 100 from patent US 6159694.
ACCESSION   AR121079
VERSION     AR121079.1  GI:14104655
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Karras,J.G.
  TITLE     Antisense modulation of stat3 expression
  JOURNAL   Patent: US 6159694-A 100 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2673 AGTGTGTGTGGGTGA 2687
              |||| ||||||||||
Db         16 AGTGAGTGTGGGTGA 2


RESULT 3836
AR124966/c
LOCUS       AR124966                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 16 from patent US 6172216.
ACCESSION   AR124966
VERSION     AR124966.1  GI:14110327
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank., Dean,N.M., Monia,B.P., Nickoloff,B.J. and
            Zhang,Q.
  TITLE     Antisense modulation of BCL-X expression
  JOURNAL   Patent: US 6172216-A 16 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2104 CGGGGGCCTTCTGGT 2118
              \\\\\ \\\\\\\\\
Db         20 CGGGGTCCTTCTGGT 6


RESULT 3837
AR130110
LOCUS       AR130110                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 13 from patent US 6187587.
ACCESSION   AR130110
VERSION     AR130110.1  GI:14118007
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Popoff,I., Brown-Driver,V.L. and Cowsert,L.M.
  TITLE     Antisense inhibition of e2f transcription factor 1 expression
  JOURNAL   Patent: US 6187587-A 13 13-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              ||||| |||||||||
Db          3 GGCGGCGGCGGCGGC 17


RESULT 3838
AR137875/c
LOCUS       AR137875                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 35 from patent US 6197564.
ACCESSION   AR137875
VERSION     AR137875.1  GI:14479384
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kofod,L.Venke., Kauppinen,M.Sakari., Christgau,S.,
            Heldt-Hansen,H.Peter., Dalb.o slashed.ge,H., Andersen,L.Nonboe.,
            Si,J.Qi., Jacobsen,T.Sejersgangrd., Munk,N. and Mullertz,A.
  TITLE     Enzymes with xylanase activity from Aspergillus aculeatus
  JOURNAL   Patent: US 6197564-A 35 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCG 65
              |||||||||| |||
Db         19 GCGGCGGGGGCAGCG 5


RESULT 3839
AR143184
LOCUS       AR143184                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 78 from patent US 6204055.
ACCESSION   AR143184
VERSION     AR143184.1  GI:15104470
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense inhibition of Fas mediated signaling
  JOURNAL   Patent: US 6204055-A 78 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
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                    /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1495 GAAAATGGAGAAACA 1509
              ||||||||| |||||
Db         19 GAAAATGGATAAACA 5


RESULT 3830
AR100054/c
LOCUS       AR100054                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 11 from patent US 6080546.
ACCESSION   AR100054
VERSION     AR100054.1  GI:12810502
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Gaarde,W. and Cowsert,L.M.
  TITLE     Antisense modulation of MEKK5 expression
  JOURNAL   Patent: US 6080546-A 11 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        264 CCTCCGCCGGGCAGC 278
              || |||||||||||
Db         16 CCGCCGCCGGGCAGC 2


RESULT 3831
AR100185/c
LOCUS       AR100185                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 35 from patent US 6080567.
ACCESSION   AR100185
VERSION     AR100185.1  GI:12810633
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kofod,L.Venke., Kauppinen,M.Sakari., Christgau,S.,
            Heldt-Hansen,H.Peter., Dalb.o slashed.ge,H., Andersen,L.Nonboe.,
            Si,J.Qi., Jacobsen,T.Sejersgangrd., Munk,N. and Mullertz,A.
  TITLE     Enzymes with xylanase activity from Aspergillus aculeatus
  JOURNAL   Patent: US 6080567-A 35 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCG 65
              |||||||||| |||
Db         19 GCGGCGGGGGCAGCG 5


RESULT 3832
AR107217
LOCUS       AR107217                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 9 from patent US 6107471.
ACCESSION   AR107217
VERSION     AR107217.1  GI:12821747
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Arahira,M. and Fukazawa,C.
  TITLE     Plant-derived, asparagine residue-specific endoprotease cDNA and a
            gene
  JOURNAL   Patent: US 6107471-A 9 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   63.2%;  Pred. No. 3.7e+03;
  Matches   12;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1135 CGAATTTCCTAGTAAACCA 1153
              | ||:||: |:|| ||:||
Db          2 CNAAYTTYATHGTNAAYCA 20


RESULT 3833
AR112276/c
LOCUS       AR112276                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 44 from patent US 6130042.
ACCESSION   AR112276
VERSION     AR112276.1  GI:14092176
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Diehl,S.R., Schenkein,H.A. and Wang,Y.-F.
  TITLE     Compositions and methods for diagnosing periodontal disease
  JOURNAL   Patent: US 6130042-A 44 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2448 TTTGAGACATGGGAT 2462
              ||||| |||||||||
Db         19 TTTGACACATGGGAT 5


RESULT 3834
AR120878/c
LOCUS       AR120878                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 180 from patent US 6159692.
ACCESSION   AR120878
VERSION     AR120878.1  GI:14104454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and
            Thompson,J.D.
  TITLE     Method and reagent for inhibiting human immunodeficiency virus
            replication
  JOURNAL   Patent: US 6159692-A 180 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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                    Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAA 2797
              || ||||||||||||
Db         15 TTAAAAAAAAAAAAA 1


RESULT 3825
A91597/c
LOCUS       A91597                    20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 124 from Patent WO9824928.
ACCESSION   A91597
VERSION     A91597.1  GI:6740552
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Pallisgaard,N. and Hokland,P.
  TITLE     DETECTION OF CHROMOSOMAL ABNORMALITIES
  JOURNAL   Patent: WO 9824928-A 124 11-JUN-1998;
            PALLISGAARD NIELS (DK); HOKLAND PETER (DK)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        681 ACCAGATGGACGAGG 695
              ||||| |||||||||
Db         16 ACCAGCTGGACGAGG 2


RESULT 3826
AR051133
LOCUS       AR051133                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5830653.
ACCESSION   AR051133
VERSION     AR051133.1  GI:5974497
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Froehler,B., Wagner,R., Matteucci,M., Jones,R.J., Gutierrez,A.J.
            and Pudlo,J.
  TITLE     Methods of using oligomers containing modified pyrimidines
  JOURNAL   Patent: US 5830653-A 14 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||| ||  |||||| ||
Db          2 TTTTNTTNATTTTTTNTT 19


RESULT 3827
AR051133/c
LOCUS       AR051133                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5830653.
ACCESSION   AR051133
VERSION     AR051133.1  GI:5974497
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Froehler,B., Wagner,R., Matteucci,M., Jones,R.J., Gutierrez,A.J.
            and Pudlo,J.
  TITLE     Methods of using oligomers containing modified pyrimidines
  JOURNAL   Patent: US 5830653-A 14 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              || ||||||  || ||||
Db         19 AANAAAAAATNAANAAAA 2


RESULT 3828
AR058747/c
LOCUS       AR058747                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 324 from patent US 5837832.
ACCESSION   AR058747
VERSION     AR058747.1  GI:5984324
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
            Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
  TITLE     Arrays of nucleic acid probes on biological chips
  JOURNAL   Patent: US 5837832-A 324 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2205 TTCAAATGGGAGACT 2219
              || ||||||||||||
Db         18 TTAAAATGGGAGACT 4


RESULT 3829
AR082336/c
LOCUS       AR082336                  20 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 180 from patent US 5972704.
ACCESSION   AR082336
VERSION     AR082336.1  GI:10009062
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and
            Thompson,J.D.
  TITLE     HIV nef targeted ribozymes
  JOURNAL   Patent: US 5972704-A 180 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
```

```
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Ikawa,Y., Ikawa,S. and Tatewaki,M.
  TITLE     Chimera gene and chimera protein of p53 family
  JOURNAL   Patent: JP 2000354488-A 9 26-DEC-2000;
            YOJI IGAWA,OTSUKA PHARMACEUTICAL CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000354488-A/9
            PD   26-DEC-2000
            PF   09-APR-1999 JP 1999139034
            PR
            PI   YOJI IKAWA,SHUNTARO IKAWA,MASUO TATEWAKI
            PC   C12N15/09,C07K14/82,C07K19/00,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1660 TCTGCATCACCCGCC 1674
              ||| ||||||||||
Db         18 TCTCCATCACCCGCC 4


RESULT 3822
BD222586
LOCUS       BD222586                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom.
ACCESSION   BD222586
VERSION     BD222586.1  GI:33032356
KEYWORDS    JP 2002522447-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom
  JOURNAL   Patent: JP 2002522447-A 4 23-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002522447-A/4
            PD   23-JUL-2002
            PF   09-AUG-1999 JP 2000563675
            PR   07-AUG-1998 US    09/130973
            PI   MUTHIAH MANOHARAN,PHILIP DAN COOK,THAZHA P PRAKASH,ANDREW M
            PI   KAWASAKI
            PC   C07H19/167,C07H19/067,C07H19/10,C07H19/20,C07H21/02,C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence: antisense sequence FH
            Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3823
BD222586/c
LOCUS       BD222586                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom.
ACCESSION   BD222586
VERSION     BD222586.1  GI:33032356
KEYWORDS    JP 2002522447-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom
  JOURNAL   Patent: JP 2002522447-A 4 23-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002522447-A/4
            PD   23-JUL-2002
            PF   09-AUG-1999 JP 2000563675
            PR   07-AUG-1998 US    09/130973
            PI   MUTHIAH MANOHARAN,PHILIP DAN COOK,THAZHA P PRAKASH,ANDREW M
            PI   KAWASAKI
            PC   C07H19/167,C07H19/067,C07H19/10,C07H19/20,C07H21/02,C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence: antisense sequence FH
            Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3824
AX048445/c
LOCUS       AX048445                  20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 44 from Patent WO0071747.
ACCESSION   AX048445
VERSION     AX048445.1  GI:12225609
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 44 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
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  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1084 AGAAGGTGAAGCTGT 1098
              ||||| |||||||||
Db         15 AGAAGCTGAAGCTGT 1


RESULT 3817
AX535777/c
LOCUS       AX535777                  19 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 16 from Patent WO02068684.
ACCESSION   AX535777
VERSION     AX535777.1  GI:25262228
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lundeberg,J., Ahmadian,A. and Nyren,P.
  TITLE     Allele-specific primer extension assay
  JOURNAL   Patent: WO 02068684-A 16 06-SEP-2002;
            Pyrosequencing AB (SE) ; DZIEGLEWSKA, Hanna Eva (GB)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        431 CCCCTGCACCAGCCG 445
              ||||||||||||| |
Db         16 CCCCTGCACCAGCAG 2


RESULT 3818
AX539268/c
LOCUS       AX539268                  19 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 55 from Patent WO02059142.
ACCESSION   AX539268
VERSION     AX539268.1  GI:25272507
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
  TITLE     Polymorphisms in the human gene for the multidrug
            resistance-associated protein 1 (mrp-1) and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 02059142-A 55 01-AUG-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        498 GAGCGGGGCTGCCCT 512
              |||| ||||||||||
Db         15 GAGCCGGGCTGCCCT 1


RESULT 3819
AX815849/c
LOCUS       AX815849                  19 bp    DNA     linear   PAT 09-DEC-2003
DEFINITION  Sequence 104 from Patent WO03066891.
ACCESSION   AX815849
VERSION     AX815849.1  GI:39646529
KEYWORDS    .
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1
  AUTHORS   Hardge,T., Schellander,K. and Wimmers,K.
  TITLE     Genetic markers for the diagnosis of the expression of inverted
            nipples in pets, breeding animals and domestic cattle
  JOURNAL   Patent: WO 03066891-A 104 14-AUG-2003;
            Foerderverein Biotechnologieforschung der deutschen
            Schweineproduktion e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Sus scrofa"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9823"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        650 GCCGAGAACCTGGGG 664
              || |||||||||||
Db         15 GCAGAGAACCTGGGG 1


RESULT 3820
AX923652/c
LOCUS       AX923652                  19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 87 from Patent WO03080638.
ACCESSION   AX923652
VERSION     AX923652.1  GI:40216668
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lacasse,E., Mcmanus,D. and Durkin,J.P.
  TITLE     Antisense iap nucleobase oligomers and uses thereof
  JOURNAL   Patent: WO 03080638-A 87 02-OCT-2003;
            Aegera Therapeutics Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="based on Homo sapiens. Each nucleobase may be part
                     of a ribonucleotide, deoxyribonucleotide, or nucleotide
                     analog~n = T or U"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2160 TTCTCCTTTTTTTTTTTT 2177
              || ||| |||||||| |
Db         19 TTNTCCNTTTTTTTTNCT 2


RESULT 3821
BD000756/c
LOCUS       BD000756                  19 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Chimera gene and chimera protein of p53 family.
ACCESSION   BD000756
VERSION     BD000756.1  GI:18623869
KEYWORDS    JP 2000354488-A/9.
```

```
ACCESSION   AR412353
VERSION     AR412353.1  GI:40167463
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleosidic compounds and oligomeric compounds
            prepared therefrom
  JOURNAL   Patent: US 6639062-A 4 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3813
AX115855/c
LOCUS       AX115855                 19 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 978 from Patent WO0129262.
ACCESSION   AX115855
VERSION     AX115855.1  GI:14032797
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 978 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        453 CAGGCAGCCAGCAGC 467
              ||||||| |||||||
Db         18 CAGGCAGTCAGCAGC 4


RESULT 3814
AX132036
LOCUS       AX132036                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3254 from Patent WO0130362.
ACCESSION   AX132036
VERSION     AX132036.1  GI:14138341
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3254 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin A1 ribozyme binding site"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1328 AACTGCTTGTCTCAT 1342
              ||||||||||||| ||
Db          3 AACTGCTTGTCTTAT 17


RESULT 3815
AX192337
LOCUS       AX192337                 19 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 31 from Patent WO0149882.
ACCESSION   AX192337
VERSION     AX192337.1  GI:15210315
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Eijk,M.J., Hogers,R.C. and Heijnen,L.
  TITLE     Method for generating oligonucleotides, in particular for the
            detection of amplified restriction fragments obtained using
            aflp_m(3)
  JOURNAL   Patent: WO 0149882-A 31 12-JUL-2001;
            Keygene N.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"
     misc_feature    3
                     /note="the deoxythymidinenucleoside at position 3 is
                     biotinylated"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2657 GGTGAGTGTGCAGTA 2671
              | |||||||||||||
Db          1 GATGAGTGTGCAGTA 15


RESULT 3816
AX412083/c
LOCUS       AX412083                 19 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 183 from Patent WO0226968.
ACCESSION   AX412083
VERSION     AX412083.1  GI:21444548
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
  TITLE     Antisense iap nucleic acids and uses thereof
  JOURNAL   Patent: WO 0226968-A 183 04-APR-2002;
            University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="based on Homo sapiens"
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RESULT 3807
AR212307
LOCUS       AR212307                19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 33 from patent US 6399754.
ACCESSION   AR212307
VERSION     AR212307.1  GI:21515846
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan.
  TITLE     Sugar modified oligonucleotides
  JOURNAL   Patent: US 6399754-A 33 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
             | ||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3808
AR212307/c
LOCUS       AR212307                19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 33 from patent US 6399754.
ACCESSION   AR212307
VERSION     AR212307.1  GI:21515846
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan.
  TITLE     Sugar modified oligonucleotides
  JOURNAL   Patent: US 6399754-A 33 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
             | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3809
AR231437
LOCUS       AR231437                19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 29 from patent US 6451991.
ACCESSION   AR231437
VERSION     AR231437.1  GI:27272520
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Martin,P., Altmann,K.-H., Cook,P.D. and Monia,B.P.
  TITLE     Sugar-modified gapped oligonucleotides
  JOURNAL   Patent: US 6451991-A 29 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
             | ||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3810
AR231437/c
LOCUS       AR231437                19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 29 from patent US 6451991.
ACCESSION   AR231437
VERSION     AR231437.1  GI:27272520
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Martin,P., Altmann,K.-H., Cook,P.D. and Monia,B.P.
  TITLE     Sugar-modified gapped oligonucleotides
  JOURNAL   Patent: US 6451991-A 29 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
             | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3811
AR412353
LOCUS       AR412353                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 4 from patent US 6639062.
ACCESSION   AR412353
VERSION     AR412353.1  GI:40167463
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleosidic compounds and oligomeric compounds
            prepared therefrom
  JOURNAL   Patent: US 6639062-A 4 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
             | ||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3812
AR412353/c
LOCUS       AR412353                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 4 from patent US 6639062.
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Qy       2785 GAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3802
AR141345/c
LOCUS       AR141345                 19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 12 from patent US 6146829.
ACCESSION   AR141345
VERSION     AR141345.1  GI:15100861
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Monia,B.P.
  TITLE     Gapped 2' modified oligonucleotides
  JOURNAL   Patent: US 6146829-A 12 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | |||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3803
AR160892/c
LOCUS       AR160892                 19 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 3 from patent US 6255112.
ACCESSION   AR160892
VERSION     AR160892.1  GI:16225906
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Thiede,M.A. and Mbalaviele,G.
  TITLE     Regulation of hematopoietic stem cell differentiation by the use of
            human mesenchymal stem cells
  JOURNAL   Patent: US 6255112-A 3 03-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1412 ATCAAAGAAGCCCTG 1426
              | |||||||||||||
Db         19 AACAAAGAAGCCCTG 5


RESULT 3804
AR179524
LOCUS       AR179524                 19 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 12 from patent US 6326199.
ACCESSION   AR179524
VERSION     AR179524.1  GI:20221079
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Monia,B.P.
  TITLE     Gapped 2' modified oligonucleotides
  JOURNAL   Patent: US 6326199-A 12 04-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3805
AR179524/c
LOCUS       AR179524                 19 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 12 from patent US 6326199.
ACCESSION   AR179524
VERSION     AR179524.1  GI:20221079
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Monia,B.P.
  TITLE     Gapped 2' modified oligonucleotides
  JOURNAL   Patent: US 6326199-A 12 04-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | |||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3806
I25705
LOCUS       I25705                   19 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 24 from patent US 5552283.
ACCESSION   I25705
VERSION     I25705.1  GI:1605575
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Diamandis,E., Dunn,J.M. and Stevens,J.K.
  TITLE     Method, reagents and kit for diagnosis and targeted screening for
            P53 mutations
  JOURNAL   Patent: US 5552283-A 24 03-SEP-1996;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        106 GCTTGGGGGCTGGGG 120
              ||| ||||||||||||
Db          1 GCTAGGGGGCTGGGG 15
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                    /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3797
AR135275
LOCUS       AR135275                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 4 from patent US 6194598.
ACCESSION   AR135275
VERSION     AR135275.1  GI:14124180
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 4 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3798
AR135275/c
LOCUS       AR135275                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 4 from patent US 6194598.
ACCESSION   AR135275
VERSION     AR135275.1  GI:14124180
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 4 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3799
AR137398
LOCUS       AR137398                  19 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 13 from patent US 6197507.
ACCESSION   AR137398
VERSION     AR137398.1  GI:14478907
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Berg,T., Tollersrud,O.Kristien. and Nilssen,O.
  TITLE     Genetic test for .alpha.-mannosidosis
  JOURNAL   Patent: US 6197507-A 13 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        560 GAGGCGGGCGCGGTG 574
              ||||||| ||||||
Db          4 GAGGCGGGAGCGGTG 18


RESULT 3800
AR137402/c
LOCUS       AR137402                  19 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 17 from patent US 6197507.
ACCESSION   AR137402
VERSION     AR137402.1  GI:14478911
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Berg,T., Tollersrud,O.Kristien. and Nilssen,O.
  TITLE     Genetic test for .alpha.-mannosidosis
  JOURNAL   Patent: US 6197507-A 17 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        560 GAGGCGGGCGCGGTG 574
              ||||||| ||||||
Db         16 GAGGCGGGAGCGGTG 2


RESULT 3801
AR141345
LOCUS       AR141345                  19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 12 from patent US 6146829.
ACCESSION   AR141345
VERSION     AR141345.1  GI:15100861
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Monia,B.P.
  TITLE     Gapped 2' modified oligonucleotides
  JOURNAL   Patent: US 6146829-A 12 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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  TITLE     2'-modified oligonucleotides
  JOURNAL   Patent: US 6005087-A 33 21-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3792
AR097400
LOCUS       AR097400                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 24 from patent US 6071726.
ACCESSION   AR097400
VERSION     AR097400.1  GI:12806130
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Diamandis,E., Dunn,J.M. and Stevens,J.K.
  TITLE     Method, reagents and kit for diagnosis and targeted screening for
            p53 mutations
  JOURNAL   Patent: US 6071726-A 24 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        106 GCTTGGGGGCTGGGG 120
              ||| ||||||||||
Db          1 GCTAGGGGGCTGGGG 15


RESULT 3793
AR111930
LOCUS       AR111930                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6127533.
ACCESSION   AR111930
VERSION     AR111930.1  GI:12828778
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 4 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3794
AR111930/c
LOCUS       AR111930                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6127533.
ACCESSION   AR111930
VERSION     AR111930.1  GI:12828778
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 4 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              | ||||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3795
AR124827
LOCUS       AR124827                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 4 from patent US 6172209.
ACCESSION   AR124827
VERSION     AR124827.1  GI:14110188
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 4 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3796
AR124827/c
LOCUS       AR124827                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 4 from patent US 6172209.
ACCESSION   AR124827
VERSION     AR124827.1  GI:14110188
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 4 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Kawasaki,A.Mamoru.
  TITLE     2'-modified oligonucleotides
  JOURNAL   Patent: US 5859221-A 33 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
             | |||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3787
AR029157/c
LOCUS       AR029157                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 33 from patent US 5859221.
ACCESSION   AR029157
VERSION     AR029157.1  GI:5941130
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Kawasaki,A.Mamoru.
  TITLE     2'-modified oligonucleotides
  JOURNAL   Patent: US 5859221-A 33 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
             | |||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3788
AR036541
LOCUS       AR036541                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 33 from patent US 5872232.
ACCESSION   AR036541
VERSION     AR036541.1  GI:5953209
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Kawasaki,A.Mamoru.
  TITLE     2'-O-modified oligonucleotides
  JOURNAL   Patent: US 5872232-A 33 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
             | |||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3789
AR036541/c
LOCUS       AR036541                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 33 from patent US 5872232.
ACCESSION   AR036541
VERSION     AR036541.1  GI:5953209
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Kawasaki,A.Mamoru.
  TITLE     2'-O-modified oligonucleotides
  JOURNAL   Patent: US 5872232-A 33 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
             | |||||||||||||
Db         18 CGTTTTTTTTTTTTT 4


RESULT 3790
AR096074
LOCUS       AR096074                 19 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 33 from patent US 6005087.
ACCESSION   AR096074
VERSION     AR096074.1  GI:10024545
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Kawasaki,A.Mamoru.
  TITLE     2'-modified oligonucleotides
  JOURNAL   Patent: US 6005087-A 33 21-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
             | |||||||||||||
Db          2 GCAAAAAAAAAAAAA 16


RESULT 3791
AR096074/c
LOCUS       AR096074                 19 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 33 from patent US 6005087.
ACCESSION   AR096074
VERSION     AR096074.1  GI:10024545
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan. and Kawasaki,A.Mamoru.
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FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        619 CCACGCACACGCCCT 633
              ||||||| ||||||
Db         18 CCACGCACTCGCCCT 4


RESULT 3783
BD217399/c
LOCUS       BD217399                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of TNFR1 expression.
ACCESSION   BD217399
VERSION     BD217399.1  GI:33027169
KEYWORDS    JP 2002519015-A/22.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense modulation of TNFR1 expression
  JOURNAL   Patent: JP 2002519015-A 22 02-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002519015-A/22
            PD   02-JUL-2002
            PF   17-JUN-1999 JP 2000557265
            PR   26-JUN-1998 US    09/106038
            PI   BRENDA F BAKER,LEX M COWSERT
            PC
            C12N15/09,A61K31/7105,A61K31/711,A61K48/00,A61P29/00,A61P43/00, PC
             C12Q1/68,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense modulation of TNFR1 expression
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        603 CCGACCTGCTGCTGC 617
              | ||||||||||||||
Db         15 CTGACCTGCTGCTGC 1


RESULT 3784
AB068476
LOCUS       AB068476                 18 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, forward primer for human STS sts-D1S1414
            at 1p36.
ACCESSION   AB068476
VERSION     AB068476.1  GI:15129280
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 18)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .18
                     /note="forward primer for human STS sts-D1S1414 at 1p36
                     sts-D1S1414 obtained from clones B313K24, B191B23,
                     B170N15, B193A17, B300E13, B172K8, B5F3, Human BAC library
                     RPCI-11"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2305 GCACGAAGCAATTTG 2319
              ||||||||||||  ||
Db          3 GCACGAAGCAATGTG 17


RESULT 3785
A51090/c
LOCUS       A51090                   19 bp    DNA     linear   PAT 10-MAR-1997
DEFINITION  Sequence 42 from Patent WO9616171.
ACCESSION   A51090
VERSION     A51090.1  GI:2303867
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Windass,J.D., Duncan,R.E., Baule,V.J. and Christian,P.D.
  TITLE     TOXINS FROM THE WASP BRACON HEBETOR
  JOURNAL   Patent: WO 9616171-A 42 30-MAY-1996;
            ZENECA LTD (GB)
COMMENT     Other publication AU 3877795 960617.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2414 GGTCTGTAAATACTG 2428
              ||||||||||||  ||
Db         16 GGTCTGTAAATAATG 2


RESULT 3786
AR029157
LOCUS       AR029157                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 33 from patent US 5859221.
ACCESSION   AR029157
VERSION     AR029157.1  GI:5941130
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COMMENT     OS   Unknown
            PN   JP 2001511000-A/294
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                 Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unknown'.
FEATURES            Location/Qualifiers
     source         1. .18
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        607 CCTGCTGCTGCCCCA 621
              || ||||||||||||
Db         15 CCAGCTGCTGCCCCA 1


RESULT 3780
BD089867
LOCUS       BD089867                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089867
VERSION     BD089867.1  GI:22635477
KEYWORDS    JP 2001321190-A/2111.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 2111 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/2111
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .18
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2305 GCACGAAGCAATTTG 2319
              ||||||||||||| ||
Db          3 GCACGAAGCAATGTG 17


RESULT 3781
BD103917/c
LOCUS       BD103917                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD103917
VERSION     BD103917.1  GI:22649491
KEYWORDS    WO 0192572-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 21 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/21
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .18
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1326 AGAACTGCTTGTCTC 1340
              ||||||||| |||||
Db         18 AGAACTGCTCGTCTC 4


RESULT 3782
BD104957/c
LOCUS       BD104957                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104957
VERSION     BD104957.1  GI:22650531
KEYWORDS    WO 0192572-A/1061.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1061 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1061
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
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  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferative disorder
  JOURNAL   Patent: EP 1340818-A 735 03-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for RARB"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2520 TTTATTCATATATAT 2534
              ||||||| |||||||
Db          3 TTTATTCGTATATAT 17


RESULT 3776
AX826483
LOCUS       AX826483                 18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 735 from Patent WO03072821.
ACCESSION   AX826483
VERSION     AX826483.1  GI:39751997
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferactive disorder
  JOURNAL   Patent: WO 03072821-A 735 04-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for RARB"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2520 TTTATTCATATATAT 2534
              ||||||| |||||||
Db          3 TTTATTCGTATATAT 17


RESULT 3777
AX837788
LOCUS       AX837788                 18 bp    DNA     linear   PAT 15-DEC-2003
DEFINITION  Sequence 4912 from Patent EP1347046.
ACCESSION   AX837788
VERSION     AX837788.1  GI:39921480
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE     Full-length cDNA sequences
  JOURNAL   Patent: EP 1347046-A 4912 24-SEP-2003;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="Description of Artificial Sequence: an artificially
                     synthesized primer se q"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1944 TGGTTGGTTTTTGTG 1958
              ||||||| |||||||
Db          3 TGGTTGGATTTTGTG 17


RESULT 3778
BD065376
LOCUS       BD065376                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065376
VERSION     BD065376.1  GI:22610979
KEYWORDS    JP 2001511000-A/11.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 11 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/11
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        269 GCCGGGCAGCACCTC 283
              ||||||| |||||||
Db          3 GCCGGGCGGCACCTC 17


RESULT 3779
BD065659/c
LOCUS       BD065659                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065659
VERSION     BD065659.1  GI:22611262
KEYWORDS    JP 2001511000-A/294.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 294 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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              |||||||||||| |||
Db         15 TCCCCCACCTCCCCT 1


RESULT 3771
AX601190/c
LOCUS       AX601190                  18 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 285 from Patent WO02092851.
ACCESSION   AX601190
VERSION     AX601190.1  GI:28401273
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Binns,M.M. and Swinburne,J.E.
  TITLE     Genetic typing
  JOURNAL   Patent: WO 02092851-A 285 21-NOV-2002;
            ANIMAL HEALTH TRUST (GB) ; The British Horseracing Board (GB)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        799 GGAGCTGGTGGGGGC 813
              ||||| |||||||||
Db         15 GGAGCAGGTGGGGGC 1


RESULT 3772
AX685128/c
LOCUS       AX685128                  18 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 5 from Patent WO0222889.
ACCESSION   AX685128
VERSION     AX685128.1  GI:29371479
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lieber,C.M., Woolley,A.T., Hahm,J.I. and Housman,D.
  TITLE     Direct haplotyping using carbon nanotube probes
  JOURNAL   Patent: WO 0222889-A 5 21-MAR-2002;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US) ; Massachusetts
            Institute Of Technology (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic PNA label"
     misc_feature    7. .8
                     /note="Lys"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              || ||||||  ||||||
Db         17 GACAAAAAANNAAAAAA 1


RESULT 3773
AX767735/c
LOCUS       AX767735                  18 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 383 from Patent WO03044226.
ACCESSION   AX767735
VERSION     AX767735.1  GI:32436340
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
            Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lymphoid cell
            proliferative disorder
  JOURNAL   Patent: WO 03044226-A 383 30-MAY-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for APC"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        970 AGCCAAATCGAAAAA 984
              | ||||||||||||||
Db         18 ACCCAAATCGAAAAA 4


RESULT 3774
AX796171/c
LOCUS       AX796171                  18 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 514 from Patent WO03052135.
ACCESSION   AX796171
VERSION     AX796171.1  GI:37516837
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
            and Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lung cell
            proliferative disorder
  JOURNAL   Patent: WO 03052135-A 514 26-JUN-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for APC"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        970 AGCCAAATCGAAAAA 984
              | ||||||||||||||
Db         18 ACCCAAATCGAAAAA 4


RESULT 3775
AX822843
LOCUS       AX822843                  18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 735 from Patent EP1340818.
ACCESSION   AX822843
VERSION     AX822843.1  GI:39749479
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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  JOURNAL   Patent: WO 0105963-A 33 25-JAN-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2176
              ||||||||  ||||||
Db         15 CTCCTTTTGTTTTTT 1


RESULT 3767
AX268173/c
LOCUS       AX268173                 18 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 59 from Patent WO0168851.
ACCESSION   AX268173
VERSION     AX268173.1  GI:16516641
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Padigaru,M., Vernet,C.A., Fernandes,E., Shimkets,R.A.,
            Spaderna,S.K., Majumder,K. and Li,L.
  TITLE     Polypeptides and nucleic acids encoding same
  JOURNAL   Patent: WO 0168851-A 59 20-SEP-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1602 TCCTGGCCTGGGGGA 1616
              ||||||||||  ||||
Db         17 TCCTGGCCTGTGGGA 3


RESULT 3768
AX557193
LOCUS       AX557193                 18 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 91 from Patent WO0244353.
ACCESSION   AX557193
VERSION     AX557193.1  GI:25900192
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wolffe,A.P.
  TITLE     Human heparanase gene regulatory sequences
  JOURNAL   Patent: WO 0244353-A 91 06-JUN-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="SBS# 5468 target"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2673 AGTGTGTGTGGGTGA 2687
              ||||  ||||||||||
Db          3 AGTGGGTGTGGGTGA 17


RESULT 3769
AX599315/c
LOCUS       AX599315                 18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 655 from Patent WO02077272.
ACCESSION   AX599315
VERSION     AX599315.1  GI:28399457
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 655 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for APC"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        970 AGCCAAATCGAAAAA 984
              | ||||||||||||||
Db         18 ACCCAAATCGAAAAA 4


RESULT 3770
AX599746/c
LOCUS       AX599746                 18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 1086 from Patent WO02077272.
ACCESSION   AX599746
VERSION     AX599746.1  GI:28399894
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 1086 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CSF1"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        252 TCCCCCACCTCTCCT 266
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Qy       1340 CATTTCAGCCTGATT 1354
              ||||||||||||| |
Db          1 CATTTCAGCCTGAAT 15


RESULT 3762
AR431658/c
LOCUS       AR431658                  18 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 27 from patent US 6653078.
ACCESSION   AR431658
VERSION     AR431658.1  GI:40193795
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lewis,M.K., Kephart,D., Rhodes,R.B., Shultz,J.W., Leippe,D.,
            Mandrekar,M., Andrews,C.A., Hartnett,J.R., Gu,T., Wood,K.V. and
            Welch,R.
  TITLE     Multiplex method for nucleic acid detection
  JOURNAL   Patent: US 6653078-A 27 25-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        108 TTGGGGGCTGGGGGG 122
              ||||||||||| |||
Db         17 TTGGGGGCTGGAGGG 3


RESULT 3763
AX078831/c
LOCUS       AX078831                  18 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 5 from Patent WO0105963.
ACCESSION   AX078831
VERSION     AX078831.1  GI:13158448
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Fundytus,M.E., Coderre,T.J., Cohen,S.R., Henry,J.L. and Vainio,A.
  TITLE     Antisense oligonucleotides for metabotropic glutamate receptor type
            1 (mglur1)
  JOURNAL   Patent: WO 0105963-A 5 25-JAN-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2176
              ||||||||| ||||||
Db         15 CTCCTTTGTTTTTT 1


RESULT 3764
AX078842/c
LOCUS       AX078842                  18 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 16 from Patent WO0105963.
ACCESSION   AX078842
VERSION     AX078842.1  GI:13158459
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Fundytus,M.E., Coderre,T.J., Cohen,S.R., Henry,J.L. and Vainio,A.
  TITLE     Antisense oligonucleotides for metabotropic glutamate receptor type
            1 (mglur1)
  JOURNAL   Patent: WO 0105963-A 16 25-JAN-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2176
              ||||||||| ||||||
Db         15 CTCCTTTGTTTTTT 1


RESULT 3765
AX078848/c
LOCUS       AX078848                  18 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 22 from Patent WO0105963.
ACCESSION   AX078848
VERSION     AX078848.1  GI:13158465
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Fundytus,M.E., Coderre,T.J., Cohen,S.R., Henry,J.L. and Vainio,A.
  TITLE     Antisense oligonucleotides for metabotropic glutamate receptor type
            1 (mglur1)
  JOURNAL   Patent: WO 0105963-A 22 25-JAN-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2176
              ||||||||| ||||||
Db         15 CTCCTTTGTTTTTT 1


RESULT 3766
AX078859/c
LOCUS       AX078859                  18 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 33 from Patent WO0105963.
ACCESSION   AX078859
VERSION     AX078859.1  GI:13158476
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Fundytus,M.E., Coderre,T.J., Cohen,S.R., Henry,J.L. and Vainio,A.
  TITLE     Antisense oligonucleotides for metabotropic glutamate receptor type
            1 (mglur1)
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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1326 AGAACTGCTTGTCTC 1340
              ||||||||| |||||
Db         15 AGAACTGCTCGTCTC 1


RESULT 3757
AR229573
LOCUS       AR229573                  18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 18 from patent US 6449562.
ACCESSION   AR229573
VERSION     AR229573.1  GI:27269200
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chandler,V.S., Fulton,J.R. and Chandler,M.B.
  TITLE     Multiplexed analysis of clinical specimens apparatus and method
  JOURNAL   Patent: US 6449562-A 18 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1326 AGAACTGCTTGTCTC 1340
              ||||||||| |||||
Db          4 AGAACTGCTCGTCTC 18


RESULT 3758
AR292914/c
LOCUS       AR292914                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4649 from patent US 6537751.
ACCESSION   AR292914
VERSION     AR292914.1  GI:31680198
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4649 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1501 GGAGAAACACAGGAA 1515
              ||||||||| |||||
Db         16 GGAGAAACAGAGGAA 2


RESULT 3759
AR295535
LOCUS       AR295535                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 7270 from patent US 6537751.
ACCESSION   AR295535
VERSION     AR295535.1  GI:31682819
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 7270 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1907 CAGATCAACAATACC 1921
              ||| ||||||||||||
Db          3 CAGCTCAACAATACC 17


RESULT 3760
AR324012/c
LOCUS       AR324012                  18 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1414 from patent US 6566127.
ACCESSION   AR324012
VERSION     AR324012.1  GI:33709820
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1414 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        474 GGCCCGGCCGCCAGA 488
              | ||||||||||||||
Db         15 GACCCGGCCGCCAGA 1


RESULT 3761
AR324101
LOCUS       AR324101                  18 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1503 from patent US 6566127.
ACCESSION   AR324101
VERSION     AR324101.1  GI:33709909
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1503 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1936 TAAGGTAATGGTTGG 1950
              ||||| |||||||||
Db         18 TAAGGGAATGGTTGG 4


RESULT 3752
AR181460/c
LOCUS       AR181460                 18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 18 from patent US 6335184.
ACCESSION   AR181460
VERSION     AR181460.1  GI:20223674
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Reyes,A.Arevalo., Wallace,R.Bruce. and Ugozzoli,L.A.
  TITLE     Linked linear amplification of nucleic acids
  JOURNAL   Patent: US 6335184-A 18 01-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1936 TAAGGTAATGGTTGG 1950
              ||||| |||||||||
Db         18 TAAGGGAATGGTTGG 4


RESULT 3753
AR187498/c
LOCUS       AR187498                 18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2986 from patent US 6346398.
ACCESSION   AR187498
VERSION     AR187498.1  GI:20233463
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2986 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        474 GGCCCGGCCGCCAGA 488
              | |||||||||||||
Db         15 GACCCGGCCGCCAGA 1


RESULT 3754
AR187588
LOCUS       AR187588                 18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 3076 from patent US 6346398.
ACCESSION   AR187588
VERSION     AR187588.1  GI:20233553
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 3076 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1340 CATTTCAGCCTGATT 1354
              ||||||||||||| |
Db          1 CATTTCAGCCTGAAT 15


RESULT 3755
AR210977/c
LOCUS       AR210977                 18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 77 from patent US 6391551.
ACCESSION   AR210977
VERSION     AR210977.1  GI:21513849
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,
            Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,
            Olson,R.J., Wood,K.V. and Welch,R.
  TITLE     Detection of nucleic acid hybrids
  JOURNAL   Patent: US 6391551-A 77 21-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        108 TTGGGGGCTGGGGGG 122
              |||||||||| |||
Db         17 TTGGGGGCTGGAGGG 3


RESULT 3756
AR229572/c
LOCUS       AR229572                 18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 17 from patent US 6449562.
ACCESSION   AR229572
VERSION     AR229572.1  GI:27269199
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chandler,V.S., Fulton,J.R. and Chandler,M.B.
  TITLE     Multiplexed analysis of clinical specimens apparatus and method
  JOURNAL   Patent: US 6449562-A 17 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
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            C07H21/04,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/ PC
            00,A61P1/16,
            PC   A61P3/00,A61P11/06,A61P25/28,A61P29/00,A61P29/00,A61P35/00, PC
              A61P35/04,
            PC   A61P37/06,A61P43/00,C12N15/09,C12Q1/02,C12Q1/68,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 CCTGGAGAAAATGGA 1503
              || ||||||||||||
Db         18 CCAGGAGAAAATGGA 4


RESULT 3748
BD227756/c
LOCUS       BD227756                  18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of integrin alph 4 expression.
ACCESSION   BD227756
VERSION     BD227756.1  GI:33037526
KEYWORDS    JP 2002526555-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,F.C., Condon,T.P. and Cowsert,L.M.
  TITLE     Antisense modulation of integrin alph 4 expression
  JOURNAL   Patent: JP 2002526555-A 18 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526555-A/18
            PD   20-AUG-2002
            PF   19-AUG-1999 JP 2000574727
            PR   05-OCT-1998 US    09/166203
            PI   FRANK C BENNETT,THOMAS P CONDON,LEX M COWSERT PC
            C07H21/04,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/ PC
            00,A61P1/16,
            PC   A61P3/00,A61P11/06,A61P25/28,A61P29/00,A61P29/00,A61P35/00, PC
              A61P35/04,
            PC   A61P37/06,A61P43/00,C12N15/09,C12Q1/02,C12Q1/68,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2481 TTTAATGGTGATGGG 2495
              |||||| ||||||||
Db         15 TTTAATTGTGATGGG 1


RESULT 3749
I73187
LOCUS       I73187                    18 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 1 from patent US 5686242.
ACCESSION   I73187
VERSION     I73187.1  GI:3009326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bruice,T.W. and Lima,W.F.
  TITLE     Determination of oligonucleotides for therapeutics, diagnostics and
            research reagents
  JOURNAL   Patent: US 5686242-A 1 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2180
              | ||||||||||||
Db          4 TGTTTTTTTTTTTT 18


RESULT 3750
I73187/c
LOCUS       I73187                    18 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 1 from patent US 5686242.
ACCESSION   I73187
VERSION     I73187.1  GI:3009326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bruice,T.W. and Lima,W.F.
  TITLE     Determination of oligonucleotides for therapeutics, diagnostics and
            research reagents
  JOURNAL   Patent: US 5686242-A 1 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2800
              |||||||||||||
Db         18 AAAAAAAAAAAACA 4


RESULT 3751
AR181458/c
LOCUS       AR181458                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 16 from patent US 6335184.
ACCESSION   AR181458
VERSION     AR181458.1  GI:20223672
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Reyes,A.Arevalo., Wallace,R.Bruce. and Ugozzoli,L.A.
  TITLE     Linked linear amplification of nucleic acids
  JOURNAL   Patent: US 6335184-A 16 01-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 CCTGGAGAAAATGGA 1503
              || ||||||||||||
Db         18 CCAGGAGAAAATGGA 4


RESULT 3743
AR162696/c
LOCUS       AR162696                 18 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 18 from patent US 6258790.
ACCESSION   AR162696
VERSION     AR162696.1  GI:16230017
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,C.Frank., Condon,T.P. and Cowsert,L.M.
  TITLE     Antisense modulation of integrin .alpha.4 expression
  JOURNAL   Patent: US 6258790-A 18 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2481 TTTAATGGTGATGGG 2495
              |||||| ||||||||
Db         15 TTTAATTGTGATGGG 1


RESULT 3744
AR163233/c
LOCUS       AR163233                 18 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 27 from patent US 6270973.
ACCESSION   AR163233
VERSION     AR163233.1  GI:16233766
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lewis,M.K., Kephart,D., Rhodes,R.Byron., Shultz,J.William.,
            Leippe,D., Mandrekar,M., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,
            Wood,K.V. and Welch,R.
  TITLE     Multiplex method for nucleic acid detection
  JOURNAL   Patent: US 6270973-A 27 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       108 TTGGGGGCTGGGGGG 122
             ||||||||||| |||
Db         17 TTGGGGGCTGGAGGG 3


RESULT 3745
AR165895/c
LOCUS       AR165895                 18 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 13 from patent US 6280936.
ACCESSION   AR165895
VERSION     AR165895.1  GI:16240982
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Burgin,A., Beigelman,L. and Bellon,L.
  TITLE     Method for screening nucleic acid catalysts
  JOURNAL   Patent: US 6280936-A 13 28-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        676 GCCTCACCAGATGGA 690
              |||||| ||||||||
Db         17 GCCTCATCAGATGGA 3


RESULT 3746
AR176958/c
LOCUS       AR176958                 18 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 61 from patent US 6312902.
ACCESSION   AR176958
VERSION     AR176958.1  GI:17919313
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,
            Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,
            Olson,R.J. and Welch,R.
  TITLE     Nucleic acid detection
  JOURNAL   Patent: US 6312902-A 61 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        108 TTGGGGGCTGGGGGG 122
              ||||||||||| |||
Db         17 TTGGGGGCTGGAGGG 3


RESULT 3747
BD227752/c
LOCUS       BD227752                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of integrin alph 4 expression.
ACCESSION   BD227752
VERSION     BD227752.1  GI:33037522
KEYWORDS    JP 2002526555-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,F.C., Condon,T.P. and Cowsert,L.M.
  TITLE     Antisense modulation of integrin alph 4 expression
  JOURNAL   Patent: JP 2002526555-A 14 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526555-A/14
            PD   20-AUG-2002
            PF   19-AUG-1999 JP 2000574727
            PR   05-OCT-1998 US    09/166203
            PI   FRANK C BENNETT,THOMAS P CONDON,LEX M COWSERT PC
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     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2481 TTTAATGGTGATGGG 2495
              |||||| ||||||||
Db         15 TTTAATTGTGATGGG 1


RESULT 3738
AR087086/c
LOCUS       AR087086                 18 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 36 from patent US 5985664.
ACCESSION   AR087086
VERSION     AR087086.1  GI:10013852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense modulation of Sentrin expression
  JOURNAL   Patent: US 5985664-A 36 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1753 GCTCTTTATTCATTA 1767
              |||| ||||||||||
Db         16 GCTCATTATTCATTA 2


RESULT 3739
AR096351/c
LOCUS       AR096351                 18 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 22 from patent US 6007995.
ACCESSION   AR096351
VERSION     AR096351.1  GI:10025085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense inhibition of TNFR1 expression
  JOURNAL   Patent: US 6007995-A 22 28-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        603 CCGACCTGCTGCTGC 617
              | ||||||||||||||
Db         15 CTGACCTGCTGCTGC 1


RESULT 3740
AR112277/c
LOCUS       AR112277                 18 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 45 from patent US 6130042.
ACCESSION   AR112277
VERSION     AR112277.1  GI:14092177
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Diehl,S.R., Schenkein,H.A. and Wang,Y.-F.
  TITLE     Compositions and methods for diagnosing periodontal disease
  JOURNAL   Patent: US 6130042-A 45 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2448 TTTGAGACATGGGAT 2462
              ||||| |||||||||
Db         18 TTTGACACATGGGAT 4


RESULT 3741
AR153218/c
LOCUS       AR153218                 18 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 220 from patent US 6235480.
ACCESSION   AR153218
VERSION     AR153218.1  GI:15120750
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,
            Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,
            Olson,R.J., Wood,K.V. and Welch,R.
  TITLE     Detection of nucleic acid hybrids
  JOURNAL   Patent: US 6235480-A 220 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        108 TTGGGGGCTGGGGGG 122
              ||||||||||| |||
Db         17 TTGGGGGCTGGAGGG 3


RESULT 3742
AR162692/c
LOCUS       AR162692                 18 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 14 from patent US 6258790.
ACCESSION   AR162692
VERSION     AR162692.1  GI:16230010
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,C.Frank., Condon,T.P. and Cowsert,L.M.
  TITLE     Antisense modulation of integrin .alpha.4 expression
  JOURNAL   Patent: US 6258790-A 14 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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                    /organism="unidentified"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        269 GCCGGGCAGCACCTC 283
              ||||||| |||||||
Db          3 GCCGGGCGGCACCTC 17


RESULT 3733
A88146/c
LOCUS       A88146                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 294 from Patent WO9833904.
ACCESSION   A88146
VERSION     A88146.1  GI:6736716
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 294 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        607 CCTGCTGCTGCCCCA 621
              || |||||||||||||
Db         15 CCAGCTGCTGCCCCA 1


RESULT 3734
A89830
LOCUS       A89830                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 11 from Patent EP0856579.
ACCESSION   A89830
VERSION     A89830.1  GI:6738344
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 11 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        269 GCCGGGCAGCACCTC 283
              ||||||| |||||||
Db          3 GCCGGGCGGCACCTC 17


RESULT 3735
A90113/c
LOCUS       A90113                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 294 from Patent EP0856579.
ACCESSION   A90113
VERSION     A90113.1  GI:6738627
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 294 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        607 CCTGCTGCTGCCCCA 621
              || |||||||||||||
Db         15 CCAGCTGCTGCCCCA 1


RESULT 3736
AR080709/c
LOCUS       AR080709                 18 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 14 from patent US 5968826.
ACCESSION   AR080709
VERSION     AR080709.1  GI:10007439
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,C.Frank., Condon,T.P. and Cowsert,L.M.
  TITLE     Antisense inhibition of integrin .alpha.4 expression
  JOURNAL   Patent: US 5968826-A 14 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1489 CCTGGAGAAAATGGA 1503
              || |||||||||||||
Db         18 CCAGGAGAAAATGGA 4


RESULT 3737
AR080713/c
LOCUS       AR080713                 18 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 18 from patent US 5968826.
ACCESSION   AR080713
VERSION     AR080713.1  GI:10007443
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Bennett,C.Frank., Condon,T.P. and Cowsert,L.M.
  TITLE     Antisense inhibition of integrin .alpha.4 expression
  JOURNAL   Patent: US 5968826-A 18 19-OCT-1999;
FEATURES             Location/Qualifiers
```

```
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD200954
VERSION     BD200954.1  GI:33010724
KEYWORDS    JP 2002509721-A/3980.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 3980 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/3980
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        881 AAATACAAAGTGACA 895
              ||||| |||||||||
Db         16 AAATAAAAAGTGACA 2


RESULT 3730
BD201172
LOCUS       BD201172                 17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD201172
VERSION     BD201172.1  GI:33010942
KEYWORDS    JP 2002509721-A/4198.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 4198 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/4198
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1971 TTACCTTGAAAAAAA 1985
              | ||||||||||||||
Db          3 TAACCTTGAAAAAAA 17


RESULT 3731
A64857
LOCUS       A64857                   18 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 14 from Patent WO9731114.
ACCESSION   A64857
VERSION     A64857.1  GI:4530848
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Burnham,M.K. and Hodgson,J.E.
  TITLE     POLYNUCLEOTIDES AND AMINOACID SEQUENCES FROM STAPHYLOCOCCUS AUREUS
  JOURNAL   Patent: WO 9731114-A 14 28-AUG-1997;
            SMITHKLINE BEECHAM PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        775 CCCTCTGAACCTCCC 789
              ||||||||||||| ||
Db          4 CCCTCTGAACCTTCC 18


RESULT 3732
A87863
LOCUS       A87863                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 11 from Patent WO9833904.
ACCESSION   A87863
VERSION     A87863.1  GI:6736433
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 11 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
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Qy        619 CCACGCACACGCCCT 633
              ||||||||| |||||
Db         17 CCACGCACAGGCCCT 3


RESULT 3726
BD105061/c
LOCUS       BD105061                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD105061
VERSION     BD105061.1  GI:22650635
KEYWORDS    WO 0192572-A/1165.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1165 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1165
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        619 CCACGCACACGCCCT 633
              |||||||| ||||||
Db         17 CCACGCACTCGCCCT 3


RESULT 3727
BD105063/c
LOCUS       BD105063                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD105063
VERSION     BD105063.1  GI:22650637
KEYWORDS    WO 0192572-A/1167.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1167 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1167
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        619 CCACGCACACGCCCT 633
              ||||||||| |||||
Db         17 CCACGCACAGGCCCT 3


RESULT 3728
BD105064/c
LOCUS       BD105064                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD105064
VERSION     BD105064.1  GI:22650638
KEYWORDS    WO 0192572-A/1168.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1168 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1168
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        619 CCACGCACACGCCCT 633
              |||||||| ||||||
Db         17 CCACGCACGCGCCCT 3


RESULT 3729
BD200954/c
LOCUS       BD200954                  17 bp    RNA     linear   PAT 17-JUL-2003
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            PD   31-JUL-2001
            PF   20-JAN-2000 JP 2000011458
            PI   YASUSHI HIRAMINE,YUKO MURAKAMI
            PC   C12N15/09,C07K14/475,C12N5/10,C12P21/02//(C12P21/02,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00
            CC   Designated oligonucleotide primer to amplify gene FH   Key
                    Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1601 CTCCTGGCCTGGGGG 1615
              ||||||| ||||||
Db         16 CTCCTGGCTTGGGGG 2


RESULT 3723
BD058091/c
LOCUS       BD058091                 17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for breast cancer.
ACCESSION   BD058091
VERSION     BD058091.1  GI:22603697
KEYWORDS    JP 2001518881-A/3.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sivaraman,V.S., Wang,H.Y. and Malbon,C.C.
  TITLE     Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for breast cancer
  JOURNAL   Patent: JP 2001518881-A 3 16-OCT-2001;
            THE RESEARCH FOUNDATION OF STATE UNIV OF NEW YORK
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001518881-A/3
            PD   16-OCT-2001
            PF   19-MAR-1998 JP 1998541700
            PI   VIMALA S SIVARAMAN,HSIEN YU WANG,CRAIG C MALBON PC
            C12N15/11,A61K31/70,C12Q1/68//A61K48/00
            CC   The molecular type is mRNA which is antisense. FH   Key
                 Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              ||||| |||||||||
Db         15 GGCGGCGGCGGCGGC 1


RESULT 3724
BD058092/c
LOCUS       BD058092                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for breast cancer.
ACCESSION   BD058092
VERSION     BD058092.1  GI:22603698
KEYWORDS    JP 2001518881-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sivaraman,V.S., Wang,H.Y. and Malbon,C.C.
  TITLE     Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for breast cancer
  JOURNAL   Patent: JP 2001518881-A 4 16-OCT-2001;
            THE RESEARCH FOUNDATION OF STATE UNIV OF NEW YORK
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001518881-A/4
            PD   16-OCT-2001
            PF   19-MAR-1998 JP 1998541700
            PI   VIMALA S SIVARAMAN,HSIEN YU WANG,CRAIG C MALBON PC
            C12N15/11,A61K31/70,C12Q1/68//A61K48/00
            CC   The molecular type is cDNA which is antisense. FH   Key
                 Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              ||||| |||||||||
Db         15 GGCGGCGGCGGCGGC 1


RESULT 3725
BD104958/c
LOCUS       BD104958                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104958
VERSION     BD104958.1  GI:22650532
KEYWORDS    WO 0192572-A/1062.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1062 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1062
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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DEFINITION  Sequence 2024 from Patent WO03040369.
ACCESSION   AX758703
VERSION     AX758703.1  GI:32253319
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 2024 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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Qy       2161 TCTCCTTTTTTTTTT 2175
              ||| ||||||||||
Db          3 TCTTCTTTTTTTTTT 17


RESULT 3719
AX759009/c
LOCUS       AX759009                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 2330 from Patent WO03040369.
ACCESSION   AX759009
VERSION     AX759009.1  GI:32253625
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 2330 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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Qy       1791 TCTTTCCTTCTCTGA 1805
              |||||||||| |||
Db         17 TCTTTCCTTCTTTGA 3


RESULT 3720
AX759584/c
LOCUS       AX759584                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 2905 from Patent WO03040369.
ACCESSION   AX759584
VERSION     AX759584.1  GI:32254200
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 2905 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        173 TGGAAAATAACCGAT 187
              ||||||||||| |||
Db         16 TGGAAAATAACAGAT 2


RESULT 3721
AX762667
LOCUS       AX762667                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 5988 from Patent WO03040369.
ACCESSION   AX762667
VERSION     AX762667.1  GI:32257283
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 5988 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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Qy       2113 TCTGGTTTTAGGAAA 2127
              |||||| ||||||||
Db          3 TCTGGTATTAGGAAA 17


RESULT 3722
BD015290/c
LOCUS       BD015290                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for promoting cell growth.
ACCESSION   BD015290
VERSION     BD015290.1  GI:22556428
KEYWORDS    JP 2001204471-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Hiramine,Y. and Murakami,Y.
  TITLE     Method for promoting cell growth
  JOURNAL   Patent: JP 2001204471-A 3 31-JUL-2001;
            SUMITOMO CHEMICAL CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001204471-A/3
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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        432 CCCTGCACCAGCCGG 446
              ||||||| |||||||
Db         17 CCCTGCAGCAGCCGG 3


RESULT 3714
AX751000/c
LOCUS       AX751000                 17 bp    DNA     linear   PAT 20-JUN-2003
DEFINITION  Sequence 216 from Patent WO03033703.
ACCESSION   AX751000
VERSION     AX751000.1  GI:32133328
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human gtp-activator protein for rab-like gtpase
  JOURNAL   Patent: WO 03033703-A 216 24-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"

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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        432 CCCTGCACCAGCCGG 446
              ||||||| |||||||
Db         16 CCCTGCAGCAGCCGG 2


RESULT 3715
AX757727
LOCUS       AX757727                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 1048 from Patent WO03040369.
ACCESSION   AX757727
VERSION     AX757727.1  GI:32252343
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 1048 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTT 2177
              ||||||||| |||||
Db          3 TCCTTTTTTCTTTTT 17


RESULT 3716
AX758401/c
LOCUS       AX758401                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 1722 from Patent WO03040369.
ACCESSION   AX758401
VERSION     AX758401.1  GI:32253017
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 1722 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"

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  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
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Qy       2569 TGTTCTTGGCTTGGA 2583
              | |||||||||||||
Db         17 TTTTCTTGGCTTGGA 3


RESULT 3717
AX758644/c
LOCUS       AX758644                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 1965 from Patent WO03040369.
ACCESSION   AX758644
VERSION     AX758644.1  GI:32253260
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 1965 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2264 ATATTTATTTCAGAT 2278
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Db         16 ATATTGATTTCAGAT 2


RESULT 3718
AX758703
LOCUS       AX758703                 17 bp    DNA     linear   PAT 25-JUN-2003
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LOCUS       AX732979                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4613 from Patent WO03025175.
ACCESSION   AX732979
VERSION     AX732979.1  GI:30512322
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 4613 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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Qy       2264 ATATTTATTTCAGAT 2278
              ||||||||||  ||||
Db         16 ATATTTATTTTAGAT 2


RESULT 3710
AX737962/c
LOCUS       AX737962                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3552 from Patent WO03025177.
ACCESSION   AX737962
VERSION     AX737962.1  GI:30517250
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3552 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1791 TCTTTCCTTCTCTGA 1805
              ||||||||||| |||
Db         17 TCTTTCCTTCTTTGA 3


RESULT 3711
AX738283/c
LOCUS       AX738283                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3873 from Patent WO03025177.
ACCESSION   AX738283
VERSION     AX738283.1  GI:30517571
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3873 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"

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  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        173 TGGAAAATAACCGAT 187
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Db         16 TGGAAAATAACAGAT 2


RESULT 3712
AX744261
LOCUS       AX744261                 17 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 226 from Patent WO03031621.
ACCESSION   AX744261
VERSION     AX744261.1  GI:30722928
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 226 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2111 CTTCTGGTTTTAGGA 2125
              ||||||| ||||||
Db          1 CTTCTGGTCTTAGGA 15


RESULT 3713
AX750999/c
LOCUS       AX750999                 17 bp    DNA     linear   PAT 20-JUN-2003
DEFINITION  Sequence 215 from Patent WO03033703.
ACCESSION   AX750999
VERSION     AX750999.1  GI:32133327
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human gtp-activator protein for rab-like gtpase
  JOURNAL   Patent: WO 03033703-A 215 24-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        902 GAAGTACAGAGGCGA 916
              ||||||| |||||||
Db         17 GAAGTACTGAGGCGA 3


RESULT 3705
AX725350
LOCUS       AX725350                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3037 from Patent WO03025176.
ACCESSION   AX725350
VERSION     AX725350.1  GI:30504693
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 3037 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATA 2474
              ||||||| |||||||
Db          1 GATCCAAATTTAATA 15


RESULT 3706
AX729187/c
LOCUS       AX729187                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 821 from Patent WO03025175.
ACCESSION   AX729187
VERSION     AX729187.1  GI:30508530
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 821 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1414 CAAAGAAGCCCTGAT 1428
              ||||||| ||||||
Db         16 CAAAGAAGGCCTGAT 2


RESULT 3707
AX729876
LOCUS       AX729876                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1510 from Patent WO03025175.
ACCESSION   AX729876
VERSION     AX729876.1  GI:30509219
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1510 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        425 ATCAACCCCCTGCAC 439
              ||||||| |||||||
Db          2 ATCAACCACCTGCAC 16


RESULT 3708
AX732099/c
LOCUS       AX732099                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3733 from Patent WO03025175.
ACCESSION   AX732099
VERSION     AX732099.1  GI:30511442
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 3733 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1791 TCTTTCCTTCTCTGA 1805
              |||||||||||| |||
Db         17 TCTTTCCTTCTTTGA 3


RESULT 3709
AX732979/c
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SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 416 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTT 2175
              |||| ||||||||||
Db          3 TCTCTTTTTTTTTTT 17


RESULT 3701
AX723158
LOCUS       AX723158                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 845 from Patent WO03025176.
ACCESSION   AX723158
VERSION     AX723158.1  GI:30423659
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 845 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2588 TCTATTTAATTGAAA 2602
              |||||||| ||||||
Db          3 TCTATTTATTTGAAA 17


RESULT 3702
AX723265/c
LOCUS       AX723265                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 952 from Patent WO03025176.
ACCESSION   AX723265
VERSION     AX723265.1  GI:30423766
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 952 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1463 CAGAGTCCAGCTGAT 1477
              ||||||| |||||||
Db         16 CAGAGTCAAGCTGAT 2


RESULT 3703
AX724168
LOCUS       AX724168                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1855 from Patent WO03025176.
ACCESSION   AX724168
VERSION     AX724168.1  GI:30503511
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 1855 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTT 2177
              |||||| ||||||||
Db          3 TCCTTTATTTTTTTT 17


RESULT 3704
AX725075/c
LOCUS       AX725075                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2762 from Patent WO03025176.
ACCESSION   AX725075
VERSION     AX725075.1  GI:30504418
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 2762 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTT 2177
              | ||||||||||||||
Db          3 TTCTTTTTTTTTTTT 17


RESULT 3696
AX692521/c
LOCUS       AX692521                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5253 from Patent EP1281758.
ACCESSION   AX692521
VERSION     AX692521.1  GI:29415479
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5253 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||| ||
Db         17 AAAAAAAAAAAAGAA 3


RESULT 3697
AX692529
LOCUS       AX692529                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5261 from Patent EP1281758.
ACCESSION   AX692529
VERSION     AX692529.1  GI:29415487
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5261 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTA 2187
              ||||||||||||| |
Db          1 TTTTTTTTTTTTTGA 15


RESULT 3698
AX692529/c
LOCUS       AX692529                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5261 from Patent EP1281758.
ACCESSION   AX692529
VERSION     AX692529.1  GI:29415487
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5261 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAA 2798
              | |||||||||||||
Db         15 TCAAAAAAAAAAAAA 1


RESULT 3699
AX708159/c
LOCUS       AX708159                  17 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 2 from Patent WO02072886.
ACCESSION   AX708159
VERSION     AX708159.1  GI:29564092
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Estibeiro,P.
  TITLE     Complex element micro-array and methods of use
  JOURNAL   Patent: WO 02072886-A 2 19-SEP-2002;
            Expresson Biosystems Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTT 2177
              ||| ||||||||||||
Db         15 TCCGTTTTTTTTTTT 1


RESULT 3700
AX722729
LOCUS       AX722729                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 416 from Patent WO03025176.
ACCESSION   AX722729
VERSION     AX722729.1  GI:30423230
KEYWORDS    .
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DEFINITION  Sequence 2882 from Patent WO03004526.
ACCESSION   AX674437
VERSION     AX674437.1  GI:29332785
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 2882 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2113 TCTGGTTTTAGGAAA 2127
              |||||| ||||||||
Db          3 TCTGGTATTAGGAAA 17


RESULT 3692
AX674708/c
LOCUS       AX674708                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 3153 from Patent WO03004526.
ACCESSION   AX674708
VERSION     AX674708.1  GI:29333056
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 3153 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        761 TCCATGACCAAGAAC 775
              ||||||||||||| |
Db         15 TCCATGACCAAGATC 1


RESULT 3693
AX688047
LOCUS       AX688047                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 779 from Patent EP1281758.
ACCESSION   AX688047
VERSION     AX688047.1  GI:29410745
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 779 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1196 GAGATGGCAGCTAGG 1210
              ||||||||||||| ||
Db          2 GAGATGGCAGCTGGG 16


RESULT 3694
AX688048
LOCUS       AX688048                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 780 from Patent EP1281758.
ACCESSION   AX688048
VERSION     AX688048.1  GI:29410746
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 780 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1196 GAGATGGCAGCTAGG 1210
              ||||||||||||| ||
Db          1 GAGATGGCAGCTGGG 15


RESULT 3695
AX692521
LOCUS       AX692521                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5253 from Patent EP1281758.
ACCESSION   AX692521
VERSION     AX692521.1  GI:29415479
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5253 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
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FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1425 TGATTGTCATAGACA 1439
              ||||||| |||||||
Db         16 TGATTGTAATAGACA 2


RESULT 3687
AX500256/c
LOCUS       AX500256                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1563 from Patent EP1229046.
ACCESSION   AX500256
VERSION     AX500256.1  GI:23382549
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1563 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1425 TGATTGTCATAGACA 1439
              ||||||| |||||||
Db         15 TGATTGTAATAGACA 1


RESULT 3688
AX600667
LOCUS       AX600667                  17 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 26 from Patent WO02092853.
ACCESSION   AX600667
VERSION     AX600667.1  GI:28400621
KEYWORDS    .
SOURCE      Moorella thermoacetica
  ORGANISM  Moorella thermoacetica
            Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
            Thermoanaerobacteriaceae; Moorella group; Moorella.
REFERENCE   1
  AUTHORS   Breen,A.W. and Singleton,F.L.
  TITLE     Detection of spore forming bacteria
  JOURNAL   Patent: WO 02092853-A 26 21-NOV-2002;
            HERCULES INCORPORATED (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Moorella thermoacetica"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1525"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        368 GCCTACTCCCAGTCG 382
              | ||||||||||||||
Db          3 GACTACTCCCAGTCG 17


RESULT 3689
AX672113
LOCUS       AX672113                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 558 from Patent WO03004526.
ACCESSION   AX672113
VERSION     AX672113.1  GI:29330461
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 558 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1766 TAAGCTTTTTTTTTT 1780
              | ||||||||||||||
Db          3 TCAGCTTTTTTTTTT 17


RESULT 3690
AX673606
LOCUS       AX673606                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 2051 from Patent WO03004526.
ACCESSION   AX673606
VERSION     AX673606.1  GI:29331954
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 2051 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTT 2177
              ||||||||| |||||
Db          3 TCCTTTTTTCTTTTT 17


RESULT 3691
AX674437
LOCUS       AX674437                  17 bp    DNA     linear   PAT 27-MAR-2003
```

```
Qy        979 GAAAAATGGAGGCCG 993
              ||||| |||||||||
Db         15 GAAAACTGGAGGCCG 1


RESULT 3682
AX499271
LOCUS       AX499271                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 578 from Patent EP1229046.
ACCESSION   AX499271
VERSION     AX499271.1  GI:23381564
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 578 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        193 CAAGTACGAAGAGGA 207
              |||| ||||||||||
Db          3 CAAGGACGAAGAGGA 17


RESULT 3683
AX499272
LOCUS       AX499272                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 579 from Patent EP1229046.
ACCESSION   AX499272
VERSION     AX499272.1  GI:23381565
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 579 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        193 CAAGTACGAAGAGGA 207
              |||| ||||||||||
Db          2 CAAGGACGAAGAGGA 16


RESULT 3684
AX499273
LOCUS       AX499273                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 580 from Patent EP1229046.
ACCESSION   AX499273
VERSION     AX499273.1  GI:23381566
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 580 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        193 CAAGTACGAAGAGGA 207
              |||| ||||||||||
Db          1 CAAGGACGAAGAGGA 15


RESULT 3685
AX500254/c
LOCUS       AX500254                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1561 from Patent EP1229046.
ACCESSION   AX500254
VERSION     AX500254.1  GI:23382547
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1561 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1425 TGATTGTCATAGACA 1439
              ||||||| |||||||
Db         17 TGATTGTAATAGACA 3


RESULT 3686
AX500255/c
LOCUS       AX500255                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 1562 from Patent EP1229046.
ACCESSION   AX500255
VERSION     AX500255.1  GI:23382548
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 1562 07-AUG-2002;
            Aeomica, Inc. (US)
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KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
  TITLE     Method and reagent for the inhibition of checkpoint kinase-1 (chk
            1) enzyme
  JOURNAL   Patent: WO 0157206-A 445 09-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1654 ACTGGTTCTGCATCA 1668
              ||||||||||||| |
Db         17 ACTGGTTCTGCATGA 3


RESULT 3678
AX227726/c
LOCUS       AX227726                 17 bp    RNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 1098 from Patent WO0157206.
ACCESSION   AX227726
VERSION     AX227726.1  GI:15556867
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
  TITLE     Method and reagent for the inhibition of checkpoint kinase-1 (chk
            1) enzyme
  JOURNAL   Patent: WO 0157206-A 1098 09-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1654 ACTGGTTCTGCATCA 1668
              ||||||||||||| |
Db         16 ACTGGTTCTGCATGA 2


RESULT 3679
AX422050/c
LOCUS       AX422050                 17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 386 from Patent WO0188124.
ACCESSION   AX422050
VERSION     AX422050.1  GI:21525432
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 386 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        979 GAAAAATGGAGGCCG 993
              ||||| |||||||||
Db         17 GAAAACTGGAGGCCG 3


RESULT 3680
AX422761/c
LOCUS       AX422761                 17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 1097 from Patent WO0188124.
ACCESSION   AX422761
VERSION     AX422761.1  GI:21526143
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1097 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        979 GAAAAATGGAGGCCG 993
              ||||| |||||||||
Db         16 GAAAACTGGAGGCCG 2


RESULT 3681
AX422762/c
LOCUS       AX422762                 17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 1098 from Patent WO0188124.
ACCESSION   AX422762
VERSION     AX422762.1  GI:21526144
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 1098 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1822 TTTAGAATCTTTTAA 1836
              ||| ||||||||||||
Db          1 TTTGGAATCTTTTAA 15


RESULT 3673
AX215487/c
LOCUS       AX215487                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 929 from Patent WO0159103.
ACCESSION   AX215487
VERSION     AX215487.1  GI:15525530
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 929 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        558 TGGAGGCGGGCGCGG 572
              ||||||| ||||||||
Db         16 TGGAGGGGGGCGCGG 2


RESULT 3674
AX215750/c
LOCUS       AX215750                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 1192 from Patent WO0159103.
ACCESSION   AX215750
VERSION     AX215750.1  GI:15525793
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 1192 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2479 CTTTTAATGGTGATG 2493
              ||| ||||||||||||
Db         16 CTTCTAATGGTGATG 2


RESULT 3675
AX216792
LOCUS       AX216792                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 2234 from Patent WO0159103.
ACCESSION   AX216792
VERSION     AX216792.1  GI:15526853
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 2234 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1822 TTTAGAATCTTTTAA 1836
              ||| ||||||||||||
Db          3 TTTGGAATCTTTTAA 17


RESULT 3676
AX216895
LOCUS       AX216895                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 2337 from Patent WO0159103.
ACCESSION   AX216895
VERSION     AX216895.1  GI:15526956
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 2337 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         55 CGGGGGCGGCGGCAG 69
              ||| ||||||||||||
Db          2 CGGCGGCGGCGGCAG 16


RESULT 3677
AX227073/c
LOCUS       AX227073                  17 bp    RNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 445 from Patent WO0157206.
ACCESSION   AX227073
VERSION     AX227073.1  GI:15556214
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Qy       2488 GTGATGGGGTAATCT 2502
              ||||||| |||||||
Db         15 GTGATGGAGTAATCT 1


RESULT 3668
AR328925
LOCUS       AR328925                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 6327 from patent US 6566127.
ACCESSION   AR328925
VERSION     AR328925.1  GI:33714733
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 6327 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAAT 1517
              ||| ||||||||||||
Db          3 AGAGACACAGGAAAT 17


RESULT 3669
AR434231
LOCUS       AR434231                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 654 from patent US 6656700.
ACCESSION   AR434231
VERSION     AR434231.1  GI:40197074
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 654 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCA 465
              |||||| ||||||||
Db          3 CACAGGTAGCCAGCA 17


RESULT 3670
AR434234
LOCUS       AR434234                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 657 from patent US 6656700.
ACCESSION   AR434234
VERSION     AR434234.1  GI:40197077
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 657 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        452 ACAGGCAGCCAGCAG 466
              ||||| |||||||||
Db          1 ACAGGTAGCCAGCAG 15


RESULT 3671
AX099948
LOCUS       AX099948                  17 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 8 from Patent WO0120034.
ACCESSION   AX099948
VERSION     AX099948.1  GI:13538958
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Voss,J. and Timm,J.
  TITLE     Methods and compositions for the screening of cell cycle modulators
  JOURNAL   Patent: WO 0120034-A 8 22-MAR-2001;
            BASF AKTIENGESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1984 AAGAAAAGTGTGTAT 1998
              ||||||||| |||||
Db          1 AAGAAAAGTATGTAT 15


RESULT 3672
AX214956
LOCUS       AX214956                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 398 from Patent WO0159103.
ACCESSION   AX214956
VERSION     AX214956.1  GI:15524999
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 398 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
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Qy       1561 GACTGCAAAAATCCT 1575
              ||||||||||  ||||
Db         17 GACTGCAAAAGTCCT 3


RESULT 3663
AR323176/c
LOCUS       AR323176                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 578 from patent US 6566127.
ACCESSION   AR323176
VERSION     AR323176.1  GI:33708984
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 578 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              ||||||||||  ||||
Db         16 GACTGCAAAAGTCCT 2


RESULT 3664
AR323177/c
LOCUS       AR323177                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 579 from patent US 6566127.
ACCESSION   AR323177
VERSION     AR323177.1  GI:33708985
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 579 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              ||||||||||  ||||
Db         15 GACTGCAAAAGTCCT 1


RESULT 3665
AR323332
LOCUS       AR323332                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 734 from patent US 6566127.
ACCESSION   AR323332
VERSION     AR323332.1  GI:33709140
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 734 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTAACT 2190
              ||||||||||| |||
Db          1 TTTTTTTTTTGACT 15


RESULT 3666
AR324232
LOCUS       AR324232                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1634 from patent US 6566127.
ACCESSION   AR324232
VERSION     AR324232.1  GI:33710040
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1634 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2698 TGGAATTGAACTCTC 2712
              ||||||||||||  ||
Db          3 TGGAATTGAACTATC 17


RESULT 3667
AR325894/c
LOCUS       AR325894                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3296 from patent US 6566127.
ACCESSION   AR325894
VERSION     AR325894.1  GI.33711702
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 3296 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              ||||||||||  ||||
Db         16 GACTGCAAAAGTCCT 2


RESULT 3658
AR186546/c
LOCUS       AR186546                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2034 from patent US 6346398.
ACCESSION   AR186546
VERSION     AR186546.1  GI:20232511
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2034 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              ||||||||||  ||||
Db         15 GACTGCAAAAGTCCT 1


RESULT 3659
AR186701
LOCUS       AR186701                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2189 from patent US 6346398.
ACCESSION   AR186701
VERSION     AR186701.1  GI:20232666
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2189 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACT 2190
              ||||||||||| |||
Db          1 TTTTTTTTTTTGACT 15


RESULT 3660
AR188379
LOCUS       AR188379                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 3867 from patent US 6346398.
ACCESSION   AR188379
VERSION     AR188379.1  GI:20234344
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 3867 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2698 TGGAATTGAACTCTC 2712
              ||||||||||||  ||
Db          3 TGGAATTGAACTATC 17


RESULT 3661
AR192002/c
LOCUS       AR192002                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 7490 from patent US 6346398.
ACCESSION   AR192002
VERSION     AR192002.1  GI:20237967
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 7490 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2488 GTGATGGGGTAATCT 2502
              |||||||  |||||||
Db         15 GTGATGGAGTAATCT 1


RESULT 3662
AR323175/c
LOCUS       AR323175                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 577 from patent US 6566127.
ACCESSION   AR323175
VERSION     AR323175.1  GI:33708983
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 577 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6370 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6370
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTTT 2192
              ||||||||||| |||
Db          3 TTTTTTTTTAATTTT 17


RESULT 3654
I53884/c
LOCUS       I53884                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1625 from patent US 5646042.
ACCESSION   I53884
VERSION     I53884.1  GI:2475087
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 1625 08-JUL-1997;
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2147 CTGATTGATTTTTTT 2161
              ||| ||||||||||||
Db         15 CTGCTTGATTTTTTT 1


RESULT 3655
I54166
LOCUS       I54166                    17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1907 from patent US 5646042.
ACCESSION   I54166
VERSION     I54166.1  GI:2475369
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb targeted ribozymes
  JOURNAL   Patent: US 5646042-A 1907 08-JUL-1997;
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAA 2794
              ||||| |||||||||
Db          3 GAATTTAAAAAAAAA 17


RESULT 3656
AR186544/c
LOCUS       AR186544                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2032 from patent US 6346398.
ACCESSION   AR186544
VERSION     AR186544.1  GI:20232509
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2032 12-FEB-2002;
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              |||||||||| ||||
Db         17 GACTGCAAAAGTCCT 3


RESULT 3657
AR186545/c
LOCUS       AR186545                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2033 from patent US 6346398.
ACCESSION   AR186545
VERSION     AR186545.1  GI:20232510
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2033 12-FEB-2002;
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
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SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6300 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6300
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES            Location/Qualifiers
     source         1. .17
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              ||||||||||  ||||
Db          3 AAGCTTTTTTATTTT 17


RESULT 3651
BD258508
LOCUS       BD258508                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258508
VERSION     BD258508.1  GI:33068278
KEYWORDS    JP 2002541795-A/6301.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6301 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6301
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES            Location/Qualifiers
     source         1. .17
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              ||||||||||  ||||
Db          2 AAGCTTTTTTATTTT 16


RESULT 3652
BD258509
LOCUS       BD258509                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258509
VERSION     BD258509.1  GI:33068279
KEYWORDS    JP 2002541795-A/6302.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6302 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6302
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES            Location/Qualifiers
     source         1. .17
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              ||||||||||  ||||
Db          1 AAGCTTTTTTATTTT 15


RESULT 3653
BD258577
LOCUS       BD258577                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258577
VERSION     BD258577.1  GI:33068347
KEYWORDS    JP 2002541795-A/6370.
SOURCE      unidentified
  ORGANISM  unidentified
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FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              ||||| |||||||||
Db         15 GGCGGCGGCGGCGGC 1


RESULT 3647
AR164081/c
LOCUS       AR164081                 17 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 4 from patent US 6271210.
ACCESSION   AR164081
VERSION     AR164081.1  GI:16235020
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sivaraman,V.S., Wang,H.-y. and Malbon,C.C.
  TITLE     Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for cancer
  JOURNAL   Patent: US 6271210-A 4 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              ||||| |||||||||
Db         15 GGCGGCGGCGGCGGC 1


RESULT 3648
BD254622
LOCUS       BD254622                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD254622
VERSION     BD254622.1  GI:33064392
KEYWORDS    JP 2002541795-A/2415.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2415 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/2415
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2736 ATTGTTGTGTGTATG 2750
              |||||||| ||||||
Db          1 ATTGTTGTTTGTATG 15


RESULT 3649
BD258292
LOCUS       BD258292                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258292
VERSION     BD258292.1  GI:33068062
KEYWORDS    JP 2002541795-A/6085.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6085 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6085
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
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            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        600 GCTCCGACCTGCTGC 614
              ||||| |||||||||
Db          3 GCTCCTACCTGCTGC 17


RESULT 3650
BD258507
LOCUS       BD258507                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258507
VERSION     BD258507.1  GI:33068277
KEYWORDS    JP 2002541795-A/6300.
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  JOURNAL   Patent: US 5817796-A 1907 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAA 2794
              ||||| |||||||||
Db          3 GAATTTAAAAAAAAA 17


RESULT 3642
AR088824/c
LOCUS       AR088824                  17 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from patent US 5990294.
ACCESSION   AR088824
VERSION     AR088824.1  GI:10015587
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Murphy,G.P., Boynton,A.L. and Sehgal,A.
  TITLE     Nucleotide and amino acid sequences of C4-2, a tumor suppressor
            gene, and methods of use thereof
  JOURNAL   Patent: US 5990294-A 5 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1891 ATGTGCCCTAGATCA 1905
              ||||||| |||||||
Db         16 ATGTGCCTTAGATCA 2


RESULT 3643
AR158488
LOCUS       AR158488                  17 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 110 from patent US 6251588.
ACCESSION   AR158488
VERSION     AR158488.1  GI:16220530
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 110 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        141 GACTGTTTTGGGGGA 155
              | |||||||||||||
Db          3 GTCTGTTTTGGGGGA 17


RESULT 3644
AR158489
LOCUS       AR158489                  17 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 111 from patent US 6251588.
ACCESSION   AR158489
VERSION     AR158489.1  GI:16220531
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 111 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        141 GACTGTTTTGGGGGA 155
              | |||||||||||||
Db          2 GTCTGTTTTGGGGGA 16


RESULT 3645
AR158490
LOCUS       AR158490                  17 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 112 from patent US 6251588.
ACCESSION   AR158490
VERSION     AR158490.1  GI:16220532
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 112 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        141 GACTGTTTTGGGGGA 155
              | |||||||||||||
Db          1 GTCTGTTTTGGGGGA 15


RESULT 3646
AR164080/c
LOCUS       AR164080                  17 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 3 from patent US 6271210.
ACCESSION   AR164080
VERSION     AR164080.1  GI:16235018
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sivaraman,V.S., Wang,H.-y. and Malbon,C.C.
  TITLE     Antisense oligonucleotides for mitogen-activated protein kinases as
            therapy for cancer
  JOURNAL   Patent: US 6271210-A 3 07-AUG-2001;
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                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||| |
Db         17 AAAAAAAAAAAAAGA 3


RESULT 3637
AX757892/c
LOCUS       AX757892                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 1213 from Patent WO03040369.
ACCESSION   AX757892
VERSION     AX757892.1  GI:32252508
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 1213 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||| |
Db         17 AAAAAAAAAAAAAGA 3


RESULT 3638
A05414/c
LOCUS       A05414                    17 bp    DNA     linear   PAT 12-APR-1994
DEFINITION  Synthetic oligonucleotide primer HuOcta1BACK.
ACCESSION   A05414
VERSION     A05414.1  GI:512617
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   .
  JOURNAL   Patent: WO 9005144-A 38 17-MAY-1990;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2256 TTATTTGCATATTTA 2270
              ||||||||||||| |
Db         17 TTATTTGCATATTCA 3


RESULT 3639
A09621/c
LOCUS       A09621                    17 bp    DNA     linear   PAT 12-OCT-1993
DEFINITION  Oligonucleotide.
ACCESSION   A09621
VERSION     A09621.1  GI:490594
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Winter,G.P., Guessow,D. and Ward,E.S.
  TITLE     Single domain ligands, receptors comprising said ligands, methods
            for their production, and use of said ligands and receptors
  JOURNAL   Patent: EP 0368684-A 38 16-MAY-1990;
            MEDICAL RESEARCH COUNCIL
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2256 TTATTTGCATATTTA 2270
              ||||||||||||| |
Db         17 TTATTTGCATATTCA 3


RESULT 3640
AR046832/c
LOCUS       AR046832                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1625 from patent US 5817796.
ACCESSION   AR046832
VERSION     AR046832.1  GI:5968297
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
  JOURNAL   Patent: US 5817796-A 1625 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2147 CTGATTGATTTTTTT 2161
              ||| ||||||||||||
Db         15 CTGCTTGATTTTTTT 1


RESULT 3641
AR047114
LOCUS       AR047114                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1907 from patent US 5817796.
ACCESSION   AR047114
VERSION     AR047114.1  GI:5968579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  TITLE     C-myb ribozymes having 2'-5'-linked adenylate residues
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            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAA 2796
              ||| ||||||||||
Db         17 ATTCAAAAAAAAAAA 3


RESULT 3634
BD255423/c
LOCUS       BD255423                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255423
VERSION     BD255423.1  GI:33065193
KEYWORDS    JP 2002541795-A/3216.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 3216 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/3216
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAA 2796
              ||| ||||||||||
Db         16 ATTCAAAAAAAAAAA 2


RESULT 3635
BD255424/c
LOCUS       BD255424                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255424
VERSION     BD255424.1  GI:33065194
KEYWORDS    JP 2002541795-A/3217.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 3217 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/3217
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAA 2796
              ||| ||||||||||
Db         15 ATTCAAAAAAAAAAA 1


RESULT 3636
AX738493/c
LOCUS       AX738493                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4083 from Patent WO03025177.
ACCESSION   AX738493
VERSION     AX738493.1  GI:30517781
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 4083 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
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            PF   22-JUN-1999 JP 2000556068
            PR   24-JUN-1998 EP   98870143.9
            PI   LIEVEN STUYVER
            PC   C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
            CC   Method of detecting mutation selected by drug in HIV protease
            CC           gene
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Aids-associated retrovirus'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Aids-associated retrovirus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:11966"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1970 TTTACCTTGAAAAAA 1984
              ||||||||||| ||||
Db         16 TTTACCTTGATAAAA 2


RESULT 3630
E33197/c
LOCUS       E33197                   16 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Reagent for detecting gene polymorphism of apolipoprotein E gene
            and alpha-1antichymotrypsin gene and detection method.
ACCESSION   E33197
VERSION     E33197.1  GI:13022360
KEYWORDS    JP 2000050898-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Norinobu,K. and Toshiaki,B.
  TITLE     Reagent for detecting gene polymorphism of apolipoprotein E gene
            and alpha-1antichymotrypsin gene and detection method
  JOURNAL   Patent: JP 2000050898-A 9 22-FEB-2000;
            NISSHO CORP
COMMENT     OS   Unidentified
            PN   JP 2000050898-A/9
            PD   22-FEB-2000
            PF   06-AUG-1998 JP 1998235033
            PR
            PI   NORINOBU KUSABA,TOSHIAKI BABA
            PC   C12Q1/68,A61B5/00,C12N15/09,G01N33/566,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        482 CGCCAGAGCCAGGAG 496
              | ||||||||||||||
Db         16 CCCCAGAGCCAGGAG 2


RESULT 3631
AR328462/c
LOCUS       AR328462                 16 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 5864 from patent US 6566127.
ACCESSION   AR328462
VERSION     AR328462.1  GI:33714270
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 5864 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCT 1575
              ||||||||||| ||||
Db         16 GACTGCAAAAGTCCT 2


RESULT 3632
AX007646/c
LOCUS       AX007646                 16 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 188 from Patent WO9967428.
ACCESSION   AX007646
VERSION     AX007646.1  GI:9995343
KEYWORDS    .
SOURCE      Aids-associated retrovirus
  ORGANISM  Aids-associated retrovirus
            Viruses; Retroid viruses; Retroviridae.
REFERENCE   1
  AUTHORS   Stuyver,L.
  TITLE     Method for detection of drug-selected mutations in the hiv protease
            gene
  JOURNAL   Patent: WO 9967428-A 188 29-DEC-1999;
            INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Aids-associated retrovirus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11966"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1970 TTTACCTTGAAAAAA 1984
              ||||||||||| ||||
Db         16 TTTACCTTGATAAAA 2


RESULT 3633
BD255422/c
LOCUS       BD255422                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255422
VERSION     BD255422.1  GI:33065192
KEYWORDS    JP 2002541795-A/3215.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 3215 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/3215
            PD   10-DEC-2002
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 164 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||| ||||||
Db          1 TTTTTTTATTTTTT 15


RESULT 3626
AR241876/c
LOCUS       AR241876                  15 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 164 from patent US 6472154.
ACCESSION   AR241876
VERSION     AR241876.1  GI:27287688
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 164 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||| ||||||||
Db         15 AAAAAATAAAAAAAA 1


RESULT 3627
AR278935
LOCUS       AR278935                  15 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 13 from patent US 6514693.
ACCESSION   AR278935
VERSION     AR278935.1  GI:29713578
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Lansdorp,P.
  TITLE     Method for detecting multiple copies of a repeat sequence in a
            nucleic acid molecule
  JOURNAL   Patent: US 6514693-A 13 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              ||||| |||||||||
Db          1 GGCGGCGGCGGCGGC 15


RESULT 3628
BD208567/c
LOCUS       BD208567                  15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD208567
VERSION     BD208567.1  GI:33018337
KEYWORDS    JP 2002512791-A/2157.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 2157 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/2157
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                 virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2204 CTTCAAATGGGAGAC 2218
              |||||||| ||||||
Db         15 CTTCAAATAGGAGAC 1


RESULT 3629
BD233092/c
LOCUS       BD233092                  16 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of detecting mutation selected by drug in HIV protease gene.
ACCESSION   BD233092
VERSION     BD233092.1  GI:33042862
KEYWORDS    JP 2002518065-A/188.
SOURCE      Aids-associated retrovirus
  ORGANISM  Aids-associated retrovirus
            Viruses; Retroid viruses; Retroviridae.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stuyver,L.
  TITLE     Method of detecting mutation selected by drug in HIV protease gene
  JOURNAL   Patent: JP 2002518065-A 188 25-JUN-2002;
            INNOGENETICS NV
COMMENT     OS   Aids-associated retrovirus
            PN   JP 2002518065-A/188
            PD   25-JUN-2002
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VERSION     AR084532.1  GI:10011303
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 21 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              ||||| |||||||||
Db          1 GGCGGCGGCGGCGGC 15


RESULT 3622
BD244856
LOCUS       BD244856                 15 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide primer capable of making the non-specific double
            strand formation unstable.
ACCESSION   BD244856
VERSION     BD244856.1  GI:33054626
KEYWORDS    JP 2002532063-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pelletier,J. and Das,M.
  TITLE     Oligonucleotide primer capable of making the non-specific double
            strand formation unstable
  JOURNAL   Patent: JP 2002532063-A 1 02-OCT-2002;
            MCGILL UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002532063-A/1
            PD   02-OCT-2002
            PF   06-OCT-1999 JP 2000574722
            PR   07-OCT-1998 CA      2246623
            PI   JERRY PELLETIER,MANJULA DAS
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||| |||||||
Db          1 AAAAAAATAAAAAAA 15


RESULT 3623
BD244856/c
LOCUS       BD244856                 15 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide primer capable of making the non-specific double
            strand formation unstable.
ACCESSION   BD244856
VERSION     BD244856.1  GI:33054626
KEYWORDS    JP 2002532063-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pelletier,J. and Das,M.
  TITLE     Oligonucleotide primer capable of making the non-specific double
            strand formation unstable
  JOURNAL   Patent: JP 2002532063-A 1 02-OCT-2002;
            MCGILL UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002532063-A/1
            PD   02-OCT-2002
            PF   06-OCT-1999 JP 2000574722
            PR   07-OCT-1998 CA      2246623
            PI   JERRY PELLETIER,MANJULA DAS
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||| |||||||
Db         15 TTTTTTTATTTTTTT 1


RESULT 3624
I25868/c
LOCUS       I25868                   15 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 2 from patent US 5552535.
ACCESSION   I25868
VERSION     I25868.1  GI:1605738
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   McLean,M.J., Holland,D., Garman,A.J. and Sheppard,R.C.
  TITLE     Multiple oligonucleotide containing oligomers and the cleanable
            linkers used in their preparation
  JOURNAL   Patent: US 5552535-A 2 03-SEP-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAA 2797
              | ||||||||||||
Db         15 TCGAAAAAAAAAAAA 1


RESULT 3625
AR241876
LOCUS       AR241876                 15 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 164 from patent US 6472154.
ACCESSION   AR241876
VERSION     AR241876.1  GI:27287688
KEYWORDS    .
SOURCE      Unknown.
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromomolecular structures
  JOURNAL   Patent: US 5571677-A 5 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAAC 2189
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTCAC 15


RESULT 3617
A15242
LOCUS       A15242                   15 bp    DNA     linear   PAT 22-MAR-1994
DEFINITION  Oligonucleotide AH14.
ACCESSION   A15242
VERSION     A15242.1  GI:512690
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ueda,I., Niwa,M., Saito,Y., Yamada,H. and Ishii,Y.
  TITLE     A process for the production of alpha-human atrial natriuretic
            polypeptide
  JOURNAL   Patent: EP 0206769-A 15 30-DEC-1986;
            FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1264 CAGCCAAGACCGGAC 1278
              ||||| |||||||||
Db          1 CAGCCCAGACCGGAC 15


RESULT 3618
A16457
LOCUS       A16457                   15 bp    DNA     linear   PAT 17-MAR-1994
DEFINITION  oligonucleotide AH14.
ACCESSION   A16457
VERSION     A16457.1  GI:489864
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ueda,I., Niwa,M., Saito,Y., Yamada,H. and Ishii,Y.
  TITLE     A process for the production of alpha-human atrial natriuretic
            polypeptide
  JOURNAL   Patent: EP 0440311-A 32 07-AUG-1991;
            FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1264 CAGCCAAGACCGGAC 1278
              ||||| |||||||||
Db          1 CAGCCCAGACCGGAC 15


RESULT 3619
AR084518
LOCUS       AR084518                 15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 7 from patent US 5981185.
ACCESSION   AR084518
VERSION     AR084518.1  GI:10011289
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 7 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              | ||||||||||||||
Db          1 ACAAAAAAAAAAAAA 15


RESULT 3620
AR084518/c
LOCUS       AR084518                 15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 7 from patent US 5981185.
ACCESSION   AR084518
VERSION     AR084518.1  GI:10011289
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 7 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||| |
Db         15 TTTTTTTTTTTTTGT 1


RESULT 3621
AR084532
LOCUS       AR084532                 15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 21 from patent US 5981185.
ACCESSION   AR084532
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LOCUS       AR045206                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5817795.
ACCESSION   AR045206
VERSION     AR045206.1  GI:5966671
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic and therapeutic
            applications
  JOURNAL   Patent: US 5817795-A 5 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAAC 2189
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTCAC 15


RESULT 3612
AR051237
LOCUS       AR051237                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5830658.
ACCESSION   AR051237
VERSION     AR051237.1  GI:5974601
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5830658-A 5 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAAC 2189
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTCAC 15


RESULT 3613
AR084519
LOCUS       AR084519                 15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 8 from patent US 5981185.
ACCESSION   AR084519
VERSION     AR084519.1  GI:10011290
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 8 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAA 2797
              || |||||||||||
Db          1 TTTAAAAAAAAAAAA 15


RESULT 3614
AR127784
LOCUS       AR127784                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 5 from patent US 6180777.
ACCESSION   AR127784
VERSION     AR127784.1  GI:14114379
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Horn,T.
  TITLE     Synthesis of branched nucleic acids
  JOURNAL   Patent: US 6180777-A 5 30-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAAC 2189
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTCAC 15


RESULT 3615
I16031
LOCUS       I16031                   15 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 5 from patent US 5473060.
ACCESSION   I16031
VERSION     I16031.1  GI:1250939
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic applications
  JOURNAL   Patent: US 5473060-A 5 05-DEC-1995;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAAC 2189
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTCAC 15


RESULT 3616
I28366
LOCUS       I28366                   15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 5 from patent US 5571677.
ACCESSION   I28366
VERSION     I28366.1  GI:1819142
```

```
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 180 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Homozygote Primer Sequence"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 4.4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||  ||  | |
Db          1 TTTTTTTTTTTTCAAGGTCG 20


RESULT 3607
AR056160
LOCUS       AR056160                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 364 from patent US 5837542.
ACCESSION   AR056160
VERSION     AR056160.1  GI:5981737
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 364 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTA 2187
              ||||||||||||| |
Db          1 TTTTTTTTTTTTCA 15


RESULT 3608
AR113918
LOCUS       AR113918                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 364 from patent US 6132967.
ACCESSION   AR113918
VERSION     AR113918.1  GI:14094240
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 364 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTA 2187
              ||||||||||||| |
Db          1 TTTTTTTTTTTTCA 15


RESULT 3609
AX633203
LOCUS       AX633203                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 342 from Patent EP1260586.
ACCESSION   AX633203
VERSION     AX633203.1  GI:28468817
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 342 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTA 2187
              ||||||||||||| |
Db          1 TTTTTTTTTTTTCA 15


RESULT 3610
AR002256
LOCUS       AR002256                 15 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5741643.
ACCESSION   AR002256
VERSION     AR002256.1  GI:3963810
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps
  JOURNAL   Patent: US 5741643-A 5 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.4;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAAC 2189
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTCAC 15


RESULT 3611
AR045206
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                     /db_xref="taxon:32630"
                     /note="Synthetic"
     misc_feature    5. .6
                     /note="The residue between C at position 5 and T at
                     position 6 is acridi ne"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 22;
  Best Local Similarity   80.0%;  Pred. No. 4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||| |||||| | ||| |||
Db         21 GAAGAAAAAAGAGAAAGAAA 2


RESULT 3602
I16929/c
LOCUS       I16929                   24 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 4 from patent US 5482836.
ACCESSION   I16929
VERSION     I16929.1  GI:1251837
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Cantor,C.R., Ito,T. and Smith,C.L.
  TITLE     DNA purification by triplex-affinity capture and affinity capture
            electrophoresis
  JOURNAL   Patent: US 5482836-A 4 09-JAN-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 24;
  Best Local Similarity   80.0%;  Pred. No. 4.3e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||||| ||| || |||| |
Db         22 GAAAAAGAAAGAAGAAAAGA 3


RESULT 3603
AX043318/c
LOCUS       AX043318                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 884 from Patent WO0065088.
ACCESSION   AX043318
VERSION     AX043318.1  GI:11341926
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 884 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 4.4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAA 2797
              | | | | ||||||||||||
Db         20 TCGTAGTTAAAAAAAAAAAA 1


RESULT 3604
AX042955
LOCUS       AX042955                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 521 from Patent WO0065088.
ACCESSION   AX042955
VERSION     AX042955.1  GI:11341563
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 521 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 4.4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
              |||||||||||| |  || |
Db          1 TTTTTTTTTTTTGTGGAATT 20


RESULT 3605
AX043216
LOCUS       AX043216                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 782 from Patent WO0065088.
ACCESSION   AX043216
VERSION     AX043216.1  GI:11341824
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 782 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 4.4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACT 2190
              |||||||||||| ||  | |
Db          1 TTTTTTTTTTTTGTTCCAGT 20


RESULT 3606
AX042614
LOCUS       AX042614                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 180 from Patent WO0065088.
ACCESSION   AX042614
VERSION     AX042614.1  GI:11341222
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .20
                     /note="forward primer for human STS sts-R101B17F at 1p36
                     sts-R101B17F obtained from clones B202F13, B116O10,
                     B367H11, B101B17, Human BAC library RPCI-11"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2423 ATACTGGTGCACTTCTTACG 2442
              ||||||| ||| |||  |||
Db         20 ATACTGGAGCATTTCCCACG 1


RESULT 3598
AX713257
LOCUS       AX713257                21 bp    DNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 143 from Patent WO03018837.
ACCESSION   AX713257
VERSION     AX713257.1  GI:29823846
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Waschuetza,S., Schnakenberg,E. and Lustig,M.
  TITLE     Method and diagnostic kit for the molecular diagnosis of
            pharmacologically relevant genes
  JOURNAL   Patent: WO 03018837-A 143 06-MAR-2003;
            Adnagen AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotid"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 21;
  Best Local Similarity   80.0%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              |||  |||||  ||||||||
Db          2 TGATTAAAAATTAAAAAAAA 21


RESULT 3599
AR029876/c
LOCUS       AR029876                22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 65 from patent US 5861244.
ACCESSION   AR029876
VERSION     AR029876.1  GI:5943090
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 65 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 22;
  Best Local Similarity   80.0%;  Pred. No. 4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||| ||||| | || ||||
Db         21 GAAATAAAAAGAGAAGAAAA 2


RESULT 3600
AX267016/c
LOCUS       AX267016                22 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 5 from Patent WO0173001.
ACCESSION   AX267016
VERSION     AX267016.1  GI:16515801
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Seidman,M.M. and Majumdar,A.
  TITLE     Establishment of cellular manipulations which enhance
            oligo-mediated gene targeting
  JOURNAL   Patent: WO 0173001-A 5 04-OCT-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic"
     misc_feature    5. .6
                     /note="The residue between C at position 5 and T at
                     position 6 is pyrene"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 22;
  Best Local Similarity   80.0%;  Pred. No. 4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||| |||||| | ||| |||
Db         21 GAAGAAAAAAGAGAAAGAAA 2


RESULT 3601
AX267017/c
LOCUS       AX267017                22 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 6 from Patent WO0173001.
ACCESSION   AX267017
VERSION     AX267017.1  GI:16515802
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Seidman,M.M. and Majumdar,A.
  TITLE     Establishment of cellular manipulations which enhance
            oligo-mediated gene targeting
  JOURNAL   Patent: WO 0173001-A 6 04-OCT-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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REFERENCE   1
  AUTHORS   Leprini,A., Gherzi,R., Siri,A., Querze,G., Viti,F. and Zardi,L.
  TITLE     The human tenascin-R gene
  JOURNAL   J. Biol. Chem. 271 (49), 31251-31254 (1996)
  MEDLINE   97094894
   PUBMED   8940128
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Zardi,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-SEP-1996) L. Zardi, Istituto Nazionale per la Ricerca
            sul Cancro, Laboratory of Cell Biology, Largo R.Benzi, 10, 16132
            Genova, ITALY
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /dev_stage="adult"
     intron          <1. .9
                     /number=14
     gene            10. .20
                     /gene="tenascin-R"
     exon            10. .>20
                     /gene="tenascin-R"
                     /number=15

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1552 AAGGAACAGGACTGCAAAAA 1571
              | ||  ||||||||||||  |
Db         20 AGGGTCCAGGACTGCAAAGA 1


RESULT 3595
AB068343
LOCUS       AB068343                 20 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, reverse primer for human STS sts-stSG1888
            at 1p36.
ACCESSION   AB068343
VERSION     AB068343.1  GI:15129147
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .20
                     /note="reverse primer for human STS sts-stSG1888 at 1p36
                     sts-stSG1888 obtained from clones B244O11, B364C12,
                     B76J14, B220M17, B218A5, B218I5, Human BAC library
                     RPCI-11"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         20 TGTCCAGTGACCCGGACAGC 39
              ||| | |||||| ||| ||
Db          1 TGTTCTGTGACCCTGACTGC 20


RESULT 3596
AB068345
LOCUS       AB068345                 20 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, reverse primer for human STS sts-NIB2114
            at 1p36.
ACCESSION   AB068345
VERSION     AB068345.1  GI:15129149
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .20
                     /note="reverse primer for human STS sts-NIB2114 at 1p36
                     sts-NIB2114 obtained from clones B244O11, B364C12, B76J14,
                     B220M17, B218A5, B218I5, Human BAC library RPCI-11"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         20 TGTCCAGTGACCCGGACAGC 39
              ||| | |||||| ||| ||
Db          1 TGTTCTGTGACCCTGACTGC 20


RESULT 3597
AB069220/c
LOCUS       AB069220                 20 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, forward primer for human STS sts-R101B17F
            at 1p36.
ACCESSION   AB069220
VERSION     AB069220.1  GI:15130024
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
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Qy       2094 CGTGTTCAAACGGGGGCCTT 2113
              ||| |||||| | ||||||
Db         20 CGTTCTCAAACTGTGGCCTT 1


RESULT 3591
BD195388
LOCUS       BD195388                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Male infertility Y-deletion detection battery.
ACCESSION   BD195388
VERSION     BD195388.1  GI:33005158
KEYWORDS    JP 2002510962-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   First,M.K. and Muallem,A.
  TITLE     Male infertility Y-deletion detection battery
  JOURNAL   Patent: JP 2002510962-A 1 09-APR-2002;
            PROMEGA CORP
COMMENT     OS   Unidentified
            PN   JP 2002510962-A/1
            PD   09-APR-2002
            PF   04-DEC-1997 JP 1998525914
            PR   04-DEC-1996 US    08/753979
            PI   MARIJO KENT FIRST,ARIEGE MUALLEM
            PC   C12Q1/68
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Male infertility Y-deletion detection battery FH   Key
                 Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1078 CTTAGTAGAAGGTGAAGCTG 1097
              ||||| | || ||||||| |
Db          1 CTTAGGAAAAAGTGAAGCCG 20


RESULT 3592
BD205800/c
LOCUS       BD205800                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  A method for detecting microorganisms in products.
ACCESSION   BD205800
VERSION     BD205800.1  GI:33015570
KEYWORDS    JP 2002514439-A/42.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Gerbling,K.P., Lauter,F.R. and Grohmann,L.
  TITLE     A method for detecting microorganisms in products
  JOURNAL   Patent: JP 2002514439-A 42 21-MAY-2002;
            BIOINSIDE GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002514439-A/42
            PD   21-MAY-2002
            PF   10-MAY-1999 JP 2000548504
            PR   12-MAY-1998 DE 198 22 108.8
            PI   KLAUS PETER GERBLING,FRANK ROMAN LAUTER,LUTZ GROHMANN PC
            C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: primer
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2427 TGGTGCACTTCTTACGACTT 2446
              ||||   ||| ||||||||||
Db         20 TGGTTACCTTGTTACGACTT 1


RESULT 3593
BD206090
LOCUS       BD206090                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Insulin-like growth factor II antisense oligonucleotide sequence
            and method of using the same for controlling cell proliferation.
ACCESSION   BD206090
VERSION     BD206090.1  GI:33015860
KEYWORDS    JP 2002512792-A/17.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wright,J.A., Young,A.H. and Lee,Y.S.
  TITLE     Insulin-like growth factor II antisense oligonucleotide sequence
            and method of using the same for controlling cell proliferation
  JOURNAL   Patent: JP 2002512792-A 17 08-MAY-2002;
            GENESENSE TECHNOLOGIES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002512792-A/17
            PD   08-MAY-2002
            PF   23-APR-1999 JP 2000545998
            PR   23-APR-1998 US    60/082791
            PI   JIM A WRIGHT,AIPING H YOUNG,YOON S LEE
            PC   C12N15/09,A61K31/711,A61K45/06,A61K48/00,A61P35/04,C12N15/00
            CC   Insulin-like growth factor II antisense oligonucleotide  CC
                 sequence and
            CC   method of using the same for controlling cell proliferation.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        251 GTCCCCCACCTCTCCTCCGC 270
              |||| ||| ||| || ||||
Db          1 GTCCACCAGCTCCCCGCCGC 20


RESULT 3594
HSTNRAS14/c
LOCUS       HSTNRAS14                 20 bp    DNA     linear   PRI 05-JUN-1997
DEFINITION  Homo sapiens TN-R gene acceptor splice site intron 14.
ACCESSION   Y13522 Y07980
VERSION     Y13522.1  GI:2181887
KEYWORDS    tenascin-R.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            BML INC,JAPAN MEAT INFORMATION SERVICE CENTER
COMMENT     OS   Bos sp. (bovine)
            PN   JP 2002209581-A/3
            PD   30-JUL-2002
            PF   12-JAN-2001 JP 2001005368
            PI   HIROSHI NAGAISHI,TSUYOSHI SAITO,AKIKO KOSUGA,HIROSHI TAHARA,
            PI   TADASHI YAMAZAKI
            PC   C12N15/09,A01K67/00,C12Q1/68,C12N15/00
            CC   Method for distinguishing bovine variety
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Bos sp. (bovine)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Bos sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:29061"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        778 TCTGAACCTCCCCTGTCAGA 797
              |||| | || ||||| ||||
Db         20 TCTGCAACTTCCCTGACAGA 1


RESULT 3588
BD167996
LOCUS       BD167996                 20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of constructing mutation DNA library and utilization
            thereof.
ACCESSION   BD167996
VERSION     BD167996.1  GI:27873808
KEYWORDS    WO 0226964-A/43.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tsuji,T. and Yanagawa,H.
  TITLE     Method of constructing mutation DNA library and utilization thereof
  JOURNAL   Patent: WO 0226964-A 43 04-APR-2002;
            MITSUBISHI CHEMICAL CORP,TORU TSUJI,HIROSHI YANAGAWA
COMMENT     OS   Artificial Sequence
            PN   WO 0226964-A/43
            PD   04-APR-2002
            PF   26-SEP-2001 WO 2001JP008387
            PR   27-SEP-2000 JP 00P   293692,06-FEB-2001 JP 01P   029138 PI
            TORU TSUJI,HIROSHI YANAGAWA
            PC   C12N15/09,C12P21/02
            CC   Description of Artificial Sequence:Synthesized FH   Key
            Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        596 CGCCGCTCCGACCTGCTGCT 615
              | || ||  ||||||||||||
Db          1 CCCCTCTATGACCTGCTGCT 20


RESULT 3589
BD177804
LOCUS       BD177804                 20 bp    DNA     linear   PAT 16-APR-2003
DEFINITION  A method for snp typing.
ACCESSION   BD177804
VERSION     BD177804.1  GI:30015067
KEYWORDS    JP 2002300894-A/94.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Nakamura,Y., Tanaka,T., Onishi,Y., Ozaki,K. and Yamada,A.
  TITLE     A method for snp typing
  JOURNAL   Patent: JP 2002300894-A 94 15-OCT-2002;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
COMMENT     OS   Artificial Sequence
            PN   JP 2002300894-A/94
            PD   15-OCT-2002
            PF   29-JAN-2002 JP 2002019752
            PI   YUSUKE NAKAMURA,TOSHIHIRO TANAKA,YOZO ONISHI,KOICHI OZAKI, PI
             AKIRA YAMADA
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence:Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1197 AGATGGCAGCTAGGAAGAAC 1216
              |||  ||||| |||||| ||
Db          1 AGAACGCAGCAAGGAAGCAC 20


RESULT 3590
BD177830/c
LOCUS       BD177830                 20 bp    DNA     linear   PAT 16-APR-2003
DEFINITION  A method for snp typing.
ACCESSION   BD177830
VERSION     BD177830.1  GI:30015093
KEYWORDS    JP 2002300894-A/120.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Nakamura,Y., Tanaka,T., Onishi,Y., Ozaki,K. and Yamada,A.
  TITLE     A method for snp typing
  JOURNAL   Patent: JP 2002300894-A 120 15-OCT-2002;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
COMMENT     OS   Artificial Sequence
            PN   JP 2002300894-A/120
            PD   15-OCT-2002
            PF   29-JAN-2002 JP 2002019752
            PI   YUSUKE NAKAMURA,TOSHIHIRO TANAKA,YOZO ONISHI,KOICHI OZAKI, PI
             AKIRA YAMADA
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence:Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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VERSION     BD130033.1  GI:23224978
KEYWORDS    JP 2002500895-A/323.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wilson,A.R.B., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
            Miller,A. and North,M.
  TITLE     Asthma-associated gene
  JOURNAL   Patent: JP 2002500895-A 323 15-JAN-2002;
            AXYS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002500895-A/323
            PD   15-JAN-2002
            PF   21-JAN-1998 JP 2000528715
            PI   ANGELA R BROOKS WILSON,ALAN BUCKLER,LON
            CARDON,ALISOUN H CAREY,
            PI   MARGARET GALVIN,ANDREW MILLER,MICHAEL NORTH
            PC   C12Q1/68,A01K67/027,C07K14/47,C12N15/09,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Asthma-associated gene
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1619 AGTTTGTTACCTACCTTACT 1638
              |||| |||||||||  | ||
Db         20 AGTTAGTTACCTACTGTGCT 1


RESULT 3585
BD138289/c
LOCUS       BD138289                 20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Antisense modulation of human MDM2 expression.
ACCESSION   BD138289
VERSION     BD138289.1  GI:23233234
KEYWORDS    JP 2002508944-A/215.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of human MDM2 expression
  JOURNAL   Patent: JP 2002508944-A 215 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002508944-A/215
            PD   26-MAR-2002
            PF   26-MAR-1999 JP 2000538025
            PR   26-MAR-1998 US    09/048810
            PI   LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

            PI   COWSERT
            PC   C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
            PC   C12Q1/68,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense modulation of human MDM2 expression FH   Key
                Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2520 TTTATTCATATATATACAGG 2539
              |||||||| ||||||  | |
Db         20 TTTATTCACATATATCAAAG 1


RESULT 3586
BD144137
LOCUS       BD144137                 20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Oligonucleotide for detecting HIV-1 and detection method.
ACCESSION   BD144137
VERSION     BD144137.1  GI:27849895
KEYWORDS    JP 2002125687-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ishizuka,T., Ishiguro,T. and Saito,J.
  TITLE     Oligonucleotide for detecting HIV-1 and detection method
  JOURNAL   Patent: JP 2002125687-A 7 08-MAY-2002;
            TOSOH CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002125687-A/7
            PD   08-MAY-2002
            PF   30-OCT-2000 JP 2000334937
            PI   TETSUYA ISHIZUKA,TAKAHIKO ISHIGURO,JUICHI SAITO PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Oligonucleotide capable of binding specifically to a specified

            CC            site of
            CC   HIV-1 RNA
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTT 2174
              ||||||  | |||||  ||||
Db          1 TTTTTTCTTACTTTGTTTT 20


RESULT 3587
BD166405/c
LOCUS       BD166405                 20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for distinguishing bovine variety.
ACCESSION   BD166405
VERSION     BD166405.1  GI:27872217
KEYWORDS    JP 2002209581-A/3.
SOURCE      Bos sp.
  ORGANISM  Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Nagaishi,H., Saito,T., Kosuga,A., Tahara,H. and Yamazaki,T.
  TITLE     Method for distinguishing bovine variety
  JOURNAL   Patent: JP 2002209581-A 3 30-JUL-2002;
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                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         20 TGTCCAGTGACCCGGACAGC 39
              ||| | ||||||| ||| ||
Db          1 TGTTCTGTGACCCTGACTGC 20


RESULT 3581
BD088308
LOCUS       BD088308                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD088308
VERSION     BD088308.1  GI:22633918
KEYWORDS    JP 2001321190-A/552.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 552 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/552
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         20 TGTCCAGTGACCCGGACAGC 39
              ||| | ||||||| ||| ||
Db          1 TGTTCTGTGACCCTGACTGC 20


RESULT 3582
BD088771/c
LOCUS       BD088771                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD088771
VERSION     BD088771.1  GI:22634381
KEYWORDS    JP 2001321190-A/1015.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 1015 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/1015
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2423 ATACTGGTGCACTTCTTACG 2442
              ||||||| ||| |||  |||
Db         20 ATACTGGAGCATTTCCCACG 1


RESULT 3583
BD094607/c
LOCUS       BD094607                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Substrate for immobilizing ligand.
ACCESSION   BD094607
VERSION     BD094607.1  GI:22640195
KEYWORDS    WO 0135098-A/45.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kato,I., Izu,H. and Asada,K.
  TITLE     Substrate for immobilizing ligand
  JOURNAL   Patent: WO 0135098-A 45 17-MAY-2001;
            TAKARA SHUZO CO LTD,IKUNOSHIN KATO,HIROYUKI IZU,KIYOZO ASADA
COMMENT     OS   Artificial Sequence
            PN   WO 0135098-A/45
            PD   17-MAY-2001
            PF   24-OCT-2000 WO 2000JP007415
            PR   05-NOV-1999 JP 99P   315610
            PI   IKUNOSHIN KATO,HIROYUKI IZU,KIYOZO ASADA
            PC   G01N33/543,G01N33/521,G01N33/53,G01N33/566,G01N37/00 CC
            Designed oligonucleotide primer for amplifying a portion of  CC
                 RIP 140 gene.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        895 AGTGGCTGAAGTACAGAGGC 914
              | || |||||| | ||||||
Db         20 AATGACTGAAGCAAAGAGGC 1


RESULT 3584
BD130033/c
LOCUS       BD130033                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Asthma-associated gene.
ACCESSION   BD130033
```

```
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 262 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/262
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unknown'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        283 CTACAGCCCCGCGCCACCCC 302
              ||||   ||||||||| |||
Db         20 CTACCCGCCCGCGCCAGCCC 1


RESULT 3578
BD065818/c
LOCUS       BD065818                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065818
VERSION     BD065818.1  GI:22611421
KEYWORDS    JP 2001511000-A/453.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 453 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/453
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                  Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unknown'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTT 2180
              | | |||||||| |||| ||
Db         20 TTTACTTTTTTGTTTTGTT 1


RESULT 3579
BD073164/c
LOCUS       BD073164                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisense oligonucleotide inhibition of RAS.
ACCESSION   BD073164
VERSION     BD073164.1  GI:22618767
KEYWORDS    JP 2001509394-A/37.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Cowcert,L.M. and Manoharan,M.
  TITLE     Antisense oligonucleotide inhibition of RAS
  JOURNAL   Patent: JP 2001509394-A 37 24-JUL-2001;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2001509394-A/37
            PD   24-JUL-2001
            PF   06-JUL-1998 JP 2000502223
            PR   08-JUL-1997 US    08/889296
            PI   BRETT P MONIA,LEX M COWCERT,MUSIA MANOHARAN
            PC   C12N15/09,A61K31/7088,A61K48/00,A61P35/00,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense oligonucleotide inhibition of RAS
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         69 GACGCCTGGTCACCGTGACC 88
              | |||||||| || ||| ||
Db         20 GCCGCCTGGTTACTGTGTCC 1


RESULT 3580
BD088306
LOCUS       BD088306                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD088306
VERSION     BD088306.1  GI:22633916
KEYWORDS    JP 2001321190-A/550.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 550 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/550
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
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LOCUS       BD000413                  20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel protease and DNA encoding the protease.
ACCESSION   BD000413
VERSION     BD000413.1  GI:18623526
KEYWORDS    JP 2000325089-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Yamashita,M., Sato,M., Iida,K. and Kido,H.
  TITLE     Novel protease and DNA encoding the protease
  JOURNAL   Patent: JP 2000325089-A 12 28-NOV-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000325089-A/12
            PD   28-NOV-2000
            PF   15-MAR-2000 JP 2000071575
            PR
            PI   MAKOTO YAMASHITA,MASAYUKI SATO,KENJI IIDA,HIROSHI KIDO PC
            C12N15/09,C07K16/40,C12N1/21,C12N9/64//C12P21/08,(C12N15/09, PC
            C12R1:91),
            PC   (C12N1/21,C12R1:19),C12N15/00,(C12N15/00,C12R1:91) CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        349 CCCTCCCTACCAGCAGCTGG 368
              || ||| | |||| ||||||
Db          1 CCATCCTTCCCAGAAGCTGG 20


RESULT 3575
BD012474
LOCUS       BD012474                  20 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  Guanosine triphosphate-binding protein-coupled receptors, genes
            thereof and production and use of the same.
ACCESSION   BD012474
VERSION     BD012474.1  GI:22092663
KEYWORDS    WO 0109322-A/12.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T.,
            Kishimoto,T., Yano,K., Kanzaki,K. and Inoue,Y.
  TITLE     Guanosine triphosphate-binding protein-coupled receptors, genes
            thereof and production and use of the same
  JOURNAL   Patent: WO 0109322-A 12 08-FEB-2001;
            HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,
            KOJI HAYASHI,KAORU SAITO,JUNICHI YAMAMOTO,SHIZUKO ISHII, OMOYASU
            SUGIYAMA, AI WAKAMATSU,KEIICHI NAGAI,TETSUJI OTSUKI,TOSHIMITSU
            KISHIMOTO, KAZUHIRO YANO,KOJI KANZAKI,YOSHIHISA INOUE
COMMENT     PN   WO 0109322-A/12
            PD   08-FEB-2001
            PF   28-JUL-2000 WO 2000JP005069
            PR   29-JUL-1999 JP 99P   248036,27-AUG-1999 JP 99P   300253 PR
            11-JAN-2000 JP 00P   118776,02-MAY-2000 JP 00P   183767 PR
            18-OCT-1999 US    60/159590,17-FEB-2000 US    60/183322 PI   TOSHIO
            OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI, PI   KAORU SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI,TOSHIMITSU KISHIMOTO, PI
            KAZUHIRO YANO,
            PI   KOJI KANZAKI,YOSHIHISA INOUE
            PC   C12N15/12,C12N5/10,C12N1/15,C12N1/19,C12N1/21,C12P21/02, PC
            C07K14/705,
            PC   C07K16/28,C12Q1/02
            CC   Description of Artificial Sequence: an artificially
            synthesized primer
            CC            C07K14/705,
            CC   sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1119 CCTATGTCTGTGAAGCCGAA 1138
              | || ||| || ||||||||
Db          1 CATAAGTCAGTCAAGCCGAA 20


RESULT 3576
BD016578
LOCUS       BD016578                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Genes and proteins participating in the upstream of degradation
            passage of aromatic polycyclic compound.
ACCESSION   BD016578
VERSION     BD016578.1  GI:22557754
KEYWORDS    JP 2001245662-A/66.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Saito,A., Tamatsubo,K. and Adachi,K.
  TITLE     Genes and proteins participating in the upstream of degradation
            passage of aromatic polycyclic compound
  JOURNAL   Patent: JP 2001245662-A 66 11-SEP-2001;
            MARINE BIOTECHNOLOGY INST CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001245662-A/66
            PD   11-SEP-2001
            PF   03-MAR-2000 JP 2000059523
            PI   ATSUSHI SAITO,KAZUAKI TAMATSUBO,KYOKO ADACHI
            PC   C12N15/09,C12N9/02,C12N15/00
            CC   Description of Artificial Sequence: Synthetic primer KP212. FH
              Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        603 CCGACCTGCTGCTGCCCCAC 622
              |||| ||||| |||| | ||
Db          1 CCGAACTGCTCCTGCTCGAC 20


RESULT 3577
BD065627/c
LOCUS       BD065627                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065627
VERSION     BD065627.1  GI:22611230
KEYWORDS    JP 2001511000-A/262.
SOURCE      unidentified
  ORGANISM  unidentified
```

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FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1488 CCCTGGAGAAAATGGAGAAA 1507
              |||||||||| || |  |||
Db          1 CCCTGGAGAACATAGGCAAA 20


RESULT 3570
AX767571
LOCUS       AX767571                 20 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 219 from Patent WO03044226.
ACCESSION   AX767571
VERSION     AX767571.1  GI:32436176
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
            Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lymphoid cell
            proliferative disorder
  JOURNAL   Patent: WO 03044226-A 219 30-MAY-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection primer for CSNK2B"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2683 GGTGAAATGGAGATTTGGAA 2702
              || ||||||||||  || ||
Db          1 GGGGAAATGGAGAAGTGTAA 20


RESULT 3571
AX804600
LOCUS       AX804600                 20 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 768 from Patent WO03060160.
ACCESSION   AX804600
VERSION     AX804600.1  GI:38521741
KEYWORDS    .
SOURCE      Oreochromis niloticus (Nile tilapia)
  ORGANISM  Oreochromis niloticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Labroidei; Cichlidae; Oreochromis.
REFERENCE   1
  AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
  TITLE     Verification of food origin based on nucleic acid pattern
            recognition
  JOURNAL   Patent: WO 03060160-A 768 24-JUL-2003;
            Genomar ASA (NO)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oreochromis niloticus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:8128"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1010 TTGGACAAGATCGGGTTGAA 1029
              |||||||| |  ||| ||||
Db          1 TTGGACAACAATGGGATGAA 20


RESULT 3572
AX839715
LOCUS       AX839715                 20 bp    DNA     linear   PAT 15-DEC-2003
DEFINITION  Sequence 49 from Patent WO03055912.
ACCESSION   AX839715
VERSION     AX839715.1  GI:39922890
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fagan,R.J., Phelps,C.B., Gutteridge,A. and Power,C.
  TITLE     Secreted proteins
  JOURNAL   Patent: WO 03055912-A 49 10-JUL-2003;
            ARES TRADING S.A. (CH)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3A7 forward primer"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2322 GCTGCTTGTCACCCCCAAGT 2341
              ||||||| ||  | ||||||
Db          1 GCTGCTTCTCCACACCAAGT 20


RESULT 3573
AX922674
LOCUS       AX922674                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1014 from Patent WO02068649.
ACCESSION   AX922674
VERSION     AX922674.1  GI:40215624
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   .
  JOURNAL   Patent: WO 02068649-A 1014 06-SEP-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Ag2956 Reverse"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1069 CCTGACATCCTTAGTAGAAG 1088
              || || |||||| | |||||
Db          1 CCAGAGATCCTTGGCAGAAG 20


RESULT 3574
BD000413
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```
ACCESSION   AX590963
VERSION     AX590963.1  GI:27949513
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Cookson,W.O., Moffat,M.F., Allen,M. and Lench,N.
  TITLE     Enzyme and snp marker for disease
  JOURNAL   Patent: WO 02086113-A 403 31-OCT-2002;
            Isis Innovation Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1630 TACCTTACTATTTAAAGAGC 1649
              ||  ||| ||||||||||  |
Db          1 TAAATTAGTATTTAAAGACC 20


RESULT 3566
AX599049
LOCUS       AX599049                 20 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 389 from Patent WO02077272.
ACCESSION   AX599049
VERSION     AX599049.1  GI:28399189
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 389 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection primer for CSNK2B"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2683 GGTGAAATGGAGATTTGGAA 2702
              || ||||||||||  || ||
Db          1 GGGGAAATGGAGAAGTGTAA 20


RESULT 3567
AX599172
LOCUS       AX599172                 20 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 512 from Patent WO02077272.
ACCESSION   AX599172
VERSION     AX599172.1  GI:28399314
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 512 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection primer for CSNK2B"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2683 GGTGAAATGGAGATTTGGAA 2702
              || ||||||||||  || ||
Db          1 GGGGAAATGGAGAAGTGTAA 20


RESULT 3568
AX657302
LOCUS       AX657302                 20 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 15 from Patent WO02100896.
ACCESSION   AX657302
VERSION     AX657302.1  GI:29160042
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   dalla Venezia,N.L., Magnard,C.M., Lenoir,G.M. and
            Sinilnikova-Erard,O.
  TITLE     Method for diagnosing cancer susceptibility
  JOURNAL   Patent: WO 02100896-A 15 19-DEC-2002;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR);
            UNIVERSITE CLAUDE BERNARD - LYON 1 (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="amorce PCR"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2356 TGTATTTTAAGAAACAGTGC 2375
              ||||  | |||||||||  ||
Db          1 TGTACCTCAAGAAACAGGGC 20


RESULT 3569
AX662867
LOCUS       AX662867                 20 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 78 from Patent WO02061134.
ACCESSION   AX662867
VERSION     AX662867.1  GI:29163448
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Roninson,I.B. and Chang,B.D.
  TITLE     Reagents and methods for identifying and modulating expression of
            tumor senescence genes
  JOURNAL   Patent: WO 02061134-A 78 08-AUG-2002;
            THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)
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FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="TAG004"
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  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2343 CCCGTGGAGGTTCTGTATTT 2362
              || |||||||| ||| |||
Db         20 CCAGTGGAGGTCATGTTTTT 1


RESULT 3561
AX547214/c
LOCUS       AX547214                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 353 from Patent WO02053141.
ACCESSION   AX547214
VERSION     AX547214.1  GI:25812358
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 353 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1543 AGAGTAGGGAAGGAACAGGA 1562
              ||| |  |||||||| |||
Db         20 AGACTGAGGAAGGAACTGGA 1


RESULT 3562
AX547386/c
LOCUS       AX547386                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 525 from Patent WO02053141.
ACCESSION   AX547386
VERSION     AX547386.1  GI:25812530
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 525 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              |||||||||| |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 3563
AX547637
LOCUS       AX547637                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 776 from Patent WO02053141.
ACCESSION   AX547637
VERSION     AX547637.1  GI:25812781
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 776 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1966 AATATTTACCTTGAAAAAAA 1985
              || ||  || ||||||||||
Db          1 AAAATCAACGTTGAAAAAAA 20


RESULT 3564
AX547716/c
LOCUS       AX547716                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 855 from Patent WO02053141.
ACCESSION   AX547716
VERSION     AX547716.1  GI:25812860
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 855 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              |||||||||| |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 3565
AX590963
LOCUS       AX590963                 20 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 403 from Patent WO02086113.
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Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||| |||||||||
Db         20 TTTTTTTAAAATTTTTTTTT 1


RESULT 3556
AX441510/c
LOCUS       AX441510                  20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 14 from Patent WO0206531.
ACCESSION   AX441510
VERSION     AX441510.1  GI:21690471
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 14 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02021"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||| |||||||||
Db         20 TTTTTTTACAATTTTTTTTT 1


RESULT 3557
AX441513/c
LOCUS       AX441513                  20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 17 from Patent WO0206531.
ACCESSION   AX441513
VERSION     AX441513.1  GI:21690474
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 17 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02024"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||| |||||||||
Db         20 TTTTTTTAGAATTTTTTTTT 1


RESULT 3558
AX482057/c
LOCUS       AX482057                  20 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 34 from Patent EP1225233.
ACCESSION   AX482057
VERSION     AX482057.1  GI:22316779
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: EP 1225233-A 34 24-JUL-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="TAG004"
     modified_base   1. .5
                     /mod_base=i

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2343 CCCGTGGAGGTTCTGTATTT 2362
              || |||||||| ||| |||
Db         20 CCAGTGGAGGTCATGTTTTT 1


RESULT 3559
AX492793
LOCUS       AX492793                  20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 5 from Patent WO02058738.
ACCESSION   AX492793
VERSION     AX492793.1  GI:23338476
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Zarling,D.A. and Reddy,G.
  TITLE     Use of rad51 inhibitors for p53 gene therapy
  JOURNAL   Patent: WO 02058738-A 5 01-AUG-2002;
            PANGENE CORP (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        563 GCGGGCGCGGTGAGCGCCCG 582
              ||||||| ||   |||||||
Db          1 GCGGGCGTGGCACGCGCCCG 20


RESULT 3560
AX511296/c
LOCUS       AX511296                  20 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 34 from Patent WO02059558.
ACCESSION   AX511296
VERSION     AX511296.1  GI:23392173
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: WO 02059558-A 34 01-AUG-2002;
            Amsterdam Support Diagnostics B.V. (NL)
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ACCESSION   AX441504
VERSION     AX441504.1  GI:21690465
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 8 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide AGT02008"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3552
AX441505
LOCUS       AX441505                  20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 9 from Patent WO0206531.
ACCESSION   AX441505
VERSION     AX441505.1  GI:21690466
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 9 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide AGT02012"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3553
AX441506
LOCUS       AX441506                  20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 10 from Patent WO0206531.
ACCESSION   AX441506
VERSION     AX441506.1  GI:21690467
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 10 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide AGT02013"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3554
AX441507
LOCUS       AX441507                  20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 11 from Patent WO0206531.
ACCESSION   AX441507
VERSION     AX441507.1  GI:21690468
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 11 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide AGT02014"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3555
AX441508/c
LOCUS       AX441508                  20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 12 from Patent WO0206531.
ACCESSION   AX441508
VERSION     AX441508.1  GI:21690469
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 12 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Complement DNA oligo AGT02009"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-chimeric phosphorothioate/phosphodiester backbone with phosphorothioate at 5' and 3' ends"

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       1966 AATATTTACCTTGAAAAAAA 1985
              || ||  || ||||||||||
Db          1 AAAATCAACGTTGAAAAAAA 20
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RESULT 3547
AX355514/c
LOCUS AX355514 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 542 from Patent WO0197843.
ACCESSION AX355514
VERSION AX355514.1 GI:18620182
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 542 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       1543 AGAGTAGGGAAGGAACAGGA 1562
              ||| |  ||||||||| |||
Db         20 AGACTGAGGAAGGAACTGGA 1
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RESULT 3548
AX418628/c
LOCUS AX418628 20 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 23 from Patent WO0210378.
ACCESSION AX418628
VERSION AX418628.1 GI:21523491
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Cowsert,L.M., Wyatt,J., Freier,S.M., Monia,B.P., Butler,M.M. and Mckay,R.
TITLE Antisense modulation of ptp1b expression
JOURNAL Patent: WO 0210378-A 23 07-FEB-2002;
ISIS PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense Oligonucleotide"

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy        903 AAGTACAGAGGCGACTGTCC 922
              | ||||||||| || | ||||
Db         20 AGGTACAGAGACGTCAGTCC 1
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RESULT 3549
AX418788/c
LOCUS AX418788 20 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 183 from Patent WO0210378.
ACCESSION AX418788
VERSION AX418788.1 GI:21523651
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Cowsert,L.M., Wyatt,J., Freier,S.M., Monia,B.P., Butler,M.M. and Mckay,R.
TITLE Antisense modulation of ptp1b expression
JOURNAL Patent: WO 0210378-A 183 07-FEB-2002;
ISIS PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense Oligonucleotide"

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       1590 ACTGGGAACCCCTCCTGGCC 1609
              ||||| | ||| |||||| |
Db         20 ACTGGAAGCCCTTCCTGGTC 1
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RESULT 3550
AX429779
LOCUS AX429779 20 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 7 from Patent EP1203826.
ACCESSION AX429779
VERSION AX429779.1 GI:21540955
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ishizuka,T., Ishiguro,T. and Saitoh,J.
TITLE Oligonucleotide for detection of hiv-1 and detection method
JOURNAL Patent: EP 1203826-A 7 08-MAY-2002;
Tosoh Corporation (JP)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide hybridizable with a specific site of HIV-1 RNA"

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2155 TTTTTTTCTCCTTTTTTTT 2174
              ||||||  | ||||| ||||
Db          1 TTTTTTCTTACTTTGTTTT 20
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RESULT 3551
AX441504
LOCUS AX441504 20 bp DNA linear PAT 02-JUL-2002
DEFINITION Sequence 8 from Patent WO0206531.

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LOCUS       AX349199                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 125 from Patent WO0202808.
ACCESSION   AX349199
VERSION     AX349199.1  GI:18615234
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Method and nucleic acids for the analysis of astrocytomas
  JOURNAL   Patent: WO 0202808-A 125 10-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="CSNK2B detection primer"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2683 GGTGAAATGGAGATTTGGAA 2702
              || |||||||||  || ||
Db          1 GGGGAAATGGAGAAGTGTAA 20


RESULT 3543
AX354307
LOCUS       AX354307                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 5 from Patent WO0194638.
ACCESSION   AX354307
VERSION     AX354307.1  GI:18619166
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,C., Egholm,M. and Haff,L.
  TITLE     Asynchronous primed pcr
  JOURNAL   Patent: WO 0194638-A 5 13-DEC-2001;
            Applera Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        247 GCGGGTCCCCCACCTCTCCT 266
              || |||||||  | ||||||
Db          1 GCTGGTCCCCGTCTTCTCCT 20


RESULT 3544
AX354976/c
LOCUS       AX354976                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 4 from Patent WO0197843.
ACCESSION   AX354976
VERSION     AX354976.1  GI:18619643
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 4 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide~Chimeric
                     phosphorothioate/phosphodiester backbone with
                     phosphorothioate at 5' and 3' ends"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 3545
AX354977/c
LOCUS       AX354977                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 5 from Patent WO0197843.
ACCESSION   AX354977
VERSION     AX354977.1  GI:18619644
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 5 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide~phosphorodithioate
                     backbone"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 3546
AX354981
LOCUS       AX354981                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 9 from Patent WO0197843.
ACCESSION   AX354981
VERSION     AX354981.1  GI:18619648
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 9 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                     /note="Beschreibung der kunstlichen
                     Sequenz:Oligonukleotid"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2695 ATTTGGAATTGAACTCTCTG 2714
              ||||||| ||||| | | ||
Db          1 ATTTGGAGTTGAAGTATTTG 20


RESULT 3538
AX294124/c
LOCUS       AX294124                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 5886 from Patent WO0179548.
ACCESSION   AX294124
VERSION     AX294124.1  GI:17055807
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 5886 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1593 GGGAACCCCTCCTGGCCTGG 1612
              |||||| | |||| || |||
Db         20 GGGAACTCGTCCTTGCATGG 1


RESULT 3539
AX294426
LOCUS       AX294426                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 6188 from Patent WO0179548.
ACCESSION   AX294426
VERSION     AX294426.1  GI:17056109
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 6188 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1358 CACGGGTTTGGCAGCCAGGC 1377
              ||||| |||| |||||  ||
Db          1 CACGGCTTTGTCAGCCGTGC 20


RESULT 3540
AX298602/c
LOCUS       AX298602                  20 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 236 from Patent WO0183749.
ACCESSION   AX298602
VERSION     AX298602.1  GI:17128592
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
            Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
  TITLE     Gene and sequence variation associated with sensing carbohydrate
            compounds and other sweeteners
  JOURNAL   Patent: WO 0183749-A 236 08-NOV-2001;
            WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
            (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10095"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1331 TGCTTGTCTCATTTCAGCCT 1350
              | |||||||  |||| ||||
Db         20 TCCTTGTCTGCTTTCTGCCT 1


RESULT 3541
AX298787
LOCUS       AX298787                  20 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 421 from Patent WO0183749.
ACCESSION   AX298787
VERSION     AX298787.1  GI:17128777
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
            Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
  TITLE     Gene and sequence variation associated with sensing carbohydrate
            compounds and other sweeteners
  JOURNAL   Patent: WO 0183749-A 421 08-NOV-2001;
            WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
            (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10095"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1562 ACTGCAAAAATCCTTCTCCA 1581
              ||||||||  |||  |||||
Db          1 ACTGCAAATGTCCAACTCCA 20


RESULT 3542
AX349199
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LOCUS       AX167934                 20 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 118 from Patent WO0142307.
ACCESSION   AX167934
VERSION     AX167934.1  GI:14597254
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Saito,K., Ohe,N. and Satoh,H.
  TITLE     Mutant er_g(a) and test systems for transactivation
  JOURNAL   Patent: WO 0142307-A 118 14-JUN-2001;
            Sumitomo Chemical Company, Limited (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Designed oligonucleotide probe for Southern
                     hybridization"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        365 CTGGCCTACTCCCAGTCGGC 384
              ||||||| |||| | ||||
Db          1 CTGGCCTTGTCCCTGACGGC 20


RESULT 3534
AX167935
LOCUS       AX167935                 20 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 119 from Patent WO0142307.
ACCESSION   AX167935
VERSION     AX167935.1  GI:14597255
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Saito,K., Ohe,N. and Satoh,H.
  TITLE     Mutant er_g(a) and test systems for transactivation
  JOURNAL   Patent: WO 0142307-A 119 14-JUN-2001;
            Sumitomo Chemical Company, Limited (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Designed oligonucleotide probe for Southern
                     hybridization"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        369 CCTACTCCCAGTCGGCCGAC 388
              ||| |||| | ||||||||
Db          1 CCTTGTCCCTGACGGCCGAC 20


RESULT 3535
AX231607
LOCUS       AX231607                 20 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 5 from Patent WO0163289.
ACCESSION   AX231607
VERSION     AX231607.1  GI:15592504
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boyd,R.S., Stamps,A.C., Terrett,J.A. and Tyson,K.L.
  TITLE     Diagnosis of breast cancer using bcmp-11 as marker
  JOURNAL   Patent: WO 0163289-A 5 30-AUG-2001;
            Oxford GlycoSciences (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        849 CTGGAAGATTGTCGCTCCTC 868
              ||||| |||||||  | |||
Db          1 CTGGAGGATTGTCAATACTC 20


RESULT 3536
AX231700
LOCUS       AX231700                 20 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 88 from Patent WO0162784.
ACCESSION   AX231700
VERSION     AX231700.1  GI:15592510
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boyd,R.S., Stamps,A.C. and Terrett,J.A.
  TITLE     Use of breast cancer associated membrane proteins (bcmp) for
            treatment, prophylaxis and diagnosis of breast cancer
  JOURNAL   Patent: WO 0162784-A 88 30-AUG-2001;
            Oxford GlycoSciences (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        849 CTGGAAGATTGTCGCTCCTC 868
              ||||| |||||||  | |||
Db          1 CTGGAGGATTGTCAATACTC 20


RESULT 3537
AX252919
LOCUS       AX252919                 20 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 389 from Patent WO0168910.
ACCESSION   AX252919
VERSION     AX252919.1  GI:15986190
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K.
  TITLE     Oligonucleotides or pna oligomers and a method for detecting the
            methylation state of genomic dna in a parallel manner
  JOURNAL   Patent: WO 0168910-A 389 20-SEP-2001;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="PDGF B ribozyme recognition site"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        360 AGCAGCTGGCCTACTCCCAG 379
              | |||| || || |||||||
Db          1 ATCAGCGGGTCTCCTCCCAG 20


RESULT 3529
AX136904
LOCUS       AX136904                 20 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 6 from Patent EP1065278.
ACCESSION   AX136904
VERSION     AX136904.1  GI:14273253
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Makino,Y., Abe,Y., Ogawa,M., Takagi,M., Takenaka,S. and
            Yamashita,K.
  TITLE     Detection of partly complementary nucleic acid fragment
  JOURNAL   Patent: EP 1065278-A 6 03-JAN-2001;
            FUJI PHOTO FILM CO., LTD. (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sample nucleic acid fragment"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||    ||||||||
Db          1 TTTTTTTTAAAATTTTTTTT 20


RESULT 3530
AX148869/c
LOCUS       AX148869                 20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 71 from Patent WO0136625.
ACCESSION   AX148869
VERSION     AX148869.1  GI:14347393
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 71 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAA 2797
              | ||| ||||| | ||||||
Db         20 TTGAAATGAAAGAGAAAAAA 1


RESULT 3531
AX149016
LOCUS       AX149016                 20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 218 from Patent WO0136625.
ACCESSION   AX149016
VERSION     AX149016.1  GI:14347540
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 218 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1913 AACAATACCTTTTTTTTCAG 1932
              |||||||||||  ||   |||
Db          1 AACAATACCTTCTTCAACAG 20


RESULT 3532
AX149128
LOCUS       AX149128                 20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 330 from Patent WO0136625.
ACCESSION   AX149128
VERSION     AX149128.1  GI:14347652
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 330 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTT 2176
              |||| | |||||||| || |
Db          1 TTTTACCCCTTTTTTCTTAT 20


RESULT 3533
AX167934
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Qy        563 GCGGGCGCGGTGAGCGCCCG 582
              ||||||| ||   |||||||
Db          1 GCGGGCGTGGCACGCGCCCG 20


RESULT 3524
AX104161/c
LOCUS       AX104161                  20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 353 from Patent WO0122972.
ACCESSION   AX104161
VERSION     AX104161.1  GI:13920358
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 353 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1543 AGAGTAGGGAAGGAACAGGA 1562
              ||| |  |||||||||  |||
Db         20 AGACTGAGGAAGGAACTGGA 1


RESULT 3525
AX104333/c
LOCUS       AX104333                  20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 525 from Patent WO0122972.
ACCESSION   AX104333
VERSION     AX104333.1  GI:13920530
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 525 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 3526
AX104584
LOCUS       AX104584                  20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 776 from Patent WO0122972.
ACCESSION   AX104584
VERSION     AX104584.1  GI:13920781
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 776 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1966 AATATTTACCTTGAAAAAAA 1985
              || ||  || ||||||||||
Db          1 AAAATCAACGTTGAAAAAAA 20


RESULT 3527
AX104663/c
LOCUS       AX104663                  20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 855 from Patent WO0122972.
ACCESSION   AX104663
VERSION     AX104663.1  GI:13920860
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 855 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              ||||||||||  |||  |||
Db         20 TTTTTTGAACGTCATGTTTT 1


RESULT 3528
AX133293
LOCUS       AX133293                  20 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 4511 from Patent WO0130362.
ACCESSION   AX133293
VERSION     AX133293.1  GI:14139603
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 4511 03-MAY-2001;
            IMMUSOL, INC. (US)
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VERSION     AX066409.1  GI:12544117
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gannon,F., Denger,S. and Flouriot,G.
  TITLE     Novel isoforms of the human estrogen receptor-_g(a)
  JOURNAL   Patent: WO 0100823-A 9 04-JAN-2001;
            EUROPEAN MOLECULAR BIOLOGY LABORATORY (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1666 TCACCCGCCCCTGGACTTCT 1685
              || | || |||| |||||||
Db          1 TCTCTCGGCCCTTGACTTCT 20


RESULT 3520
AX077095/c
LOCUS       AX077095                 20 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 19 from Patent WO0107580.
ACCESSION   AX077095
VERSION     AX077095.1  GI:13121714
KEYWORDS    .
SOURCE      Oryctolagus cuniculus (rabbit)
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1
  AUTHORS   Andrews,C.A. and Hartnett,J.R.
  TITLE     Thermostable nucleoside diphosphate kinase for nucleic acid
            detection
  JOURNAL   Patent: WO 0107580-A 19 01-FEB-2001;
            PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryctolagus cuniculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9986"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        886 CAAAGTGACAGTGGCTGAAG 905
              ||| ||||  |||| |||||
Db         20 CAAGGTGAACGTGGATGAAG 1


RESULT 3521
AX078027/c
LOCUS       AX078027                 20 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 41 from Patent WO0105435.
ACCESSION   AX078027
VERSION     AX078027.1  GI:13157782
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gleave,M.
  TITLE     Antisense therapy for hormone-regulated tumors
  JOURNAL   Patent: WO 0105435-A 41 25-JAN-2001;
            THE UNIVERSITY OF BRITISH COLUMBIA (CA) ; Miyake, Hideaki (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        543 CCCACCTCTCCGGGCTGGAG 562
              ||| | |||||| |||| ||
Db         20 CCCGCATCTCCGAGCTGAAG 1


RESULT 3522
AX078046/c
LOCUS       AX078046                 20 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 60 from Patent WO0105435.
ACCESSION   AX078046
VERSION     AX078046.1  GI:13157801
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gleave,M.
  TITLE     Antisense therapy for hormone-regulated tumors
  JOURNAL   Patent: WO 0105435-A 60 25-JAN-2001;
            THE UNIVERSITY OF BRITISH COLUMBIA (CA) ; Miyake, Hideaki (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAACCTGG 662
              ||| | |||| ||| |||||
Db         20 GGGGCCGGCCCAGAGCCTGG 1


RESULT 3523
AX099900
LOCUS       AX099900                 20 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 3 from Patent WO0119397.
ACCESSION   AX099900
VERSION     AX099900.1  GI:13538926
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Reddy,G.
  TITLE     Methods and compositions utilizing rad51
  JOURNAL   Patent: WO 0119397-A 3 22-MAR-2001;
            Pangene Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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  JOURNAL   Patent: US 6610481-A 6 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||| ||| ||| ||| |||
Db         20 GAAAGAAAGAAAGAAAGAAA 1


RESULT 3515
AR432267
LOCUS       AR432267                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 67 from patent US 6653133.
ACCESSION   AR432267
VERSION     AR432267.1  GI:40194540
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M., Marcusson,E.G. and Wyatt,J.
  TITLE     Antisense modulation of Fas mediated signaling
  JOURNAL   Patent: US 6653133-A 67 25-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        231 GCAGCAATGGGAATCCGCGG 250
              ||||||| || || | ||||
Db          1 GCAGCAAGGGAAAACAGCGG 20


RESULT 3516
AX010463/c
LOCUS       AX010463                 20 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 42 from Patent WO9958713.
ACCESSION   AX010463
VERSION     AX010463.1  GI:9997306
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Grohmann,L., Gerbling,K.P. and Lauter,F.R.
  TITLE     Method for detecting microorganisms in products
  JOURNAL   Patent: WO 9958713-A 42 18-NOV-1999;
            GROHMANN LUTZ (DE); BIOINSIDE GMBH (DE); GERBLING KLAUS PETER (DE);
            LAUTER FRANK ROMAN (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2427 TGGTGCACTTCTTACGACTT 2446
              ||||   ||| |||||||||
Db         20 TGGTTACCTTGTTACGACTT 1


RESULT 3517
AX048438
LOCUS       AX048438                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 37 from Patent WO0071747.
ACCESSION   AX048438
VERSION     AX048438.1  GI:12225602
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 37 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTT 2192
              |||||||||||||| |  | |
Db          1 TTTTTTTTTTTTTGAGGTGT 20


RESULT 3518
AX048438/c
LOCUS       AX048438                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 37 from Patent WO0071747.
ACCESSION   AX048438
VERSION     AX048438.1  GI:12225602
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 37 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAA 2798
              | |  | ||||||||||||||
Db         20 ACACCTCAAAAAAAAAAAAA 1


RESULT 3519
AX066409
LOCUS       AX066409                 20 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 9 from Patent WO0100823.
ACCESSION   AX066409
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            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of protein phosphatase 2 catalytic subunit
            beta expression
  JOURNAL   Patent: US 6602713-A 51 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1070 CTGACATCCTTAGTAGAAGG 1089
              || ||| | |||||||| ||
Db         20 CTTACAGCTTTAGTAGATGG 1


RESULT 3510
AR373514/c
LOCUS       AR373514                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 84 from patent US 6602713.
ACCESSION   AR373514
VERSION     AR373514.1  GI:40075643
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of protein phosphatase 2 catalytic subunit
            beta expression
  JOURNAL   Patent: US 6602713-A 84 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1765 TTAAGCTTTTTTTTTTGAA 1784
              |||  |||| |||| |||||
Db         20 TTATCCTTTATTTTATTGAA 1


RESULT 3511
AR373631/c
LOCUS       AR373631                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 23 from patent US 6602857.
ACCESSION   AR373631
VERSION     AR373631.1  GI:40076042
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M., Wyatt,J., Monia,B.P., Butler,M.M. and McKay,R.
  TITLE     Antisense modulation of PTP1B expression
  JOURNAL   Patent: US 6602857-A 23 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        903 AAGTACAGAGGCGACTGTCC 922
              | ||||||| || | ||||
Db         20 AGGTACAGAGACGTCAGTCC 1


RESULT 3512
AR373791/c
LOCUS       AR373791                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 183 from patent US 6602857.
ACCESSION   AR373791
VERSION     AR373791.1  GI:40076202
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M., Wyatt,J., Monia,B.P., Butler,M.M. and McKay,R.
  TITLE     Antisense modulation of PTP1B expression
  JOURNAL   Patent: US 6602857-A 183 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1590 ACTGGGAACCCCTCCTGGCC 1609
              ||||| | ||| ||||||  |
Db         20 ACTGGAAGCCCTTCCTGGTC 1


RESULT 3513
AR382158
LOCUS       AR382158                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from patent US 6610481.
ACCESSION   AR382158
VERSION     AR382158.1  GI:40090567
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Koch,J.E.
  TITLE     Cascade nucleic acid amplification reaction
  JOURNAL   Patent: US 6610481-A 5 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||| ||| ||| ||| |||
Db          1 GAAAGAAAGAAAGAAAGAAA 20


RESULT 3514
AR382159/c
LOCUS       AR382159                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6610481.
ACCESSION   AR382159
VERSION     AR382159.1  GI:40090568
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Koch,J.E.
  TITLE     Cascade nucleic acid amplification reaction
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DEFINITION  Sequence 10 from patent US 6596490.
ACCESSION   AR360422
VERSION     AR360422.1  GI:33767452
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 10 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3505
AR360423
LOCUS       AR360423                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6596490.
ACCESSION   AR360423
VERSION     AR360423.1  GI:33767453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 11 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3506
AR360424/c
LOCUS       AR360424                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 12 from patent US 6596490.
ACCESSION   AR360424
VERSION     AR360424.1  GI:33767454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 12 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3507
AR360426/c
LOCUS       AR360426                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 14 from patent US 6596490.
ACCESSION   AR360426
VERSION     AR360426.1  GI:33767456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 14 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3508
AR360429/c
LOCUS       AR360429                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 17 from patent US 6596490.
ACCESSION   AR360429
VERSION     AR360429.1  GI:33767459
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 17 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3509
AR373481/c
LOCUS       AR373481                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 51 from patent US 6602713.
ACCESSION   AR373481
VERSION     AR373481.1  GI:40075610
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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RESULT 3499
AR360397/c
LOCUS       AR360397                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 12 from patent US 6596489.
ACCESSION   AR360397
VERSION     AR360397.1  GI:33767427
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 12 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
             |||||||    |||||||||
Db         20 TTTTTTTAAAATTTTTTTTT 1


RESULT 3500
AR360399/c
LOCUS       AR360399                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 14 from patent US 6596489.
ACCESSION   AR360399
VERSION     AR360399.1  GI:33767429
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 14 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
             |||||||    |||||||||
Db         20 TTTTTTTACAATTTTTTTTT 1


RESULT 3501
AR360402/c
LOCUS       AR360402                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 17 from patent US 6596489.
ACCESSION   AR360402
VERSION     AR360402.1  GI:33767432
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 17 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
             |||||||    |||||||||
Db         20 TTTTTTTAGAATTTTTTTTT 1


RESULT 3502
AR360420
LOCUS       AR360420                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6596490.
ACCESSION   AR360420
VERSION     AR360420.1  GI:33767450
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 8 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
             |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3503
AR360421
LOCUS       AR360421                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6596490.
ACCESSION   AR360421
VERSION     AR360421.1  GI:33767451
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 9 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
             |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3504
AR360422
LOCUS       AR360422                  20 bp    DNA     linear   PAT 17-AUG-2003
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RESULT 3494
AR343102
LOCUS       AR343102                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6576759.
ACCESSION   AR343102
VERSION     AR343102.1  GI:33738513
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zeng,H., Reddy,G., Vallerga,A. and Zarling,D.A.
  TITLE     Antisense inhibition of RAD51
  JOURNAL   Patent: US 6576759-A 6 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        563 GCGGGCGCGGTGAGCGCCCG 582
              ||||||| ||   |||||||
Db          1 GCGGGCGTGGCACGCGCCCG 20


RESULT 3495
AR360393
LOCUS       AR360393                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6596489.
ACCESSION   AR360393
VERSION     AR360393.1  GI:33767423
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 8 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3496
AR360394
LOCUS       AR360394                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6596489.
ACCESSION   AR360394
VERSION     AR360394.1  GI:33767424
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 9 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3497
AR360395
LOCUS       AR360395                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 10 from patent US 6596489.
ACCESSION   AR360395
VERSION     AR360395.1  GI:33767425
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 10 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20


RESULT 3498
AR360396
LOCUS       AR360396                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6596489.
ACCESSION   AR360396
VERSION     AR360396.1  GI:33767426
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 11 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||    |||||||||
Db          1 TTTTTTTAAAATTTTTTTTT 20
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                  |||||||| |    |||||||
Db          20 AGGAGAGTGGCACAGGAACA 1


RESULT 3489
AR304441/c
LOCUS       AR304441                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 66 from patent US 6544784.
ACCESSION   AR304441
VERSION     AR304441.1  GI:31693589
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bullerdiek,J., Van de Ven,W.J.M., Schoenmakers,H.F.P.M. and Mols,R.
  TITLE     Multiple-tumor aberrant growth genes
  JOURNAL   Patent: US 6544784-A 66 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2672 CAGTGTGTGTGGGTGAAATG 2691
              || |||||||| ||| |||
Db         20 CATTGTGTGTGCCTGAGATG 1


RESULT 3490
AR311041
LOCUS       AR311041                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1578 from patent US 6559294.
ACCESSION   AR311041
VERSION     AR311041.1  GI:31704467
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 1578 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        903 AAGTACAGAGGCGACTGTCC 922
              ||| || |||||||  | |||
Db          1 AAGAACGGAGGCGATTATCC 20


RESULT 3491
AR311824/c
LOCUS       AR311824                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2361 from patent US 6559294.
ACCESSION   AR311824
VERSION     AR311824.1  GI:31705250
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2361 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1114 CTTTGCCTATGTCTGTGAAG 1133
              ||||||||||    ||||||
Db         20 CTTTGCCTATAGGGGTGAAG 1


RESULT 3492
AR313463/c
LOCUS       AR313463                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4000 from patent US 6559294.
ACCESSION   AR313463
VERSION     AR313463.1  GI:31706889
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 4000 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1310 TTGGAGACGAACATACAGAA 1329
              |||  | |||||  |||||||
Db         20 TTGCTGCCGAACCTACAGAA 1


RESULT 3493
AR313846/c
LOCUS       AR313846                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4383 from patent US 6559294.
ACCESSION   AR313846
VERSION     AR313846.1  GI:31707272
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 4383 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1114 CTTTGCCTATGTCTGTGAAG 1133
              |||| ||||||| || | ||
Db         20 CTTTCCCTATGTATGGGGAG 1
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Qy       1482 ACAAAACCCTGGAGAAAATG 1501
              |||| | ||||||| || ||
Db         20 ACAACATCCTGGAGGAAGTG 1
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RESULT 3484
AR294017
LOCUS       AR294017                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5752 from patent US 6537751.
ACCESSION   AR294017
VERSION     AR294017.1  GI:31681301
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 5752 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1535 AGGTTAGGAGAGTAGGGAAG 1554
              || | ||||| | |||||||
Db          1 AGATGAGGAGTGGAGGGAAG 20
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RESULT 3485
AR297173
LOCUS       AR297173                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 8908 from patent US 6537751.
ACCESSION   AR297173
VERSION     AR297173.1  GI:31684457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 8908 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        970 AGCCAAATCGAAAAATGGAG 989
              |||||||| | |||| |||
Db          1 AGCCAAATGAACAAATAGAG 20
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RESULT 3486
AR298189
LOCUS       AR298189                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 9924 from patent US 6537751.
ACCESSION   AR298189
VERSION     AR298189.1  GI:31685473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 9924 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1493 GAGAAAATGGAGAAACACAG 1512
              || | || ||||| ||||||
Db          1 GATATAAAGGAGATACACAG 20
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RESULT 3487
AR299111/c
LOCUS       AR299111                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 10846 from patent US 6537751.
ACCESSION   AR299111
VERSION     AR299111.1  GI:31686395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 10846 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2124 GAAACTTGTAGAAACGAAGC 2143
              |||||   || |||||||||
Db         20 GAAACCACTATAAACGAAGC 1
```

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RESULT 3488
AR300314/c
LOCUS       AR300314                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 116 from patent US 6537775.
ACCESSION   AR300314
VERSION     AR300314.1  GI:31687733
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tournier-Lasserve,E., Joutel,A., Bousser,M.-G. and Bach,J.-F.
  TITLE     Gene involved in cadasil, method of diagnosis and therapeutic
            application
  JOURNAL   Patent: US 6537775-A 116 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAACA 1559
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                    /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        247 GCGGGTCCCCCACCTCTCCT 266
              ||| | ||  ||||||||||
Db         20 GCGCGGCCTGCACCTCTCCT 1


RESULT 3479
AR262371/c
LOCUS       AR262371                  20 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 7 from patent US 6323184.
ACCESSION   AR262371
VERSION     AR262371.1  GI:28073802
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zalewski,A. and Shi,Y.
  TITLE     Arteriovenous and venous graft treatments: methods and compositions
  JOURNAL   Patent: US 6323184-A 7 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        653 GAGAACCTGGGGCTCCACGA 672
              |||  ||||| ||||||  ||
Db         20 GAGCCCCTGGTGCTCCATGA 1


RESULT 3480
AR262372/c
LOCUS       AR262372                  20 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 8 from patent US 6323184.
ACCESSION   AR262372
VERSION     AR262372.1  GI:28073803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zalewski,A. and Shi,Y.
  TITLE     Arteriovenous and venous graft treatments: methods and compositions
  JOURNAL   Patent: US 6323184-A 8 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        653 GAGAACCTGGGGCTCCACGA 672
              |||  ||||| ||||||  ||
Db         20 GAGCCCCTGGTGCTCCATGA 1


RESULT 3481
AR266944/c
LOCUS       AR266944                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 89 from patent US 6495348.
ACCESSION   AR266944
VERSION     AR266944.1  GI:29696326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sherman,D.H., Mao,Y., Varoglu,M., He,M. and Sheldon,P.
  TITLE     Mitomycin biosynthetic gene cluster
  JOURNAL   Patent: US 6495348-A 89 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        507 TGCCCTCGCACCACGGGCGC 526
              ||| | |||| ||||| |||
Db         20 TGCGCGCGCAGCACGGACGC 1


RESULT 3482
AR266945
LOCUS       AR266945                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 90 from patent US 6495348.
ACCESSION   AR266945
VERSION     AR266945.1  GI:29696327
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sherman,D.H., Mao,Y., Varoglu,M., He,M. and Sheldon,P.
  TITLE     Mitomycin biosynthetic gene cluster
  JOURNAL   Patent: US 6495348-A 90 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        507 TGCCCTCGCACCACGGGCGC 526
              ||| | |||| ||||| |||
Db          1 TGCGCGCGCAGCACGGACGC 20


RESULT 3483
AR277762/c
LOCUS       AR277762                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 2 from patent US 6511800.
ACCESSION   AR277762
VERSION     AR277762.1  GI:29711579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Singh,I.
  TITLE     Methods of treating nitric oxide and cytokine mediated disorders
  JOURNAL   Patent: US 6511800-A 2 28-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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  TITLE      Immunostimulatory nucleic acid molecules for activating dendritic
             cells
  JOURNAL    Patent: US 6429199-A 99 06-AUG-2002;
FEATURES               Location/Qualifiers
     source            1. .20
                       /organism="unknown"
                       /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1966 AATATTTACCTTGAAAAAAA 1985
              || ||  || ||||||||||
Db          1 AAAATCAACGTTGAAAAAAA 20


RESULT 3474
AR232339/c
LOCUS       AR232339                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 34 from patent US 6455308.
ACCESSION   AR232339
VERSION     AR232339.1  GI:27274331
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Freier,S.M.
  TITLE     Antisense modulation of serum amyloid A4 expression
  JOURNAL   Patent: US 6455308-A 34 24-SEP-2002;
FEATURES               Location/Qualifiers
     source            1. .20
                       /organism="unknown"
                       /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1390 GGTGTCTGCCCTGCAGAACT 1409
              ||||||||  ||||  ||||
Db         20 GGTGTCTGGGCTGCTAAACT 1


RESULT 3475
AR234640
LOCUS       AR234640                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 81 from patent US 6458591.
ACCESSION   AR234640
VERSION     AR234640.1  GI:27277347
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of phosphorylase kinase Alpha 2 expression
  JOURNAL   Patent: US 6458591-A 81 01-OCT-2002;
FEATURES               Location/Qualifiers
     source            1. .20
                       /organism="unknown"
                       /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2455 CATGGGATCCAATTTTAATA 2474
              |||||||  |||  |||  ||  |
Db          1 CATGGGAGCCATTTTAAACA 20


RESULT 3476
AR234698/c
LOCUS       AR234698                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 14 from patent US 6458838.
ACCESSION   AR234698
VERSION     AR234698.1  GI:27277476
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Smith,K.D.
  TITLE     Adrenoleukodystrophy treatments
  JOURNAL   Patent: US 6458838-A 14 01-OCT-2002;
FEATURES               Location/Qualifiers
     source            1. .20
                       /organism="unknown"
                       /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        793 TCAGAAGGAGCTGGTGGGGG 812
              ||||  ||  ||||||  ||| |
Db         20 TCAGGAGAAGCTGGAGGGAG 1


RESULT 3477
AR255963/c
LOCUS       AR255963                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 22 from patent US 6482644.
ACCESSION   AR255963
VERSION     AR255963.1  GI:27305222
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense modulation of dual specific phosphatase 8 expression
  JOURNAL   Patent: US 6482644-A 22 19-NOV-2002;
FEATURES               Location/Qualifiers
     source            1. .20
                       /organism="unknown"
                       /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        532 CGGCCTACTGCCCCACCTCT 551
              | ||  | |||||  |||||||
Db         20 CCGCATCCTGCCTCACCTCT 1


RESULT 3478
AR255975/c
LOCUS       AR255975                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 34 from patent US 6482644.
ACCESSION   AR255975
VERSION     AR255975.1  GI:27305234
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense modulation of dual specific phosphatase 8 expression
  JOURNAL   Patent: US 6482644-A 34 19-NOV-2002;
FEATURES               Location/Qualifiers
     source            1. .20
                       /organism="unknown"
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REFERENCE   1  (bases 1 to 20)
  AUTHORS   Makino,Y., Abe,Y., Takagi,M., Takenaka,S., Yamashita,K. and
            Ogawa,M.
  TITLE     Protection of partial complementary nucleic acid fragment using a
            electroconductive chip and intercalator
  JOURNAL   Patent: US 6399305-A 6 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||    ||||||||
Db          1 TTTTTTTTAAAATTTTTTT 20


RESULT 3469
AR212007/c
LOCUS       AR212007                 20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 63 from patent US 6399378.
ACCESSION   AR212007
VERSION     AR212007.1  GI:21515479
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ward,D.T. and Watt,A.T.
  TITLE     Antisense modulation of RECQL2 expression
  JOURNAL   Patent: US 6399378-A 63 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1366 TGGCAGCCAGGCCATCTGTG 1385
              |||| | ||||  |||||||
Db         20 TGGCTGTCAGGTTATCTGTG 1


RESULT 3470
AR217899
LOCUS       AR217899                 20 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 17 from patent US 6417169.
ACCESSION   AR217899
VERSION     AR217899.1  GI:23318024
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wright,J.A., Young,A.H. and Lee,Y.S.
  TITLE     Insulin-like growth factor II antisense oligonucleotide sequences
            and methods of using same to inhibit cell growth
  JOURNAL   Patent: US 6417169-A 17 09-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        251 GTCCCCCACCTCTCCTCCGC 270
              |||| ||| ||| || ||||
Db          1 GTCCACCAGCTCCCCGCCGC 20


RESULT 3471
AR220184
LOCUS       AR220184                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 49 from patent US 6423543.
ACCESSION   AR220184
VERSION     AR220184.1  GI:23324627
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Marcotte,P.A. and Cowsert,L.M.
  TITLE     Antisense modulation of hepsin expression
  JOURNAL   Patent: US 6423543-A 49 23-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1627 ACCTACCTTACTATTTAAAG 1646
              |||  | ||| |||||||||
Db          1 ACCATCTTTATTATTTAAAG 20


RESULT 3472
AR221789
LOCUS       AR221789                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 1 from patent US 6428781.
ACCESSION   AR221789
VERSION     AR221789.1  GI:23328892
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sakano,K., Higashihashi,N. and Hashimoto,R.
  TITLE     Composition of an endogenous insulin-like growth factor-II
            derivative
  JOURNAL   Patent: US 6428781-A 1 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        628 CGCCCTGGATGCCGCGGGCC 647
              |||| || || ||||| |||
Db          1 CGCCATGCATCCCGCGCGCC 20


RESULT 3473
AR222265
LOCUS       AR222265                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 99 from patent US 6429199.
ACCESSION   AR222265
VERSION     AR222265.1  GI:23329730
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Krieg,A.M. and Hartmann,G.
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VERSION     I88040.1  GI:3407980
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brown,S.Joel., Dattagupta,N. and Naidu,Y.M.
  TITLE     Method for inhibiting cellular proliferation using antisense
            oligonucleotides to interleukin-6 receptor mRNA
  JOURNAL   Patent: US 5716846-A 18 10-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAGCAGG 470
              | |||| |||| || |||||
Db         20 CTCAGGAAGCCGGCTGCAGG 1


RESULT 3464
AR199794
LOCUS       AR199794                 20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 55 from patent US 6355482.
ACCESSION   AR199794
VERSION     AR199794.1  GI:20249868
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Freier,S.M.
  TITLE     Antisense inhibition of integrin beta 4 binding protein expression
  JOURNAL   Patent: US 6355482-A 55 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        351 CTCCCTACCAGCAGCTGGCC 370
              || ||||| |||| |||| |
Db          1 CTTCCTACTAGCACCTGGTC 20


RESULT 3465
AR203118
LOCUS       AR203118                 20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 37 from patent US 6365354.
ACCESSION   AR203118
VERSION     AR203118.1  GI:21499424
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Wyatt,J.
  TITLE     Antisense modulation of lysophospholipase I expression
  JOURNAL   Patent: US 6365354-A 37 02-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1782 GAACCCCATTCTTTCCTTCT 1801
              |||  ||||||||  |||||
Db          1 GAATGCCATTCTTCACTTCT 20


RESULT 3466
AR203152/c
LOCUS       AR203152                 20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 71 from patent US 6365354.
ACCESSION   AR203152
VERSION     AR203152.1  GI:21499467
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Wyatt,J.
  TITLE     Antisense modulation of lysophospholipase I expression
  JOURNAL   Patent: US 6365354-A 71 02-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2344 CCGTGGAGGTTCTGTATTTT 2363
              || || ||  ||||||||||
Db         20 CCATGCAGTGTCTGTATTTT 1


RESULT 3467
AR203166
LOCUS       AR203166                 20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 85 from patent US 6365354.
ACCESSION   AR203166
VERSION     AR203166.1  GI:21499484
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Wyatt,J.
  TITLE     Antisense modulation of lysophospholipase I expression
  JOURNAL   Patent: US 6365354-A 85 02-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2512 CATAAGGTTTTATTCATATA 2531
              |||||| || | |||| |||
Db          1 CATAAGTTTGTTTTCAAATA 20


RESULT 3468
AR211368
LOCUS       AR211368                 20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6399305.
ACCESSION   AR211368
VERSION     AR211368.1  GI:21514671
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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```
DEFINITION  Novel protein and process for producing it.
ACCESSION   E39963
VERSION     E39963.1  GI:18633313
KEYWORDS    JP 2001078777-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Goto,M., Tomoyasu,M., Morita,S. and Yamaguchi,K.
  TITLE     Novel protein and process for producing it
  JOURNAL   Patent: JP 2001078777-A 5 27-MAR-2001;
            SNOW BRAND MILK PROD CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001078777-A/5
            PD   27-MAR-2001
            PF   16-SEP-1999 JP 1999262777
            PR
            PI   MASAAKI GOTO,MASATAKU TOMOYASU,SHUJI MORITA,KYOJI YAMAGUCHI PC
              C12N15/09,A61K38/00,A61P3/04,C07K14/47,C12P21/02,C12N15/00, PC
            A61K37/02
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        712 CCAGCACCTGTTGCTGCACG 731
              | || || || |||||||||
Db          1 CAAGGACTTGCTGCTGCACG 20


RESULT 3460
E58734
LOCUS       E58734                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Osteogenesis promoter.
ACCESSION   E58734
VERSION     E58734.1  GI:18629898
KEYWORDS    JP 2000229879-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kinozaki,M., Goto,M., Yamaguchi,K., Morita,S. and Tomoyasu,M.
  TITLE     Osteogenesis promoter
  JOURNAL   Patent: JP 2000229879-A 5 22-AUG-2000;
            SNOW BRAND MILK PROD CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000229879-A/5
            PD   22-AUG-2000
            PF   10-FEB-1999 JP 1999033261
            PR
            PI   MASAHIKO KINOZAKI,MASAAKI GOTO,KYOJI YAMAGUCHI,SHUJI MORITA,
            PI   MASATAKU TOMOYASU
            PC
            A61K38/00,A61K31/00//C07K14/435,C12N15/09,C12P21/02,(C12P21/02, PC
              C12R1:91),
            PC   A61K37/02,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        712 CCAGCACCTGTTGCTGCACG 731
              | || || || |||||||||
Db          1 CAAGGACTTGCTGCTGCACG 20


RESULT 3461
I19926/c
LOCUS       I19926                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 23 from patent US 5512462.
ACCESSION   I19926
VERSION     I19926.1  GI:1600281
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cheng,S.
  TITLE     Methods and reagents for the polymerase chain reaction
            amplification of long DNA sequences
  JOURNAL   Patent: US 5512462-A 23 30-APR-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        707 GACGACCAGCACCTGTTGCT 726
              || | ||||| |||||| ||
Db         20 GATGCCCAGCGCCTGTTTCT 1


RESULT 3462
I72480/c
LOCUS       I72480                    20 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 64 from patent US 5683987.
ACCESSION   I72480
VERSION     I72480.1  GI:3008619
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Smith,L.J.
  TITLE     Therapeutic oligonucleotides targeting the human MDR1 and MRP genes
  JOURNAL   Patent: US 5683987-A 64 04-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        415 CGCCGCCGCCATCAACCCCC 434
              |||||||  |||| ||| |
Db         20 CGCCGCCATCATCATCCCGC 1


RESULT 3463
I88040/c
LOCUS       I88040                    20 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 18 from patent US 5716846.
ACCESSION   I88040
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            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1337 TCTCATTTCAGCCTGATTAC 1356
              |||| || |||||||| | |
Db         20 TCTCCTTCCAGCCTGAGTGC 1


RESULT 3456
E29890/c
LOCUS       E29890                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  HIV cofactor inhibitor.
ACCESSION   E29890
VERSION     E29890.1  GI:13021285
KEYWORDS    JP 1999292795-A/44.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hiroshi,T., Naoki,Y., Toru,K., Kazuyuki,T. and Akira,W.
  TITLE     HIV cofactor inhibitor
  JOURNAL   Patent: JP 1999292795-A 44 26-OCT-1999;
            YAMANOUCHI PHARMACEUT CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999292795-A/44
            PD   26-OCT-1999
            PF   02-APR-1998 JP 1998125452
            PR
            PI   HIROSHI TAKAHISA,NAOKI YAMAMOTO,TORU KIMURA,KAZUYUKI TAKAI, PI
              AKIRA WADA
            PC   A61K48/00,A61K31/70,A61K31/70,C12N15/09,C12N15/00 CC
            FH   Key             Location/Qualifiers
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            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2149 GATTGATTTTTTTCTCCTTT 2168
              ||||| || ||||||| | |
Db         20 GATTGTTTATTTTCTCTTCT 1


RESULT 3457
E29952
LOCUS       E29952                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  HIV cofactor inhibitor.
ACCESSION   E29952
VERSION     E29952.1  GI:13021347
KEYWORDS    JP 1999292795-A/106.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hiroshi,T., Naoki,Y., Toru,K., Kazuyuki,T. and Akira,W.
  TITLE     HIV cofactor inhibitor
  JOURNAL   Patent: JP 1999292795-A 106 26-OCT-1999;
            YAMANOUCHI PHARMACEUT CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999292795-A/106
            PD   26-OCT-1999
            PF   02-APR-1998 JP 1998125452
            PR
            PI   HIROSHI TAKAHISA,NAOKI YAMAMOTO,TORU KIMURA,KAZUYUKI TAKAI, PI
              AKIRA WADA
            PC   A61K48/00,A61K31/70,A61K31/70,C12N15/09,C12N15/00 CC
            FH   Key             Location/Qualifiers
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            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1776 TTTTTTGAACCCCATTCTTT 1795
              || | |||||||||| || |
Db          1 TTGTCTGAACCCCATCCTCT 20


RESULT 3458
E39288
LOCUS       E39288                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel protein and process for producing the same.
ACCESSION   E39288
VERSION     E39288.1  GI:18628919
KEYWORDS    JP 2000239299-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Goto,M., Tomoyasu,M., Yamaguchi,K., Kinozaki,M., Shima,N.,
            Yasuda,N. and Nakagawa,N.
  TITLE     Novel protein and process for producing the same
  JOURNAL   Patent: JP 2000239299-A 5 05-SEP-2000;
            SNOW BRAND MILK PROD CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000239299-A/5
            PD   05-SEP-2000
            PF   15-FEB-1999 JP 1999036225
            PR
            PI   MASAAKI GOTO,MASAAKI TOMOYASU,KYOJI YAMAGUCHI, PI   MASAHIKO
            KINOZAKI,
            PI   NOBUYUKI SHIMA,NAOTAKA YASUDA,NOBUAKI NAKAGAWA PC
            C07K14/47,C12N5/10,C12N15/09,C12P21/02//A61K31/00,A61K31/00, PC
            A61K38/00,
            PC   (C12P21/02,C12R1:91),C12N5/00,C12N15/00,A61K37/02 CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        712 CCAGCACCTGTTGCTGCACG 731
              | || || || |||||||||
Db          1 CAAGGACTTGCTGCTGCACG 20


RESULT 3459
E39963
LOCUS       E39963                    20 bp    DNA     linear   PAT 31-JAN-2002
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            PN   JP 2002537833-A/72
            PD   12-NOV-2002
            PF   10-MAR-2000 JP 2000603359
            PR   12-MAR-1999 US    09/266965
            PI   DAVID H SHERMAN,YINGQING MAO,MUSTAFA VAROGLU,MIN HE,PAUL C  PI
              SHELDON
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P17/10 PC
            ,C12Q1/68,G01N33/53,
            PC   G01N33/566//C12N9/00,(C12P17/10,C12R1:465),C12N15/00,C12N5/00
            CC   Mitomycin biosynthetic gene cluster
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Amycolatopsis mediterranei'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Amycolatopsis mediterranei"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:33910"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        507 TGCCCTCGCACCACGGGCGC 526
              ||| | |||| ||||| |||
Db         20 TGCGCGCGCAGCACGGACGC 1


RESULT 3453
BD269459
LOCUS       BD269459                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Mitomycin biosynthetic gene cluster.
ACCESSION   BD269459
VERSION     BD269459.1  GI:33079227
KEYWORDS    JP 2002537833-A/73.
SOURCE      Amycolatopsis mediterranei
  ORGANISM  Amycolatopsis mediterranei
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sherman,D.H., Mao,Y., Varoglu,M., He,M. and Sheldon,P.C.
  TITLE     Mitomycin biosynthetic gene cluster
  JOURNAL   Patent: JP 2002537833-A 73 12-NOV-2002;
            REGENTS OF THE UNIVERSITY OF MINNESOTA
CCMMENT     OS   Amycolatopsis mediterranei
            PN   JP 2002537833-A/73
            PD   12-NOV-2002
            PF   10-MAR-2000 JP 2000603359
            PR   12-MAR-1999 US    09/266965
            PI   DAVID H SHERMAN,YINGQING MAO,MUSTAFA VAROGLU,MIN HE,PAUL C  PI
              SHELDON
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P17/10 PC
            ,C12Q1/68,G01N33/53,
            PC   G01N33/566//C12N9/00,(C12P17/10,C12R1:465),C12N15/00,C12N5/00
            CC   Mitomycin biosynthetic gene cluster
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Amycolatopsis mediterranei'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Amycolatopsis mediterranei"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:33910"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        507 TGCCCTCGCACCACGGGCGC 526
              ||| | |||| ||||| |||
Db          1 TGCGCGCGCAGCACGGACGC 20


RESULT 3454
BD272643
LOCUS       BD272643                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide modulation of STAT3 expression.
ACCESSION   BD272643
VERSION     BD272643.1  GI:33082411
KEYWORDS    JP 2002541784-A/43.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Karras,J.G.
  TITLE     Antisense oligonucleotide modulation of STAT3 expression
  JOURNAL   Patent: JP 2002541784-A 43 10-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002541784-A/43
            PD   10-DEC-2002
            PF   06-APR-2000 JP 2000611544
            PR   08-APR-1999 US    09/288461
            PI   JAMES G KARRAS
            PC   C12N15/09,A61K31/711,A61K48/00,A61P29/00,A61P29/00,A61P35/00,
            PC   A61P37/02,
            PC   A61P43/00,C12N5/06,C12Q1/02,C12N15/00,C12N5/00 CC   Antisense
            oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1741 TGACAAGTACTGGCTCTTTA 1760
              ||||||| | ||| ||| ||
Db          1 TGACAAGGAGTGGGTCTCTA 20


RESULT 3455
E16129/c
LOCUS       E16129                   20 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  PCR primer for amplifying cDNA to mRNA.
ACCESSION   E16129
VERSION     E16129.1  GI:5710812
KEYWORDS    JP 1998136998-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Otsuka,Y., Shimazu,M., Miura,M. and Hatake,H.
  TITLE     DETERMINATION OF MESSENGER RNA
  JOURNAL   Patent: JP 1998136998-A 5 26-MAY-1998;
            MITSUBISHI KAGAKU B C L:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1998136998-A/5
            PD   26-MAY-1998
            PF   11-NOV-1996 JP 1996299136
            PI   OTSUKA YOSHIHIKO, SHIMAZU MITSUNOBU, MIURA MASAKAZU, PI
            HATAKE HIROMI
            PC   C12Q1/68,C07H21/02,C07H21/04//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
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  TITLE     Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha)
  JOURNAL   Patent: JP 2002526125-A 217 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526125-A/217
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574737
            PR   05-OCT-1998 US    09/166186,18-MAY-1999 US    09/313932 PI
            BRENDA F BAKER,FRANK C BENNETT,MADELINE M BUTLER,WILLIAM J  PI
            SHANAHAN JR
            PC   C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/
            PC   00,A61P1/16,
            PC   A61P1/18,A61P3/10,A61P17/00,A61P17/04,A61P29/00,A61P31/00, PC
             C07H21/02,
            PC   C07H21/04,C12N15/00
            CC   Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1453 CCCTGGAGACCAGAGTCCAG 1472
              ||||||   ||||| |||||
Db          1 CCCTGGTCTCCAGATTCCAG 20


RESULT 3450
BD249348
LOCUS       BD249348                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of FAS mediated signaling.
ACCESSION   BD249348
VERSION     BD249348.1  GI:33059118
KEYWORDS    JP 2002540812-A/63.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense modulation of FAS mediated signaling
  JOURNAL   Patent: JP 2002540812-A 63 03-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002540812-A/63
            PD   03-DEC-2002
            PF   10-APR-2000 JP 2000610483
            PR   12-APR-1999 US    09/290640
            PI   NICHOLAS M DEAN,ERIC G MARCUSSON
            PC   C12N15/09,A61K31/7088,A61K31/7115,A61K31/712,A61K31/7125, PC
            A61K48/00,
            PC   A61P1/16,A61P29/00,A61P35/00,A61P37/00,A61P43/00//C12N5/06, PC
              C12N15/00,
            PC   C12N5/00
            CC   Synthetic Sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       231 GCAGCAATGGGAATCCGCGG 250
             ||||||| || || | ||||
Db         1 GCAGCAAGGGAAAACAGCGG 20


RESULT 3451
BD251480
LOCUS       BD251480                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of in vitro detection of target substance in specimen
            involving labeling of the target substance with reporter gene and
            sequence needed for the in vitro expression thereof.
ACCESSION   BD251480
VERSION     BD251480.1  GI:33061250
KEYWORDS    JP 2002531143-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dautel,S., Persillon,C., Dupret,D., Masson,J.M. and Lefevre,F.
  TITLE     Method of in vitro detection of target substance in specimen
            involving labeling of the target substance with reporter gene and
            sequence needed for the in vitro expression thereof
  JOURNAL   Patent: JP 2002531143-A 8 24-SEP-2002;
            PROTEUS
COMMENT     OS   Artificial Sequence
            PN   JP 2002531143-A/8
            PD   24-SEP-2002
            PF   08-DEC-1999 JP 2000586946
            PR   08-DEC-1998 FR     98/15489
            PI   SANDRINE DAUTEL,CECILE PERSILLON,DANIEL DUPRET,JEAN MICHEL  PI
              MASSON,
            PI   FABRICE LEFEVRE
            PC   C12Q1/68,C12Q1/48,G01N33/50,G01N33/68//C12N15/09,C12N15/09, PC
              C12N15/00,
            PC   C12N15/00
            CC   PADPCR 5' Oligonucleotide
            CC   PADPCR 5' Oligonucleotide
            FH   Key             Location/Qualifiers
            FT   misc_feature    (1). .(20).
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1343 TTCAGCCTGATTACCCACGG 1362
              ||||||  |||| ||||| |
Db          1 TTCAGCAGGATTCCCCACAG 20


RESULT 3452
BD269458/c
LOCUS       BD269458                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Mitomycin biosynthetic gene cluster.
ACCESSION   BD269458
VERSION     BD269458.1  GI:33079226
KEYWORDS    JP 2002537833-A/72.
SOURCE      Amycolatopsis mediterranei
  ORGANISM  Amycolatopsis mediterranei
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sherman,D.H., Mao,Y., Varoglu,M., He,M. and Sheldon,P.C.
  TITLE     Mitomycin biosynthetic gene cluster
  JOURNAL   Patent: JP 2002537833-A 72 12-NOV-2002;
            REGENTS OF THE UNIVERSITY OF MINNESOTA
COMMENT     OS   Amycolatopsis mediterranei
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP beta expression
  JOURNAL   Patent: US 6271030-A 18 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          50 CGCGGCGGGGGCGGCGGCAG 69
               | |||| | |||||| ||||
Db          20 CCCGGCAGCGGCGGCAGCAG 1


RESULT 3445
AR163962
LOCUS       AR163962                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 160 from patent US 6271030.
ACCESSION   AR163962
VERSION     AR163962.1  GI:16234833
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP beta expression
  JOURNAL   Patent: US 6271030-A 160 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         562 GGCGGGCGCGGTGAGCGCCC 581
               ||||||||||   ||| ||
Db           1 GGCGGGCGCGGCCGGCGGCC 20


RESULT 3446
AR164029/c
LOCUS       AR164029                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 228 from patent US 6271030.
ACCESSION   AR164029
VERSION     AR164029.1  GI:16234940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP beta expression
  JOURNAL   Patent: US 6271030-A 228 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        2166 TTTTTTTTTTTTTTTTTTT 2185
               |||||  |||| ||||| ||
Db          20 TTTTTGGTTTTGTTTTTGTT 1


RESULT 3447
AR173039
LOCUS       AR173039                 20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 164 from patent US 6303374.
ACCESSION   AR173039
VERSION     AR173039.1  GI:17912530
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zhang,H. and Cowsert,L.M.
  TITLE     Antisense modulation of caspase 3 expression
  JOURNAL   Patent: US 6303374-A 164 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        1742 GACAAGTACTGGCTCTTTAT 1761
               ||||  |||| |||| ||||
Db           1 GACAGTTACTTGCTCCTTAT 20


RESULT 3448
AR176812
LOCUS       AR176812                 20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 67 from patent US 6312900.
ACCESSION   AR176812
VERSION     AR176812.1  GI:17919167
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of activating protein 1
  JOURNAL   Patent: US 6312900-A 67 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         632 CTGGATGCCGCGGGCCTGGC 651
               ||||||||||   |||| ||
Db           1 CTGGATGCCGGCTGCCTTGC 20


RESULT 3449
BD228014
LOCUS       BD228014                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha).
ACCESSION   BD228014
VERSION     BD228014.1  GI:33037784
KEYWORDS    JP 2002526125-A/217.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,F.C., Butler,M.M. and Jr,W.J.S.
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 354 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1818 AAGTTTTAGAATCTTTTAAA 1837
              || | |||||  ||||||||
Db         20 AAATCTTAGAGCCTTTTAAA 1


RESULT 3440
AR158929
LOCUS       AR158929                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 551 from patent US 6251588.
ACCESSION   AR158929
VERSION     AR158929.1  GI:16221337
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 551 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTT 2178
              || ||  |||||| ||||||
Db          1 TTACTGATTTTTTCTTTTTT 20


RESULT 3441
AR159152/c
LOCUS       AR159152                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 774 from patent US 6251588.
ACCESSION   AR159152
VERSION     AR159152.1  GI:16221728
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 774 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              ||| | || ||||||| ||||
Db         20 TGACAGAAGAAAAAATAAAA 1


RESULT 3442
AR159153/c
LOCUS       AR159153                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 775 from patent US 6251588.
ACCESSION   AR159153
VERSION     AR159153.1  GI:16221729
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 775 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              |||| | || ||||||| |||
Db         20 TTGACAGAAGAAAAAATAAA 1


RESULT 3443
AR159154/c
LOCUS       AR159154                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 776 from patent US 6251588.
ACCESSION   AR159154
VERSION     AR159154.1  GI:16221730
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 776 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2801
              ||||| | || ||||||  ||
Db         20 ATTGACAGAAGAAAAAATAA 1


RESULT 3444
AR163820/c
LOCUS       AR163820                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 18 from patent US 6271030.
ACCESSION   AR163820
VERSION     AR163820.1  GI:16234587
KEYWORDS    .
SOURCE      Unknown.
```

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ACCESSION   AR130120
VERSION     AR130120.1  GI:14118017
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Popoff,I., Brown-Driver,V.L. and Cowsert,L.M.
  TITLE     Antisense inhibition of e2f transcription factor 1 expression
  JOURNAL   Patent: US 6187587-A 23 13-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        646 CCTGGCCGAGAACCTGGGGC 665
              ||||||||||| |    ||||
Db         20 CCTGGCCGAGAGCAGTGGGC 1


RESULT 3435
AR136423
LOCUS       AR136423                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 18 from patent US 6136604.
ACCESSION   AR136423
VERSION     AR136423.1  GI:14477095
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P. and Wyatt,J.
  TITLE     Antisense inhibition of methionine aminopeptidase 2 expression
  JOURNAL   Patent: US 6136604-A 18 24-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2160 TTCTCCTTTTTTTTTTTTTT 2179
              |||| |||||| || || ||
Db          1 TTCTTCTTTTTCTTCTTCTT 20


RESULT 3436
AR143173
LOCUS       AR143173                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 67 from patent US 6204055.
ACCESSION   AR143173
VERSION     AR143173.1  GI:15104459
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M. and Marcusson,E.G.
  TITLE     Antisense inhibition of Fas mediated signaling
  JOURNAL   Patent: US 6204055-A 67 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        231 GCAGCAATGGGAATCCGCGG 250
              ||||||| || || | ||||
Db          1 GCAGCAAGGGAAAACAGCGG 20


RESULT 3437
AR150141
LOCUS       AR150141                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 217 from patent US 6228642.
ACCESSION   AR150141
VERSION     AR150141.1  GI:15114732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-(.alpha.) (TNF-.alpha.) expression
  JOURNAL   Patent: US 6228642-A 217 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1453 CCCTGGAGACCAGAGTCCAG 1472
              ||||||   ||||| |||||
Db          1 CCCTGGTCTCCAGATTCCAG 20


RESULT 3438
AR153094/c
LOCUS       AR153094                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 96 from patent US 6235480.
ACCESSION   AR153094
VERSION     AR153094.1  GI:15120626
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,
            Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,
            Olson,R.J., Wood,K.V. and Welch,R.
  TITLE     Detection of nucleic acid hybrids
  JOURNAL   Patent: US 6235480-A 96 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        886 CAAAGTGACAGTGGCTGAAG 905
              ||| ||||  |||| |||||
Db         20 CAAGGTGAACGTGGATGAAG 1


RESULT 3439
AR158732/c
LOCUS       AR158732                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 354 from patent US 6251588.
ACCESSION   AR158732
VERSION     AR158732.1  GI:16220947
KEYWORDS    .
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AR121022
LOCUS       AR121022                20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 43 from patent US 6159694.
ACCESSION   AR121022
VERSION     AR121022.1  GI:14104598
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Karras,J.G.
  TITLE     Antisense modulation of stat3 expression
  JOURNAL   Patent: US 6159694-A 43 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1741 TGACAAGTACTGGCTCTTTA 1760
              ||||||| | ||| ||| ||
Db          1 TGACAAGGAGTGGGTCTCTA 20


RESULT 3430
AR121320
LOCUS       AR121320                20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 4 from patent US 6159718.
ACCESSION   AR121320
VERSION     AR121320.1  GI:14104896
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dalboege,H., Andersen,L.Nonboe., Kofoed,L.Venke.,
            Kauppinen,M.Sakari., Christgau,S., Heldt-Hansen,H.Peter. and
            Halkier,T.
  TITLE     Enzyme with polygalacturonase activity
  JOURNAL   Patent: US 6159718-A 4 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        281 CTCTACAGCCCCGCGCCACC 300
              |||  |||||| || |||||
Db          1 CTCGCCAGCCCAGCCCCACC 20


RESULT 3431
AR121613/c
LOCUS       AR121613                20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 10 from patent US 6159946.
ACCESSION   AR121613
VERSION     AR121613.1  GI:14105189
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zalewski,A. and Shi,Y.
  TITLE     Antisense inhibition of c-myc to modulate the proliferation of
            smooth muscle cells
  JOURNAL   Patent: US 6159946-A 10 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         653 GAGAACCTGGGGCTCCACGA 672
               |||  ||||| |||||| ||
Db          20 GAGCCCCTGGTGCTCCATGA 1


RESULT 3432
AR124459/c
LOCUS       AR124459                20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 28 from patent US 6171860.
ACCESSION   AR124459
VERSION     AR124459.1  GI:14109820
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense inhibition of rank expression
  JOURNAL   Patent: US 6171860-A 28 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         705 TCGACGACCAGCACCTGTTG 724
               | | || |||||||| ||||
Db          20 TGGGCGCCCAGCACCCGTTG 1


RESULT 3433
AR126680/c
LOCUS       AR126680                20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 109 from patent US 6180353.
ACCESSION   AR126680
VERSION     AR126680.1  GI:14113273
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M. and Cowsert,L.M.
  TITLE     Antisense modulation of daxx expression
  JOURNAL   Patent: US 6180353-A 109 30-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        1992 TGTGTATCTAGCTTCTTCAG 2011
               ||||| ||| || ||| |||
Db          20 TGTGTTTCTGGCCTCTGCAG 1


RESULT 3434
AR130120/c
LOCUS       AR130120                20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 23 from patent US 6187587.
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RESULT 3424
AR102419/c
LOCUS       AR102419                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 44 from patent US 6083923.
ACCESSION   AR102419
VERSION     AR102419.1  GI:12813217
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hardee,G.E., Geary,R.S., Levin,A., Templin,M.V., Howard,R. and
            Mehta,R.C.
  TITLE     Liposomal oligonucleotide compositions for modulating RAS gene
            expression
  JOURNAL   Patent: US 6083923-A 44 04-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         69 GACGCCTGGTCACCGTGACC 88
              | |||||||| || ||| ||
Db         20 GCCGCCTGGTTACTGTGTCC 1


RESULT 3425
AR103803/c
LOCUS       AR103803                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 327 from patent US 6087485.
ACCESSION   AR103803
VERSION     AR103803.1  GI:12815391
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brooks-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
            Miller,A. and North,M.
  TITLE     Asthma related genes
  JOURNAL   Patent: US 6087485-A 327 11-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1619 AGTTTGTTACCTACCTTACT 1638
              |||| |||||||||  | ||
Db         20 AGTTAGTTACCTACTGTGCT 1


RESULT 3426
AR107635/c
LOCUS       AR107635                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 75 from patent US 6110664.
ACCESSION   AR107635
VERSION     AR107635.1  GI:12823122
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 75 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAA 2800
              || ||||| |||| ||| ||
Db         20 AAATGAAATAAAAGAAACAA 1


RESULT 3427
AR107636/c
LOCUS       AR107636                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 76 from patent US 6110664.
ACCESSION   AR107636
VERSION     AR107636.1  GI:12823123
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 76 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2801
              | ||||| |||| ||| |||
Db         20 AATGAAATAAAAGAAACAAA 1


RESULT 3428
AR116415/c
LOCUS       AR116415                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 7 from patent US 6133242.
ACCESSION   AR116415
VERSION     AR116415.1  GI:14096737
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zalewski,A. and Shi,Y.
  TITLE     Inhibition of extracellular matrix synthesis by antisense compounds
            directed to nuclear proto-oncogenes
  JOURNAL   Patent: US 6133242-A 7 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        653 GAGAACCTGGGGCTCCACGA 672
              |||  ||||| |||||| ||
Db         20 GAGCCCCTGGTGCTCCATGA 1


RESULT 3429
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                 |||||||||| | |  ||||
Db          1 GCGCGGCGGGCGGGCGGGCA 20


RESULT 3419
AR060235
LOCUS       AR060235                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5840549.
ACCESSION   AR060235
VERSION     AR060235.1  GI:5986685
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   First,M.Kent. and Muallem,A.
  TITLE     Male infertility Y-deletion detection battery
  JOURNAL   Patent: US 5840549-A 1 24-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1078 CTTAGTAGAAGGTGAAGCTG 1097
                 ||||| | || |||||||
Db          1 CTTAGGAAAAAGTGAAGCCG 20


RESULT 3420
AR086246
LOCUS       AR086246                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 67 from patent US 5985558.
ACCESSION   AR086246
VERSION     AR086246.1  GI:10013012
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
  TITLE     Antisense oligonucleotide compositions and methods for the
            inibition of c-Jun and c-Fos
  JOURNAL   Patent: US 5985558-A 67 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        632 CTGGATGCCGCGGGCCTGGC 651
              ||||||||||   |||| ||
Db          1 CTGGATGCCGGCTGCCTTGC 20


RESULT 3421
AR095027/c
LOCUS       AR095027                 20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 21 from patent US 6001991.
ACCESSION   AR095027
VERSION     AR095027.1  GI:10022505
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M. and Manoharan,M.
  TITLE     Antisense oligonucleotide modulation of MDR P-glycoprotein gene
            expression
  JOURNAL   Patent: US 6001991-A 21 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2756 TGTATAATAAAAGTATTCTT 2775
                | |||||||||| ||  |||
Db         20 TCTATAATAAAACTAAACTT 1


RESULT 3422
AR100486
LOCUS       AR100486                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 217 from patent US 6080580.
ACCESSION   AR100486
VERSION     AR100486.1  GI:12810934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-.alpha. (TNF-.alpha.) expression
  JOURNAL   Patent: US 6080580-A 217 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1453 CCCTGGAGACCAGAGTCCAG 1472
              ||||||   ||||| |||||
Db          1 CCCTGGTCTCCAGATTCCAG 20


RESULT 3423
AR100614/c
LOCUS       AR100614                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 10 from patent US 6080727.
ACCESSION   AR100614
VERSION     AR100614.1  GI:12811062
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zupi,G.
  TITLE     Oligonucleotide treatments and compositions for human melanoma
  JOURNAL   Patent: US 6080727-A 10 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        653 GAGAACCTGGGGCTCCACGA 672
              |||  ||||| |||||| ||
Db         20 GAGCCCCTGGTGCTCCATGA 1
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  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        283 CTACAGCCCCGCGCCACCCC 302
              ||||   |||||||| |||
Db         20 CTACCCGCCCGCGCCAGCCC 1


RESULT 3414
A90272/c
LOCUS       A90272                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 453 from Patent EP0856579.
ACCESSION   A90272
VERSION     A90272.1  GI:6738786
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 453 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTT 2180
              | | |||||||| |||| ||
Db         20 TTTACTTTTTTTGTTTTGTT 1


RESULT 3415
AR016151
LOCUS       AR016151                 20 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 39 from patent US 5776682.
ACCESSION   AR016151
VERSION     AR016151.1  GI:3972428
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   First,M.Kent., Agoulnik,A.I. and Muallem,A.
  TITLE     Male infertility y-deletion detection battery
  JOURNAL   Patent: US 5776682-A 39 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1078 CTTAGTAGAAGGTGAAGCTG 1097
              ||||| | || |||||||| |
Db          1 CTTAGGAAAAAGTGAAGCCG 20


RESULT 3416
AR019149
LOCUS       AR019149                 20 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 39 from patent US 5783390.
ACCESSION   AR019149
VERSION     AR019149.1  GI:3974263
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   First,M.Kent. and Agoulnik,A.I.
  TITLE     Male infertility Y-deletion detection battery
  JOURNAL   Patent: US 5783390-A 39 21-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1078 CTTAGTAGAAGGTGAAGCTG 1097
              ||||| | || |||||||| |
Db          1 CTTAGGAAAAAGTGAAGCCG 20


RESULT 3417
AR036637/c
LOCUS       AR036637                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 37 from patent US 5872242.
ACCESSION   AR036637
VERSION     AR036637.1  GI:5953305
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Cowsert,L.M. and Manoharan,M.
  TITLE     Antisense oligonucleotide inhibition of ras
  JOURNAL   Patent: US 5872242-A 37 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         69 GACGCCTGGTCACCGTGACC 88
              | |||||||| || ||| ||
Db         20 GCCGCCTGGTTACTGTGTCC 1


RESULT 3418
AR052626
LOCUS       AR052626                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 26 from patent US 5831066.
ACCESSION   AR052626
VERSION     AR052626.1  GI:5975990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 26 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         49 GCGCGGCGGGGGCGGCGGCA 68
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  JOURNAL   Anim. Genet. 27 (5), 365-368 (1996)
  MEDLINE   97083737
   PUBMED   8930081
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Hirano,T., Nakane,S., Mizoshita,K., Inoue-Murayama,M., Watanabe,T.,
            Barendse,W. and Sugimoto,Y.
  TITLE     Characterization of 42 bovine microsatellite markers
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 20)
  AUTHORS   Sugimoto,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JAN-1996) Yoshikazu Sugimoto, Japan Live Stock
            Technology Association, Shirakawa Institute of Animal Genetics;
            Nishigo Odakura, Nishishirakawa, Fukushima 961, Japan
            (E-mail:LDI03222@niftyserve.or.jp, Tel:0248-25-5641,
            Fax:0248-25-5725)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9913"
     misc_feature    <1. .20
                     /note="microsatellite DIK039 PCR sense primer"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2128 CTTGTAGAAACGAAGCCTGC 2147
              ||||| ||||| | | ||||
Db         20 CTTGTTGAAACCAGGACTGC 1


RESULT 3410
A69626
LOCUS       A69626                   20 bp    DNA     linear   PAT 07-MAY-1999
DEFINITION  Sequence 35 from Patent WO9806871.
ACCESSION   A69626
VERSION     A69626.1  GI:4774249
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shipley,J., Clark,J. and Cooper,C.
  TITLE     MATERIALS AND METHODS RELATING TO THE DIAGNOSIS AND PROPHYLACTIC
            AND THERAPEUTIC TREATMENT OF PAPILLARY RENAL CELL CARCINOMA
  JOURNAL   Patent: WO 9806871-A 35 19-FEB-1998;
            SHIPLEY JANET (GB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2642 TGGGCTGAACCCTAAGGTGA 2661
              || |||| |||| | |||||
Db          1 TGAGCTGGACCCGATGGTGA 20


RESULT 3411
A88114/c
LOCUS       A88114                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 262 from Patent WO9833904.
ACCESSION   A88114
VERSION     A88114.1  GI:6736684
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 262 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        283 CTACAGCCCCGCGCCACCCC 302
              ||||   ||||||||| |||
Db         20 CTACCCGCCCGCGCCAGCCC 1


RESULT 3412
A88305/c
LOCUS       A88305                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 453 from Patent WO9833904.
ACCESSION   A88305
VERSION     A88305.1  GI:6736875
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 453 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTT 2180
              | | |||||||| |||| ||
Db         20 TTTACTTTTTTTGTTTTGTT 1


RESULT 3413
A90081/c
LOCUS       A90081                   20 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 262 from Patent EP0856579.
ACCESSION   A90081
VERSION     A90081.1  GI:6738595
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 262 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 25;
  Best Local Similarity   88.2%;  Pred. No. 4.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1974 CCTTGAAAAAAAGAAAA 1990
              |||| ||||||| ||||
Db         17 CCTTCAAAAAAAAAAAA 1


RESULT 3406
AX048437/c
LOCUS       AX048437                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 36 from Patent WO0071747.
ACCESSION   AX048437
VERSION     AX048437.1  GI:12225601
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 36 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAA 2798
              | |  | ||||||||||||||
Db         20 ACAGCTTAAAAAAAAAAAAA 1


RESULT 3407
AX048435/c
LOCUS       AX048435                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 34 from Patent WO0071747.
ACCESSION   AX048435
VERSION     AX048435.1  GI:12225599
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 34 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAA 2798
              | |  | ||||||||||||||
Db         20 ACATCTTAAAAAAAAAAAAA 1


RESULT 3408
BOVINE01/c
LOCUS       BOVINE01                 20 bp    DNA     linear   MAM 06-FEB-1999
DEFINITION  Bovine DNA for microsatellite marker, 3' terminus.
ACCESSION   D83281
VERSION     D83281.1  GI:1199698
KEYWORDS    PCR primer.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (sites)
  AUTHORS   Hirano,T., Nakane,S., Mizoshita,K., Yamakuchi,H.,
            Inoue-Murayama,M., Watanabe,T., Barendse,W. and Sugimoto,Y.
  TITLE     Characterization of 42 highly polymorphic bovine microsatellite
            markers
  JOURNAL   Anim. Genet. 27 (5), 365-368 (1996)
  MEDLINE   97083737
   PUBMED   8930081
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Hirano,T., Nakane,S., Mizoshita,K., Inoue-Murayama,M., Watanabe,T.,
            Barendse,W. and Sugimoto,Y.
  TITLE     Characterization of 42 bovine microsatellite markers
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 20)
  AUTHORS   Sugimoto,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JAN-1996) Yoshikazu Sugimoto, Japan Live Stock
            Technology Association, Shirakawa Institute of Animal Genetics;
            Nishigo Odakura, Nishishirakawa, Fukushima 961, Japan
            (E-mail:LDI03222@niftyserve.or.jp, Tel:0248-25-5641,
            Fax:0248-25-5725)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Bos taurus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9913"
     misc_feature    <1. .20
                     /note="microsatellite DIK039 PCR sense primer"

  Query Match             0.5%;  Score 13.6;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2128 CTTGTAGAAACGAAGCCTGC 2147
              ||||| ||||| | | ||||
Db         20 CTTGTTGAAACCAGGACTGC 1


RESULT 3409
BOVINE31/c
LOCUS       BOVINE31                 20 bp    DNA     linear   MAM 06-FEB-1999
DEFINITION  Bovine DNA for microsatellite marker, 3' terminus.
ACCESSION   D83311
VERSION     D83311.1  GI:1199728
KEYWORDS    PCR primer.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (sites)
  AUTHORS   Hirano,T., Nakane,S., Mizoshita,K., Yamakuchi,H.,
            Inoue-Murayama,M., Watanabe,T., Barendse,W. and Sugimoto,Y.
  TITLE     Characterization of 42 highly polymorphic bovine microsatellite
            markers
```

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              ||||| ||||||| |||
Db          1 AAAAATAAAAAAAGAAA 17


RESULT 3401
AX042978
LOCUS       AX042978                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 544 from Patent WO0065088.
ACCESSION   AX042978
VERSION     AX042978.1  GI:11341586
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 544 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 25;
  Best Local Similarity   88.2%;  Pred. No. 4.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACT 2190
              ||||||||||||||| | |
Db          1 TTTTTTTTTTTTTCAGT 17


RESULT 3402
AX043019/c
LOCUS       AX043019                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 585 from Patent WO0065088.
ACCESSION   AX043019
VERSION     AX043019.1  GI:11341627
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 585 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 25;
  Best Local Similarity   88.2%;  Pred. No. 4.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAA 2797
              || | ||||||||||||
Db         17 AAGTTAAAAAAAAAAAA 1


RESULT 3403
AX043461
LOCUS       AX043461                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1027 from Patent WO0065088.
ACCESSION   AX043461
VERSION     AX043461.1  GI:11342069
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1027 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DRB345 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 25;
  Best Local Similarity   88.2%;  Pred. No. 4.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACT 2190
              ||||||||||||| || |
Db          1 TTTTTTTTTTTTCAATT 17


RESULT 3404
AX042904/c
LOCUS       AX042904                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 470 from Patent WO0065088.
ACCESSION   AX042904
VERSION     AX042904.1  GI:11341512
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 470 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 25;
  Best Local Similarity   72.0%;  Pred. No. 4.3e+03;
  Matches   18;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
              | ||| |     ||||||||||||
Db         25 ACAATGGGGGGTAAAAAAAAAAAAA 1


RESULT 3405
AX043257/c
LOCUS       AX043257                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 823 from Patent WO0065088.
ACCESSION   AX043257
VERSION     AX043257.1  GI:11341865
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 823 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
```

```
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .21
                     /note="reverse primer for human STS sts-R45E6R at 1p36
                     sts-R45E6R obtained from clones B369B23, B187I7, B305A18,
                     B372M12, B225E8, B45E6, B258I16, B194I13, B228P18 , Human
                     BAC library RPCI-11"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2160 TTCTCCTTTTTTTTTTT 2176
              ||| |||||||| ||||
Db         18 TTCCCCTTTTTTCTTTT 2

RESULT 3398
AR066407/c
LOCUS       AR066407                 22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 31 from patent US 5849995.
ACCESSION   AR066407
VERSION     AR066407.1  GI:5996623
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hayden,M., Lin,B. and Nasir,J.
  TITLE     Mouse model for Huntington's Disease and related DNA sequences
  JOURNAL   Patent: US 5849995-A 31 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 22;
  Best Local Similarity   88.2%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              ||||| |||||||| ||
Db         20 AAAAATAAAAAAAAGAA 4

RESULT 3399
AX011524
LOCUS       AX011524                 22 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 21 from Patent WO9955892.
ACCESSION   AX011524
VERSION     AX011524.1  GI:9998074
KEYWORDS    .
SOURCE      Caprine arthritis-encephalitis virus
  ORGANISM  Caprine arthritis-encephalitis virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Ovine/caprine
            lentivirus.
REFERENCE   1
  AUTHORS   Charneau,P., Firat,H. and Zennou,V.
  TITLE     Use of triplex structure dna sequences for transferring nucleotide
            sequences
  JOURNAL   Patent: WO 9955892-A 21 04-NOV-1999;
            CHARNEAU PIERRE (FR); FIRAT HUESEYIN (FR); PASTEUR INSTITUT (FR);
            ZENNOU VERONIQUE (FR)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Caprine arthritis-encephalitis virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11660"
     misc_feature    complement(1. .22)
                     /note="Sequence a double brin"
     misc_feature    4
                     /note="A peut etre T"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 22;
  Best Local Similarity   88.2%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              ||||| ||||||| |||
Db          1 AAAAATAAAAAAAGAAA 17

RESULT 3400
BD226411
LOCUS       BD226411                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Use of triplex structure DNA sequences for transferring nucleotide
            sequences.
ACCESSION   BD226411
VERSION     BD226411.1  GI:33036181
KEYWORDS    JP 2002512804-A/21.
SOURCE      Caprine arthritis-encephalitis virus
  ORGANISM  Caprine arthritis-encephalitis virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Ovine/caprine
            lentivirus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Charneau,P., Zennou,V. and Firat,H.
  TITLE     Use of triplex structure DNA sequences for transferring nucleotide
            sequences
  JOURNAL   Patent: JP 2002512804-A 21 08-MAY-2002;
            INSTITUT PASTEUR
COMMENT     OS   Caprine arthritis-encephalitis virus
            PN   JP 2002512804-A/21
            PD   08-MAY-2002
            PF   23-APR-1999 JP 2000546035
            PR   24-APR-1998 FR     98/05197
            PI   PIERRE CHARNEAU,VERONIQUE ZENNOU,HUESEYIN FIRAT PC
            C12N15/09,A61K48/00,C12N5/10,C12N7/00//A61K35/12,C07K14/16, PC
            C12N15/00,
            PC   C12N5/00
            CC   Strandedness: Double;
            CC   A can be T
            CC   Sequence of double strand
            FH   Key             Location/Qualifiers
            FT   misc_feature    (4)
            FT   misc_feature    complement(1. .22).
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Caprine arthritis-encephalitis virus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:11660"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 22;
  Best Local Similarity   88.2%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
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RESULT 3394
BD134288
LOCUS       BD134288                  21 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Detection of neoplasia by analysis of saliva.
ACCESSION   BD134288
VERSION     BD134288.1  GI:23229233
KEYWORDS    JP 2002505888-A/112.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Sidlanski,D.
  TITLE     Detection of neoplasia by analysis of saliva
  JOURNAL   Patent: JP 2002505888-A 112 26-FEB-2002;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Artificial Sequence
            PN   JP 2002505888-A/112
            PD   26-FEB-2002
            PF   10-MAR-1999 JP 2000535774
            PR   10-MAR-1998 US    09/038637
            PI   DAVID SIDLANSKI
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   nucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         89 CCGATTTTGGATTTACC 105
              | |||||| ||||||||
Db          5 CAGATTTTGATTTACC 21


RESULT 3395
BD140134
LOCUS       BD140134                  21 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Diagnosis and treatment of AUR-1 and/or AUR-2 related disorders.
ACCESSION   BD140134
VERSION     BD140134.1  GI:23235079
KEYWORDS    JP 2002508937-A/8.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Plowman,G.D. and Mossie,K.
  TITLE     Diagnosis and treatment of AUR-1 and/or AUR-2 related disorders
  JOURNAL   Patent: JP 2002508937-A 8 26-MAR-2002;
            SUGEN INC
COMMENT     OS   Unidentified
            PN   JP 2002508937-A/8
            PD   26-MAR-2002
            PF   21-JAN-1999 JP 2000528695
            PR   22-JAN-1998 US    09/012135
            PI   GREGORY D PLOWMAN,KEVIN MOSSIE
            PC   C12N15/09,A61K31/7088,A61K45/00,A61P35/00,C07K16/40,C12N1/15,
            PC   C12N1/19,
            PC   C12N1/21,C12N5/10,C12N9/12,C12P21/08,C12Q1/48,C12Q1/68,G01N33/
            PC   573,
            PC   C12N15/00,C12N5/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Diagnosis and treatment of AUR-1 and/or AUR-2 related  CC
                 disorders
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         595 CCGCCGCTCCGACCTGC 611
               ||||| |||||||| ||
Db           4 CCGCCACTCCGACCAGC 20


RESULT 3396
BD161939/c
LOCUS       BD161939                  21 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Polymorphism of upstream region of human cholecystokinin gene,
            identification method and reagent thereof, and method for diagnosis
            of anxiety disorders based thereon.
ACCESSION   BD161939
VERSION     BD161939.1  GI:27867697
KEYWORDS    JP 2002171990-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Yoshikawa,T. and Hattori,E.
  TITLE     Polymorphism of upstream region of human cholecystokinin gene,
            identification method and reagent thereof, and method for diagnosis
            of anxiety disorders based thereon
  JOURNAL   Patent: JP 2002171990-A 5 18-JUN-2002;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
COMMENT     OS   Artificial Sequence
            PN   JP 2002171990-A/5
            PD   18-JUN-2002
            PF   08-DEC-2000 JP 2000375090
            PI   TAKEO YOSHIKAWA,EIJI HATTORI
            PC   C12N15/09,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
            Description of Artificial Sequence: upstream primer p5 FH   Key
                  Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         898 GGCTGAAGTACAGAGGC 914
               ||||| ||||||| |||
Db          19 GGCTGGAGTACAGTGGC 3


RESULT 3397
AB069141/c
LOCUS       AB069141                  21 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, reverse primer for human STS sts-R45E6R at
            1p36.
ACCESSION   AB069141
VERSION     AB069141.1  GI:15129945
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
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  AUTHORS   Park,J.G., Kim,I.J., Kang,H.C. and Park,J.H.
  TITLE     Ret oligonucleotide microchip and method for detecting hereditary
            cancer employing same
  JOURNAL   Patent: EP 1333100-A 60 06-AUG-2003;
            National Cancer Center (KR)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="804M-(M)"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1175 CCTCATCTTGGAGGACG 1191
              ||||||| ||||| |||
Db          4 CCTCATCATGGAGTACG 20


RESULT 3391
BD000358
LOCUS       BD000358                 21 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for amplifying nucleic acids.
ACCESSION   BD000358
VERSION     BD000358.1  GI:18623437
KEYWORDS    JP 2000279184-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Preston,G.M. and Bax,J.W.
  TITLE     Method for amplifying nucleic acids
  JOURNAL   Patent: JP 2000279184-A 10 10-OCT-2000;
            ORTHO CLINICAL DIAGNOSTICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000279184-A/10
            PD   10-OCT-2000
            PF   03-FEB-2000 JP 2000032660
            PR   03-FEB-1999 US    60/118495
            PI   GREGORY M PRESTON,JOHN W BAX
            PC   C12N15/09,C12Q1/48,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        734 CAGACAGTCATTCGCAA 750
              ||||| |||| ||||||
Db          3 CAGACGGTCAGTCGCAA 19


RESULT 3392
BD056555/c
LOCUS       BD056555                 21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method to diagnose and treat pathological conditions resulting from
            deficient ion transport.
ACCESSION   BD056555
VERSION     BD056555.1  GI:22602161
KEYWORDS    JP 2001508291-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Lifton,R.P. and Simon,D.B.
  TITLE     Method to diagnose and treat pathological conditions resulting from
            deficient ion transport
  JOURNAL   Patent: JP 2001508291-A 12 26-JUN-2001;
            YALE UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2001508291-A/12
            PD   26-JUN-2001
            PF   19-DEC-1997 JP 1998530123
            PR   31-DEC-1996 US    08/778052
            PI   RICHARD P LIFTON,DAVID B SIMON
            PC   C12N15/09,C07K14/435,C07K16/00,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12Q1/68,G01N33/53,C12N15/00,C12N5/00 CC   Primer
            for analysis of human TSC gene
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1781 TGAACCCCATTCTTTCC 1797
              |||| |||||||||| ||
Db         20 TGAATCCCATTCTTCCC 4


RESULT 3393
BD089006/c
LOCUS       BD089006                 21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089006
VERSION     BD089006.1  GI:22634616
KEYWORDS    JP 2001321190-A/1250.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 1250 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/1250
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2160 TTCTCCTTTTTTTTTTT 2176
              ||| |||||||| ||||
Db         18 TTCCCCTTTTTTCTTTT 2
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  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1729 ATTATCAGAAGGTGACA 1745
              ||||||||||||| | ||
Db         18 ATTATCAGAAGGAGCCA 2


RESULT 3386
AX397812/c
LOCUS       AX397812                 21 bp    DNA     linear   PAT 27-MAY-2002
DEFINITION  Sequence 46 from Patent WO0220852.
ACCESSION   AX397812
VERSION     AX397812.1  GI:21260686
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
  TITLE     Amplification of hiv-1 sequences for detection of sequences
            associated with drug-resistance mutations
  JOURNAL   Patent: WO 0220852-A 46 14-MAR-2002;
            Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer for Gag target sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1729 ATTATCAGAAGGTGACA 1745
              ||||||||||||| | ||
Db         18 ATTATCAGAAGGAGCCA 2


RESULT 3387
AX555818/c
LOCUS       AX555818                 21 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 414 from Patent WO02070755.
ACCESSION   AX555818
VERSION     AX555818.1  GI:25899292
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lyamichev,V.I., Kaiser,M.W. and Lyamicheva,N.
  TITLE     Fen endonucleases
  JOURNAL   Patent: WO 02070755-A 414 12-SEP-2002;
            Third Wave Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1768 AGCTTTTTTTTTTTGAA 1784
              |||| ||| ||||||||
Db         20 AGCTCTTTCTTTTTGAA 4


RESULT 3388
AX594110
LOCUS       AX594110                 21 bp    DNA     linear   PAT 13-FEB-2003
DEFINITION  Sequence 188 from Patent WO0246477.
ACCESSION   AX594110
VERSION     AX594110.1  GI:28375340
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Garcia,P., Hardy,S.F., Williams,L.T. and Escobedo,J.
  TITLE     Endogenous retroviruses up-regulated in prostate cancer
  JOURNAL   Patent: WO 0246477-A 188 13-JUN-2002;
            CHIRON CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        721 GTTGCTGCACGATCAGA 737
              ||| ||||| |||||||
Db          5 GTTCCTGCAGGATCAGA 21


RESULT 3389
AX713257/c
LOCUS       AX713257                 21 bp    DNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 143 from Patent WO03018837.
ACCESSION   AX713257
VERSION     AX713257.1  GI:29823846
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Waschuetza,S., Schnakenberg,E. and Lustig,M.
  TITLE     Method and diagnostic kit for the molecular diagnosis of
            pharmacologically relevant genes
  JOURNAL   Patent: WO 03018837-A 143 06-MAR-2003;
            Adnagen AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAA 2188
              ||||||||  |||||||
Db         21 TTTTTTTAATTTTTAA 5


RESULT 3390
AX810933
LOCUS       AX810933                 21 bp    DNA     linear   PAT 02-DEC-2003
DEFINITION  Sequence 60 from Patent EP1333100.
ACCESSION   AX810933
VERSION     AX810933.1  GI:38635530
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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RESULT 3381
AX201193/c
LOCUS       AX201193                21 bp    DNA     linear   PAT 29-AUG-2001
DEFINITION  Sequence 18 from Patent WO0142457.
ACCESSION   AX201193
VERSION     AX201193.1  GI:15390945
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Iversen,P.L.
  TITLE     Antisense antibacterial method and composition
  JOURNAL   Patent: WO 0142457-A 18 14-JUN-2001;
            Avi Biopharma, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="antisense oligomer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        169 GTTGTGGAAAATAACCG 185
              ||||||| ||||||||
Db         21 GTTGTGGTTAATAACCG 5


RESULT 3382
AX201215
LOCUS       AX201215                21 bp    DNA     linear   PAT 29-AUG-2001
DEFINITION  Sequence 40 from Patent WO0142457.
ACCESSION   AX201215
VERSION     AX201215.1  GI:15390967
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Iversen,P.L.
  TITLE     Antisense antibacterial method and composition
  JOURNAL   Patent: WO 0142457-A 40 14-JUN-2001;
            Avi Biopharma, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="antisense oligomer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2009 CAGAGATCAAGTCCTCT 2025
              |||||| |||| |||||
Db          1 CAGAGAGCAAGCCCTCT 17


RESULT 3383
AX201233
LOCUS       AX201233                21 bp    DNA     linear   PAT 29-AUG-2001
DEFINITION  Sequence 58 from Patent WO0142457.
ACCESSION   AX201233
VERSION     AX201233.1  GI:15390996
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Iversen,P.L.
  TITLE     Antisense antibacterial method and composition
  JOURNAL   Patent: WO 0142457-A 58 14-JUN-2001;
            Avi Biopharma, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="antisense oligomer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1393 GTCTGCCCTGCAGAACT 1409
              |||| |||||||| |||
Db          3 GTCTCCCCTGCAGTACT 19


RESULT 3384
AX203169
LOCUS       AX203169                21 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 22 from Patent WO0153529.
ACCESSION   AX203169
VERSION     AX203169.1  GI:15392528
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Thomann,H.U. and Fitzgerald,M.S.
  TITLE     Rapid determination of gene structure using cdna sequence
  JOURNAL   Patent: WO 0153529-A 22 26-JUL-2001;
            Genome Therapeutics Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1068 TCCTGACATCCTTAGTA 1084
              | |||||||||||| ||
Db          2 TGCTGACATCCTTAATA 18


RESULT 3385
AX397777/c
LOCUS       AX397777                21 bp    DNA     linear   PAT 27-MAY-2002
DEFINITION  Sequence 11 from Patent WO0220852.
ACCESSION   AX397777
VERSION     AX397777.1  GI:21260651
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
  TITLE     Amplification of hiv-1 sequences for detection of sequences
            associated with drug-resistance mutations
  JOURNAL   Patent: WO 0220852-A 11 14-MAR-2002;
            Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer for Gag target sequence"
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            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   78.9%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        711 ACCAGCACCTGTTGCTGCA 729
              ||||||||:|| | || ||
Db         19 ACCAGCACYTGGTTCTCCA 1


RESULT 3377
AX097131
LOCUS       AX097131                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 2309 from Patent WO0118250.
ACCESSION   AX097131
VERSION     AX097131.1  GI:13513413
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 2309 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGC 248
              |||||||||| |||| |
Db          1 CAGCAATGGGYATCCCC 17


RESULT 3378
AX097215
LOCUS       AX097215                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 2393 from Patent WO0118250.
ACCESSION   AX097215
VERSION     AX097215.1  GI:13513582
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 2393 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1505 AAACACAGGAAATAAAA 1521
              ||| || ||||||||||
Db          5 AAATACKGGAAATAAAA 21


RESULT 3379
AX154141/c
LOCUS       AX154141                 21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 239 from Patent WO0138576.
ACCESSION   AX154141
VERSION     AX154141.1  GI:14535755
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0138576-A 239 31-MAY-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   78.9%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        495 AGGGAGCGGGGCTGCCCTC 513
              || |||| ||:||| ||||
Db         21 AGTGAGCTGGRCTGTCCTC 3


RESULT 3380
AX183997/c
LOCUS       AX183997                 21 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 1750 from Patent WO0142511.
ACCESSION   AX183997
VERSION     AX183997.1  GI:15135332
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
  TITLE     Ibd-related polymorphisms
  JOURNAL   Patent: WO 0142511-A 1750 14-JUN-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
            Biotherapeutics Corporation (CA)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAA 2798
              ||| ||||  ||||||||
Db         18 AATGGAAANCAAAAAAAA 1
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                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        479 GGCCGCCAGAGCCAGGA 495
              ||||||| | |||||||
Db          4 GGCCGCCCGCGCCAGGA 20


RESULT 3372
AR369458
LOCUS       AR369458                  21 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 10 from patent US 6300075.
ACCESSION   AR369458
VERSION     AR369458.1  GI:34605575
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Preston,G.M. and Backus,J.W.
  TITLE     Enhancement of the specificity of nucleic acid amplification by
            carrier nucleic acid
  JOURNAL   Patent: US 6300075-A 10 09-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        734 CAGACAGTCATTCGCAA 750
              ||||| |||| ||||||
Db          3 CAGACGGTCAGTCGCAA 19


RESULT 3373
AR370563
LOCUS       AR370563                  21 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 38 from patent US 6300491.
ACCESSION   AR370563
VERSION     AR370563.1  GI:34607316
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Bennett,C.F. and Mirabelli,C.K.
  TITLE     Oligonucleotide inhibition of cell adhesion
  JOURNAL   Patent: US 6300491-A 38 09-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2489 TGATGGGGTAATCTATA 2505
              ||| |||||||||||  |
Db          5 TGAGGGGGTAATCTACA 21


RESULT 3374
AR404583/c
LOCUS       AR404583                  21 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 30 from patent US 6627747.
ACCESSION   AR404583
VERSION     AR404583.1  GI:40153212
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Fritz,C., Youngman,P. and Guzman,L.-M.
  TITLE     Essential bacterial genes and their use
  JOURNAL   Patent: US 6627747-A 30 30-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        460 CCAGCAGCAGGCCTGGC 476
              |||||| |||| |||||
Db         21 CCAGCAACAGGACTGGC 5


RESULT 3375
AX096072/c
LOCUS       AX096072                  21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 1250 from Patent WO0118250.
ACCESSION   AX096072
VERSION     AX096072.1  GI:13512299
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1250 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   78.9%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2764 AAAAGTATTCTTGTTAGAA 2782
              ||||||  |:| |||||||
Db         20 AAAAGTGGTYTCGTTAGAA 2


RESULT 3376
AX096676/c
LOCUS       AX096676                  21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 1854 from Patent WO0118250.
ACCESSION   AX096676
VERSION     AX096676.1  GI:13512930
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1854 15-MAR-2001;
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     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2062 TTAATAAGTGGTATCTG 2078
              || |||||| |||||||
Db         19 TTCATAAGTAGTATCTG 3


RESULT 3367
AR298436
LOCUS       AR298436                  21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 10171 from patent US 6537751.
ACCESSION   AR298436
VERSION     AR298436.1  GI:31685720
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 10171 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1567 AAAAATCCTTCTCCACC 1583
              ||||| ||| |||||||
Db          1 AAAAAACCTGCTCCACC 17


RESULT 3368
AR342463
LOCUS       AR342463                  21 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 13 from patent US 6576423.
ACCESSION   AR342463
VERSION     AR342463.1  GI:33737473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Batra,S.K., Brand,R.E., Ringel,J., Faulmann,G., Lohr,M. and
            Varshney,G.C.
  TITLE     Specific mucin expression as a marker for pancreatic cancer
  JOURNAL   Patent: US 6576423-A 13 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        457 CAGCCAGCAGCAGGCCT 473
              || |||||||||| ||
Db          5 CATCCAGCAGCAGGGCT 21


RESULT 3369
AR344822/c
LOCUS       AR344822                  21 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 11 from patent US 6582920.
ACCESSION   AR344822
VERSION     AR344822.1  GI:33740903
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
  TITLE     Amplification of HIV-1 RT sequences for detection of sequences
            associated with drug-resistance mutations
  JOURNAL   Patent: US 6582920-A 11 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1729 ATTATCAGAAGGTGACA 1745
              ||||||||||||| | ||
Db         18 ATTATCAGAAGGAGCCA 2


RESULT 3370
AR344857/c
LOCUS       AR344857                  21 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 46 from patent US 6582920.
ACCESSION   AR344857
VERSION     AR344857.1  GI:33740938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
  TITLE     Amplification of HIV-1 RT sequences for detection of sequences
            associated with drug-resistance mutations
  JOURNAL   Patent: US 6582920-A 46 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1729 ATTATCAGAAGGTGACA 1745
              ||||||||||||| | ||
Db         18 ATTATCAGAAGGAGCCA 2


RESULT 3371
AR365046
LOCUS       AR365046                  21 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 30 from patent US 5457089.
ACCESSION   AR365046
VERSION     AR365046.1  GI:34428292
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Fibi,M., Zettlmeissl,G. and Kupper,H.
  TITLE     Muteins of human erythropoietin, the preparation thereof and the
            use thereof
  JOURNAL   Patent: US 5457089-A 30 10-OCT-1995;
FEATURES             Location/Qualifiers
     source          1. .21
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  JOURNAL   Patent: US 5591623-A 38 07-JAN-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2489 TGATGGGGTAATCTATA 2505
              ||| |||||||||||  |
Db          5 TGAGGGGGTAATCTACA 21


RESULT 3362
I42137/c
LOCUS       I42137                    21 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 11 from patent US 5629149.
ACCESSION   I42137
VERSION     I42137.1  GI:2467632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Santamaria,P., Boyce-Jacino,M.T., Barbosa,J.J., Rich,S.S. and
            Faras,A.J.
  TITLE     DNA sequence-based HLA typing method
  JOURNAL   Patent: US 5629149-A 11 13-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2652 CCTAAGGTGAGTGTGCA 2668
              |||||||||| |||| |
Db         21 CCTAAGGTGACTGTGTA 5


RESULT 3363
AR200253
LOCUS       AR200253                  21 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 10 from patent US 6355785.
ACCESSION   AR200253
VERSION     AR200253.1  GI:20250327
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O., Hogan,M.E.,
            Pommier,Y. and Mazumder,A.
  TITLE     Guanosine-rich oligonucleotide integrase inhibitors
  JOURNAL   Patent: US 6355785-A 10 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        106 GCTTGGGGGCTGGGGGG 122
              | ||||||| |||||||
Db          4 GGTTGGGGGGTGGGGGG 20


RESULT 3364
AR212829
LOCUS       AR212829                  21 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 76 from patent US 6403303.
ACCESSION   AR212829
VERSION     AR212829.1  GI:23309695
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Shipman,R., Leushner,J. and Dunn,J.M.
  TITLE     Method and reagents for testing for mutations in the BRCA1 gene
  JOURNAL   Patent: US 6403303-A 76 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1095 CTGTTCATTTGGCTAGG 1111
              |||||||||||  ||||
Db          3 CTGTTCATTTGCATAGG 19


RESULT 3365
AR262385
LOCUS       AR262385                  21 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 10 from patent US 6323185.
ACCESSION   AR262385
VERSION     AR262385.1  GI:28073816
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Rando,R.F., Fennewald,S., Zendegui,J.G., Ojwang,J.O. and Hogan,M.E.
  TITLE     Anti-viral guanosine-rich oligonucleotides and method of treating
            HIV
  JOURNAL   Patent: US 6323185-A 10 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        106 GCTTGGGGGCTGGGGGG 122
              | ||||||| |||||||
Db          4 GGTTGGGGGGTGGGGGG 20


RESULT 3366
AR296500/c
LOCUS       AR296500                  21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 8235 from patent US 6537751.
ACCESSION   AR296500
VERSION     AR296500.1  GI:31683784
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 8235 25-MAR-2003;
FEATURES             Location/Qualifiers
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                  ||||| |||| ||||||
Db          3 CAGACGGTCAGTCGCAA 19


RESULT 3357
E36587/c
LOCUS       E36587                    21 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Antisense nucleic acid compound for inhibiting the expression of
            p300 or CBP.
ACCESSION   E36587
VERSION     E36587.1  GI:18624728
KEYWORDS    JP 2000139464-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Uchida,K. and Yokoyama,K.
  TITLE     Antisense nucleic acid compound for inhibiting the expression of
            p300 or CBP
  JOURNAL   Patent: JP 2000139464-A 1 23-MAY-2000;
            TOAGOSEI CHEM IND CO LTD
COMMENT     OS   Unidentified
            PN   JP 2000139464-A/1
            PD   23-MAY-2000
            PF   13-NOV-1998 JP 1998341086
            PR
            PI   KIYOSHI UCHIDA,KAZUHISA YOKOYAMA
            PC   C12N15/09//A61K31/00,A61K31/70,A61K48/00,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        672 ACATGCCTCACCAGATG 688
                ||||| || ||||||||
Db         17 ACATGACTTACCAGATG 1


RESULT 3358
I20640
LOCUS       I20640                    21 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 38 from patent US 5514788.
ACCESSION   I20640
VERSION     I20640.1  GI:1600995
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Bennett,C.Frank. and Mirabelli,C.K.
  TITLE     Oligonucleotide modulation of cell adhesion
  JOURNAL   Patent: US 5514788-A 38 07-MAY-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2489 TGATGGGGTAATCTATA 2505
              ||| |||||||||||| |
Db          5 TGAGGGGGTAATCTACA 21


RESULT 3359
I27778
LOCUS       I27778                    21 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 10 from patent US 5567604.
ACCESSION   I27778
VERSION     I27778.1  GI:1818554
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Rando,R.F., Fennewald,S., Zendegui,J.G. and Ojwang,J.O.
  TITLE     Anti-viral guanosine-rich oligonucleotides
  JOURNAL   Patent: US 5567604-A 10 22-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        106 GCTTGGGGGCTGGGGGG 122
              | ||||||| |||||||
Db          4 GGTTGGGGGGTGGGGGG 20


RESULT 3360
I29090/c
LOCUS       I29090                    21 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 11 from patent US 5578443.
ACCESSION   I29090
VERSION     I29090.1  GI:1819881
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Santamaria,P., Boyce-Jacino,M.T., Barbosa,J.J., Rich,S.S. and
            Faras,A.J.
  TITLE     DNA sequence-based HLA typing method
  JOURNAL   Patent: US 5578443-A 11 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2652 CCTAAGGTGAGTGTGCA 2668
              |||||||||| |||| |
Db         21 CCTAAGGTGACTGTGTA 5


RESULT 3361
I33333
LOCUS       I33333                    21 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 38 from patent US 5591623.
ACCESSION   I33333
VERSION     I33333.1  GI:1824124
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Bennett,C.Frank. and Mirabelli,C.K.
  TITLE     Oligonucleotide modulation of cell adhesion
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Qy        595 CCGCCGCTCCGACCTGC 611
              ||||| |||||||| ||
Db          4 CCGCCACTCCGACCAGC 20


RESULT 3353
AR152832
LOCUS       AR152832                 21 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 112 from patent US 6235470.
ACCESSION   AR152832
VERSION     AR152832.1  GI:15120364
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Sidransky,D.
  TITLE     Detection of neoplasia by analysis of saliva
  JOURNAL   Patent: US 6235470-A 112 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         89 CCGATTTTGGATTTACC 105
              | |||||| ||||||||
Db          5 CAGATTTTGATTTACC 21


RESULT 3354
AR168784
LOCUS       AR168784                 21 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 10 from patent US 6288042.
ACCESSION   AR168784
VERSION     AR168784.1  GI:17904883
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
  TITLE     Anti-viral guanosine-rich tetrad forming oligonucleotides
  JOURNAL   Patent: US 6288042-A 10 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        106 GCTTGGGGGCTGGGGGG 122
              | ||||||| ||||||||
Db          4 GGTTGGGGGGTGGGGGG 20


RESULT 3355
BD228621/c
LOCUS       BD228621                 21 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Essential bacterial genes and their use.
ACCESSION   BD228621
VERSION     BD228621.1  GI:33038391
KEYWORDS    JP 2002524069-A/23.
SOURCE      Streptococcus pneumoniae
  ORGANISM  Streptococcus pneumoniae
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Fritz,C., Youngman,P. and Guzman,L.M.
  TITLE     Essential bacterial genes and their use
  JOURNAL   Patent: JP 2002524069-A 23 06-AUG-2002;
            MILLENNIUM PHARMACEUTICALS INC
COMMENT     OS   Streptococcus pneumoniae
            PN   JP 2002524069-A/23
            PD   06-AUG-2002
            PF   09-SEP-1999 JP 2000568947
            PR   09-SEP-1998 US    60/099578
            PI   CHRISTIAN FRITZ,PHILIP YOUNGMAN,LUZ MARIA GUZMAN PC
            C12N15/09,A61K45/00,A61P31/04,C07K14/315,C07K16/12,C12N1/15, PC
            C12N1/19,
            PC   C12N1/21,C12N5/10,C12Q1/02,C12Q1/18,C12Q1/68,G01N33/15 PC
            ,G01N33/50,G01N33/50,
            PC   G01N33/68,C12N15/00,C12N5/00
            CC   Essential bacterial genes and their use
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Streptococcus pneumoniae'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Streptococcus pneumoniae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1313"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        460 CCAGCAGCAGGCCTGGC 476
              |||||| |||| |||||
Db         21 CCAGCAACAGGACTGGC 5


RESULT 3356
E30929
LOCUS       E30929                   21 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Amplification and detection of HIV-1 and/or HIV-2.
ACCESSION   E30929
VERSION     E30929.1  GI:13025660
KEYWORDS    JP 1999069987-A/12.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   John,W.B., Suzan,M.A., Ann,E.K., Eric,B.R. and Thomas,J.K.
  TITLE     Amplification and detection of HIV-1 and/or HIV-2
  JOURNAL   Patent: JP 1999069987-A 12 16-MAR-1999;
            ORTHO CLINICAL DIAGNOSTICS INC
COMMENT     OS   Unidentified
            PN   JP 1999069987-A/12
            PD   16-MAR-1999
            PF   24-JUN-1998 JP 1998177059
            PR   25-JUN-1997 US    60/050759
            PI   JOHN WESLEY BACCHUS,SUZAN MERISSA ATTWOOD,ANN ELIZABETH KEIJI,
            PI   ERIC BRICE RASMUSSEN,THOMAS JOSEPH KAMINZU
            PC   C12N15/09,C12Q1/68,G01N33/566,G01N33/569,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        734 CAGACAGTCATTCGCAA 750
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                    /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        455 GGCAGCCAGCAGCAGGC 471
              ||||||||||||  |||
Db         20 GGCAGCCAGCAGATGGC 4


RESULT 3348
AR109839/c
LOCUS       AR109839                  21 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 263 from patent US 6114139.
ACCESSION   AR109839
VERSION     AR109839.1  GI:12826115
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
  TITLE     G-protein coupled receptor protein and a DNA encoding the receptor
  JOURNAL   Patent: US 6114139-A 263 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        455 GGCAGCCAGCAGCAGGC 471
              ||||||||||||  |||
Db         20 GGCAGCCAGCAGATGGC 4


RESULT 3349
AR109840/c
LOCUS       AR109840                  21 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 264 from patent US 6114139.
ACCESSION   AR109840
VERSION     AR109840.1  GI:12826116
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
  TITLE     G-protein coupled receptor protein and a DNA encoding the receptor
  JOURNAL   Patent: US 6114139-A 264 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        455 GGCAGCCAGCAGCAGGC 471
              ||||||||||||  |||
Db         20 GGCAGCCAGCAGATGGC 4


RESULT 3350
AR109845/c
LOCUS       AR109845                  21 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 269 from patent US 6114139.
ACCESSION   AR109845
VERSION     AR109845.1  GI:12826121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
  TITLE     G-protein coupled receptor protein and a DNA encoding the receptor
  JOURNAL   Patent: US 6114139-A 269 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        455 GGCAGCCAGCAGCAGGC 471
              ||||||||||||  |||
Db         20 GGCAGCCAGCAGAGGGC 4


RESULT 3351
AR123225
LOCUS       AR123225                  21 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 38 from patent US 6169079.
ACCESSION   AR123225
VERSION     AR123225.1  GI:14108191
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Bennett,C.Frank. and Mirabelli,C.K.
  TITLE     Oligonucleotide inhibition of cell adhesion
  JOURNAL   Patent: US 6169079-A 38 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2489 TGATGGGGTAATCTATA 2505
              ||| |||||||||||| |
Db          5 TGAGGGGGTAATCTACA 21


RESULT 3352
AR139687
LOCUS       AR139687                  21 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 31 from patent US 6207401.
ACCESSION   AR139687
VERSION     AR139687.1  GI:14482183
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Plowman,G. and Mossie,K.
  TITLE     Diagnosis and treatment of AUR-1 and/or AUR-2 related disorders
  JOURNAL   Patent: US 6207401-A 31 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2489 TGATGGGGTAATCTATA 2505
              ||| |||||||||||  |
Db          5 TGAGGGGGTAATCTACA 21


RESULT 3343
AR081625/c
LOCUS       AR081625                 21 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 11 from patent US 5972604.
ACCESSION   AR081625
VERSION     AR081625.1  GI:10008351
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Santamaria,P., Boyce-Jacino,M.Thomas., Barbosa,J.Joaquim.,
            Rich,S.Saul. and Faras,A.James.
  TITLE     DNA sequence-based HLA typing method
  JOURNAL   Patent: US 5972604-A 11 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2652 CCTAAGGTGAGTGTGCA 2668
              |||||||||| |||| |
Db         21 CCTAAGGTGACTGTGTA 5


RESULT 3344
AR093404
LOCUS       AR093404                 21 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 12 from patent US 6001558.
ACCESSION   AR093404
VERSION     AR093404.1  GI:10020153
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Backus,J.W., Atwood,S.M., Casey,A.E., Rasmussen,E.B. and
            Cummins,T.J.
  TITLE     Amplification and detection of HIV-1 and/or HIV 2
  JOURNAL   Patent: US 6001558-A 12 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        734 CAGACAGTCATTCGCAA 750
              ||||| |||| ||||||
Db          3 CAGACGGTCAGTCGCAA 19


RESULT 3345
AR104741
LOCUS       AR104741                 21 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 38 from patent US 6093811.
ACCESSION   AR104741
VERSION     AR104741.1  GI:12817449
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Bennett,C.Frank. and Mirabelli,C.K.
  TITLE     Oligonucleotide modulation of cell adhesion
  JOURNAL   Patent: US 6093811-A 38 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2489 TGATGGGGTAATCTATA 2505
              ||| |||||||||||  |
Db          5 TGAGGGGGTAATCTACA 21


RESULT 3346
AR105563
LOCUS       AR105563                 21 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 38 from patent US 6096722.
ACCESSION   AR105563
VERSION     AR105563.1  GI:12819160
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Bennett,C.Frank., Mirabelli,C.K. and Baker,B.
  TITLE     Antisense modulation of cell adhesion molecule expression and
            treatment of cell adhesion molecule-associated diseases
  JOURNAL   Patent: US 6096722-A 38 01-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2489 TGATGGGGTAATCTATA 2505
              ||| |||||||||||  |
Db          5 TGAGGGGGTAATCTACA 21


RESULT 3347
AR109833/c
LOCUS       AR109833                 21 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 257 from patent US 6114139.
ACCESSION   AR109833
VERSION     AR109833.1  GI:12826109
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
  TITLE     G-protein coupled receptor protein and a DNA encoding the receptor
  JOURNAL   Patent: US 6114139-A 257 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
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BD181841/c
LOCUS       BD181841                 20 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Method of surface-treating gold-plated product and surface-treated
            product, process for producing gold-plated product and gold-plated
            product, and method of immobilizing sulfur-containing molecule.
ACCESSION   BD181841
VERSION     BD181841.1  GI:30792759
KEYWORDS    JP 2002322587-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kobori,S., Nakama,K. and Miyahara,H.
  TITLE     Method of surface-treating gold-plated product and surface-treated
            product, process for producing gold-plated product and gold-plated
            product, and method of immobilizing sulfur-containing molecule
  JOURNAL   Patent: JP 2002322587-A 1 08-NOV-2002;
            KYOCERA CORP,TUM GENE INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002322587-A/1
            PD   08-NOV-2002
            PF   31-JAN-2002 JP 2002023914
            PI   SHINICHI KOBORI,KAZUHIRO NAKAMA,HIROYOSHI MIYAHARA PC
            C25D3/48,C25D5/48,C25D5/50,G01N33/553,G01N37/00//C12N15/09, PC
            C12Q1/68,
            PC   C12N15/00
            CC   Method of surface-treating gold-plated product and surface- CC
                 treated
            CC   product, process for producing gold-plated product and gold-
            CC   plated
            CC   product, and method of immobilizing sulfur-containing molecule
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        219 GCCACGACGGGGAGCAGC 235
              ||||||  |||||||||
Db         19 GCCACGGGGGGAGCAGC 3


RESULT 3340
DOGP41401
LOCUS       DOGP41401                21 bp    DNA     linear   MAM 07-MAR-1996
DEFINITION  Dog (Clone: CXX.414) primer for STS 414, 5' end.
ACCESSION   L24302
VERSION     L24302.1  GI:401996
KEYWORDS    PCR identification; PCR primer; STS.
SEGMENT     1 of 2
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
  TITLE     One hundred and one new simple sequence repeat-based markers for
            the canine genome
  JOURNAL   Mamm. Genome 6 (3), 192-195 (1995)
  MEDLINE   95268214
   PUBMED   7749226
COMMENT     Original source text: Canis familiaris (library: E. Ostrander, in
            pBluescript+) adult spleen DNA.
            Submitted by:
            Fred Hutchinson Cancer Research Center
            Transplantation Biology Dept
            1124 Columbia; Mailstop M318
            Seattle, WA 98104, USA
            e-mail: EAOstrander@lbl.gov
            PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
            PCR Profile:  Denaturation:    94 degrees C for 1.00 minute
            Annealing:       55 or 59 degrees C for 0.45 minutes
            Polymerization:  74 degrees C for 1.00 minutes
            PCR Cycles:      33
            Final Extension:  74 degrees C for 5.00 minutes.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
                     /tissue_type="spleen"
                     /dev_stage="adult"
                     /tissue_lib="E. Ostrander, in pBluescript+"
     primer_bind     1. .21

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTT 2178
              | ||| ||||||||||
Db          2 CCCCTATTTTTTTTTT 18


RESULT 3341
A20740
LOCUS       A20740                   21 bp    DNA     linear   PAT 18-MAY-1994
DEFINITION  oligonucleotide EPO 47.
ACCESSION   A20740
VERSION     A20740.1  GI:514070
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Fibi,M., Zettlmeissl,G. and Kuepper,H.
  TITLE     Human erythropoietin muteins, their production and their use
  JOURNAL   Patent: EP 0409113-A 31 23-JAN-1991;
            BEHRINGWERKE Aktiengesellschaft
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        479 GGCCGCCAGAGCCAGGA 495
              ||||||| | |||||||
Db          4 GGCCGCCCGCGCCAGGA 20


RESULT 3342
AR062638
LOCUS       AR062638                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 38 from patent US 5843738.
ACCESSION   AR062638
VERSION     AR062638.1  GI:5990329
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Bennett,C.Frank. and Mirabelli,C.K.
  TITLE     Oligonucleotide modulation of cell adhesion
  JOURNAL   Patent: US 5843738-A 38 01-DEC-1998;
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  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1647 AGCCTTCACTGGTTCTG 1663
              ||||||| ||| |||||
Db         20 AGCCTTCTCTGTTTCTG 4


RESULT 3336
BD143073
LOCUS       BD143073                 20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Aurora 2 kinase inhibitor.
ACCESSION   BD143073
VERSION     BD143073.1  GI:27848831
KEYWORDS    JP 2002095479-A/3.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fujino,Y.
  TITLE     Aurora 2 kinase inhibitor
  JOURNAL   Patent: JP 2002095479-A 3 02-APR-2002;
            MITSUBISHI TOKYO PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002095479-A/3
            PD   02-APR-2002
            PF   22-SEP-2000 JP 2000287928
            PI   YASUHIRO FUJINO
            PC   C12N15/09,A61K31/7088,A61K45/00,A61K48/00,A61P35/00,A61P43/00,
            PC   C12N9/99,
            PC   C12N15/00
            CC   Aurora 2 kinase inhibitor
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        595 CCGCCGCTCCGACCTGC 611
              ||||| |||||||| ||
Db          3 CCGCCACTCCGACCAGC 19


RESULT 3337
BD170783
LOCUS       BD170783                 20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel ferrocene-type polycyclic hydrocarbon derivatives, novel
            ferrocene-type naphthalenedimide derivatives, process for producing
            the same, intercalaters comprising the derivatives and method of
            electrochemically detecting gene.
ACCESSION   BD170783
VERSION     BD170783.1  GI:27876595
KEYWORDS    WO 02053571-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Takenaka,S., Takamiya,H. and Takagi,M.
  TITLE     Novel ferrocene-type polycyclic hydrocarbon derivatives, novel
            ferrocene-type naphthalenedimide derivatives, process for producing
            the same, intercalaters comprising the derivatives and method of
            electrochemically detecting gene
  JOURNAL   Patent: WO 02053571-A 1 11-JUL-2002;
            TUM GENE INC,SHIGEORI TAKENAKA,HIROKI TAKAMIYA,MAKOTO TAKAGI
COMMENT     OS   Homo sapiens (human)
            PN   WO 02053571-A/1
            PD   11-JUL-2002
            PF   28-DEC-2001 WO 2001JP011653
            PR   28-DEC-2000 JP 00P   402076
            PI   SHIGEORI TAKENAKA,HIROKI TAKAMIYA,MAKOTO TAKAGI PC
            C07F17/02,C12Q1/68,C12N15/09,G01N27/327,G01N33/50,G01N37/00 CC
            Novel ferrocene-type polycyclic hydrocarbon derivatives, novel CC
            ferrocene-type naphthalenedimide derivatives, process for  CC
                producing the
            CC   same, intercalaters comprising the derivatives and method of
            CC   electrochemically detecting gene
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        219 GCCACGACGGGAGCAGC 235
              |||||| |||||||||
Db          2 GCCACGGGGGGAGCAGC 18


RESULT 3338
BD175645
LOCUS       BD175645                 20 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Process for producing DNA.
ACCESSION   BD175645
VERSION     BD175645.1  GI:29121343
KEYWORDS    JP 2002253236-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aozuka,S.
  TITLE     Process for producing DNA
  JOURNAL   Patent: JP 2002253236-A 21 10-SEP-2002;
            NISSHINBO INDUSTRIES INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002253236-A/21
            PD   10-SEP-2002
            PF   26-JUL-2001 JP 2001226158
            PI   SATOSHI AOZUKA
            PC   C12N15/09,C12N15/00
            CC   Description of Artificial Sequence: synthetic DNA FH   Key
                    Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2120 TTAGGAAACTTGTAGAA 2136
              ||| ||||| |||||||
Db          2 TTAAGAAACATGTAGAA 18


RESULT 3339
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            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1457 GGAGACCAGAGTCCAGC 1473
              ||||||| |||| |||
Db          3 GGAGACCAAAGTCGAGC 19


RESULT 3333
BD079273
LOCUS       BD079273                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Receptors for peptides from insects.
ACCESSION   BD079273
VERSION     BD079273.1  GI:22624876
KEYWORDS    JP 2001299369-A/64.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Antonicek,H.P., Friedrich,G. and Schulte,T.
  TITLE     Receptors for peptides from insects
  JOURNAL   Patent: JP 2001299369-A 64 30-OCT-2001;
            BAYER AG
COMMENT     OS   Artificial Sequence
            PN   JP 2001299369-A/64
            PD   30-OCT-2001
            PF   06-MAR-2001 JP 2001061585
            PR   18-MAR-2000 DE   10013618.4
            PI   HORST PETER ANTONICEK,GABI FRIEDRICH,THOMAS SCHULTE PC
            C12N15/09,A01K67/033,C07K14/705,C07K16/28,C12N1/21,C12N5/10, PC
            C12P21/02,
            PC   C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566//C12P21/08,
            PC   (C12P21/02,C12R1:19),(C12P21/02,C12R1:91),(C12Q1/02,C12R1:91),
            PC   (C12P21/08,C12R1:91),C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        598 CCGCTCCGACCTGCTGC 614
              | ||||| |||||||||
Db          4 CAGCTCCTACCTGCTGC 20


RESULT 3334
BD087042
LOCUS       BD087042                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Erythrovirus and application thereof.
ACCESSION   BD087042
VERSION     BD087042.1  GI:22632652
KEYWORDS    JP 2001525163-A/6.
SOURCE      Erythrovirus
  ORGANISM  Erythrovirus
            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Nguyen,Q.T., Garbarg,C.A. and Auguste,V.
  TITLE     Erythrovirus and application thereof
  JOURNAL   Patent: JP 2001525163-A 6 11-DEC-2001;
            ASSISTANCE PUBLIQUE HOPITAUX DE PARIS
COMMENT     OS   Erythrovirus
            PN   JP 2001525163-A/6
            PD   11-DEC-2001
            PF   03-DEC-1998 JP 2000523317
            PR   03-DEC-1997 FR     97/15197
            PI   QUANG TRI NGUYEN,CHENON ANTOINE GARBARG,VERONIQUE AUGUSTE PC
            C12N15/09,A61K39/12,A61K48/00,C07K14/015,C07K16/08,C12Q1/68, PC
            G01N33/53,
            PC   C12N15/00
            CC   Erythrovirus and application thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Erythrovirus'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="Erythrovirus"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:40121"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        893 ACAGTGGCTGAAGTACA 909
              |||| |||||| |||||
Db          1 ACAGAGGCTGATGTACA 17


RESULT 3335
BD128029/c
LOCUS       BD128029                 20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD128029
VERSION     BD128029.1  GI:23222974
KEYWORDS    JP 2002017375-A/3460.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
            Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
            Koga,H.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002017375-A 3460 22-JAN-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2002017375-A/3460
            PD   22-JAN-2002
            PF   07-JUL-2000 JP 2000253172
            PI   TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
            PI   ISHII,
            PI   YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
            SHINICHI KOJIMA,
            PI   TETSUJI OTSUKI,HISASHI KOGA
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Description of Artificial Sequence: an artificially  CC
            synthesized primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
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            ALAN LEAD
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1729 ATTATCAGAAGGTGACA 1745
              ||||||||||| | ||
Db         19 ATTATCAGAAGGAGCCA 3


RESULT 3330
BD007718
LOCUS       BD007718                  20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Dioxin receptor gene and utilization thereof.
ACCESSION   BD007718
VERSION     BD007718.1  GI:18636091
KEYWORDS    JP 2001078782-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Oe,N.
  TITLE     Dioxin receptor gene and utilization thereof
  JOURNAL   Patent: JP 2001078782-A 13 27-MAR-2001;
            SUMITOMO CHEMICAL CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001078782-A/13
            PD   27-MAR-2001
            PF   27-APR-2000 JP 2000127243
            PR
            PI   NORIHISA OE
            PC   C12N15/09,C07K14/705,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC
            C12N7/00,
            PC   C12P21/02,C12Q1/02,G01N33/15,G01N33/50,G01N33/566,C12N15/00,
            PC   C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2243 AGGTACTGAAGCTTTAT 2259
              ||| |||||||| ||||
Db          4 AGGAACTGAAGCATTAT 20


RESULT 3331
BD012429/c
LOCUS       BD012429                  20 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  A novel gene encoding TSP1-like protein.
ACCESSION   BD012429
VERSION     BD012429.1  GI:22092618
KEYWORDS    WO 0109321-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T.,
            Murakami,K., Yano,K., Kanzaki,K. and Inoue,Y.
  TITLE     A novel gene encoding TSP1-like protein
  JOURNAL   Patent: WO 0109321-A 13 08-FEB-2001;
            HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,
            KOJI HAYASHI,KAORU SAITO,JUNICHI YAMAMOTO,SHIZUKO ISHII, OMOYASU
            SUGIYAMA, AI WAKAMATSU,KEIICHI NAGAI,TETSUJI OTSUKI,KOJI MURAKAMI,
            AZUHIRO YANO, KOJI KANZAKI,YOSHIHISA INOUE
COMMENT     OS   Artificial Sequence
            PN   WO 0109321-A/13
            PD   08-FEB-2001
            PF   28-JUL-2000 WO 2000JP005068
            PR   29-JUL-1999 JP 99P   248036,27-AUG-1999 JP 99P   300253 PR
            11-JAN-2000 JP 00P   118776,02-MAY-2000 JP 00P   183767 PR
            18-OCT-1999 US    60/159590,17-FEB-2000 US    60/183322 PI   TOSHIO
            OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI, PI   KAORU SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI,KOJI MURAKAMI,KAZUHIRO YANO, PI
            KOJI KANZAKI,
            PI   YOSHIHISA INOUE
            PC   C12N15/12,C07K14/47,C07K16/18,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized
            primer
            CC            KOJI KANZAKI,
            CC   sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1210 GAAGAACATGCTATTGG 1226
              |||| |||||| |||||
Db         17 GAAGCACATGCGATTGG 1


RESULT 3332
BD074731
LOCUS       BD074731                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisence oligonucleotide composition and modulation method of JNK
            protein.
ACCESSION   BD074731
VERSION     BD074731.1  GI:22620334
KEYWORDS    JP 2001514905-A/155.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mckay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
  TITLE     Antisence oligonucleotide composition and modulation method of JNK
            protein
  JOURNAL   Patent: JP 2001514905-A 155 18-SEP-2001;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001514905-A/155
            PD   18-SEP-2001
            PF   07-AUG-1998 JP 2000509875
            PR   13-AUG-1997 US    08/910629
            PI   ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
            NERO,WILLIAM A GAARDE
            PC   C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
            PC   C12N15/00
            CC   antisense sequence
            FH   Key             Location/Qualifiers
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            artificial sequences.
REFERENCE   1
  AUTHORS   Spytek,K.A., Li,L., Wolenc,A.R., Vernet,C.A., Eisen,A., Liu,X.,
            Malyankar,U., Shimkets,R.A., Tchernev,V.T., Spaderna,S.K.,
            Gorman,L., Kekuda,R., Patturajan,M., Gusev,V., Gangolli,E.A.,
            Guo,X., Shenoy,S., Rastelli,L., Casman,S.J., Boldog,F.,
            Burgess,C.E., Edinger,S., Ellerman,K., Gunther,E., Smithson,G.,
            Millet,I. and Macdougall,J.R.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 02062999-A 284 15-AUG-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically synthesized"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1123 TGTCTGTGAAGCCGAAT 1139
              | ||||||||||| ||||
Db         20 TCTCTGTGAAGCTGAAT 4


RESULT 3326
AX671167/c
LOCUS       AX671167                  20 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 7 from Patent WO03004511.
ACCESSION   AX671167
VERSION     AX671167.1  GI:29329623
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Renzi,P., Allam,M. and Allakhverdi,Z.
  TITLE     Methods for increasing in vivo efficacy of oligonucleotides and
            inhibiting inflammation in mammals
  JOURNAL   Patent: WO 03004511-A 7 16-JAN-2003;
            Topigen Pharmaceutiques Inc (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence is completely synthesized"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              | ||||||||||| |||
Db         18 GGGGCGGGGGCGGGGGC 2


RESULT 3327
AX810932
LOCUS       AX810932                  20 bp    DNA     linear   PAT 02-DEC-2003
DEFINITION  Sequence 59 from Patent EP1333100.
ACCESSION   AX810932
VERSION     AX810932.1  GI:38635529
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Park,J.G., Kim,I.J., Kang,H.C. and Park,J.H.
  TITLE     Ret oligonucleotide microchip and method for detecting hereditary
            cancer employing same
  JOURNAL   Patent: EP 1333100-A 59 06-AUG-2003;
            National Cancer Center (KR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="804M-(L)"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1175 CCTCATCTTGGAGGACG 1191
              ||||||| ||||| |||
Db          3 CCTCATCCTGGAGTACG 19


RESULT 3328
AX810938
LOCUS       AX810938                  20 bp    DNA     linear   PAT 02-DEC-2003
DEFINITION  Sequence 65 from Patent EP1333100.
ACCESSION   AX810938
VERSION     AX810938.1  GI:38635535
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Park,J.G., Kim,I.J., Kang,H.C. and Park,J.H.
  TITLE     Ret oligonucleotide microchip and method for detecting hereditary
            cancer employing same
  JOURNAL   Patent: EP 1333100-A 65 06-AUG-2003;
            National Cancer Center (KR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="804W-(V)"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1175 CCTCATCTTGGAGGACG 1191
              ||||||| ||||| |||
Db          3 CCTCATCGTGGAGTACG 19


RESULT 3329
BD000131/c
LOCUS       BD000131                  20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Detection of nucleic acid in cell by thermophilic strand
            substitutive  amplification.
ACCESSION   BD000131
VERSION     BD000131.1  GI:18623210
KEYWORDS    JP 2000300281-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Romains,K.L., Osutoreroba,N.V., Clive,M.V. and Lead,R.A.
  TITLE     Detection of nucleic acid in cell by thermophilic strand
            substitutive amplification
  JOURNAL   Patent: JP 2000300281-A 5 31-OCT-2000;
            BECTON DICKINSON & CO
COMMENT     OS   Artificial Sequence
            PN   JP 2000300281-A/5
            PD   31-OCT-2000
            PF   03-APR-2000 JP 2000101133
            PR   21-SEP-1995 US    08/531747,21-SEP-1995 US    08/531749 PI
            KENTON L ROMAINS,NATARI V OSUTOREROBA,MARK VAN CLIVE, PI   ROBERT
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  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        219 GCCACGACGGGAGCAGC 235
              ||||||  |||||||||
Db         19 GCCACGGGGGGAGCAGC 3


RESULT 3321
AX511782/c
LOCUS       AX511782                  20 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 189 from Patent WO02055705.
ACCESSION   AX511782
VERSION     AX511782.1  GI:23392482
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mezes,P.S., Rastelli,L., Herrmann,J.L., Macdougall,J.R., Zhong,H.,
            Casman,S.J., Boldog,F., Shimkets,R.A., Gorman,L., Crasta,O.R.,
            Mysore,K.K., Folkerts,O., Martin,G.B., Eisen,A., Spaderna,S.K.,
            Vernet,C.A., Bergh,C., Spytek,K.A., Dipippo,V.A., Zerhusen,B.D.,
            Peyman,J.A., Ellerman,K., Stone,D.J., Grosse,W.M., Alsobrook,J.P.,
            Lepley,D.M., Rieger,D.K., Burgess,C.E. and Edinger,S.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 02055705-A 189 18-JUL-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide primer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1123 TGTCTGTGAAGCCGAAT 1139
              | ||||||||||| ||||
Db         20 TCTCTGTGAAGCTGAAT 4


RESULT 3322
AX547000
LOCUS       AX547000                  20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 139 from Patent WO02053141.
ACCESSION   AX547000
VERSION     AX547000.1  GI:25812144
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 139 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        520 CGGGCGCCCGGCCGGCC 536
              ||| || ||||||||||
Db          2 CGGCCGGCCGGCCGGCC 18


RESULT 3323
AX547000/c
LOCUS       AX547000                  20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 139 from Patent WO02053141.
ACCESSION   AX547000
VERSION     AX547000.1  GI:25812144
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 139 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        520 CGGGCGCCCGGCCGGCC 536
              ||| || ||||||||||
Db         19 CGGCCGGCCGGCCGGCC 3


RESULT 3324
AX613393/c
LOCUS       AX613393                  20 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 4418 from Patent WO02072882.
ACCESSION   AX613393
VERSION     AX613393.1  GI:28408822
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 4418 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1544 GAGTAGGGAAGGAACAG 1560
              ||||||| |||| ||||
Db         17 GAGTAGGTAAGGCACAG 1


RESULT 3325
AX662602/c
LOCUS       AX662602                  20 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 284 from Patent WO02062999.
ACCESSION   AX662602
VERSION     AX662602.1  GI:29163271
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
  TITLE     Amplification of hiv-1 sequences for detection of sequences
            associated with drug-resistance mutations
  JOURNAL   Patent: WO 0220852-A 47 14-MAR-2002;
            Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer for Gag target sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1729 ATTATCAGAAGGTGACA 1745
              ||||||||||||  | ||
Db         20 ATTATCAGAAGGAGCCA 4


RESULT 3317
AX449244/c
LOCUS       AX449244                  20 bp    DNA     linear   PAT 03-JUL-2002
DEFINITION  Sequence 22 from Patent WO0206327.
ACCESSION   AX449244
VERSION     AX449244.1  GI:21698002
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wang,Z. and Xiao,W.
  TITLE     A method for prognosing cancer and the proteins involved
  JOURNAL   Patent: WO 0206327-A 22 24-JAN-2002;
            Northwestern University (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2318 TGTTGCTGCTTGTCACC 2334
              ||  ||||  |||||||||
Db         18 TGATGCTACTTGTCACC 2


RESULT 3318
AX452338/c
LOCUS       AX452338                  20 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 24 from Patent WO0242441.
ACCESSION   AX452338
VERSION     AX452338.1  GI:21712249
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Laemmle,B., Gerritsen,H.E., Furlan,M., Turecek,P., Schwarz,H.P.,
            Scheiflinger,F., Antoine,G., Kerschbaumer,R., Tagliavacca,L.,
            Zimmermann,K. and Voelkel,D.
  TITLE     Von willebrand factor (vwf) cleaving protease polypeptide, nucleic
            acid encoding the polypeptide and use of polypeptide
  JOURNAL   Patent: WO 0242441-A 24 30-MAY-2002;
            Baxter Aktiengesellschaft (AT)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     primer_bind     1. .20

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1591 CTGGGAACCCCTCCTGG 1607
              |||||  ||||||||  ||
Db         17 CTGGGGACCCCTCCAGG 1


RESULT 3319
AX462490/c
LOCUS       AX462490                  20 bp    DNA     linear   PAT 15-JUL-2002
DEFINITION  Sequence 234 from Patent EP1217079.
ACCESSION   AX462490
VERSION     AX462490.1  GI:21885703
KEYWORDS    .
SOURCE      Aegilops tauschii
  ORGANISM  Aegilops tauschii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Aegilops.
REFERENCE   1
  AUTHORS   Bernard,M., Sourdille,P. and Guyomarch,H.
  TITLE     Microsatellite markers from Triticum tauschii
  JOURNAL   Patent: EP 1217079-A 234 26-JUN-2002;
            INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Aegilops tauschii"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:37682"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        675 TGCCTCACCAGATGGAC 691
              |||||||||||  | ||
Db         20 TGCCTCACCAGAAGAAC 4


RESULT 3320
AX482700/c
LOCUS       AX482700                  20 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 1 from Patent WO02057488.
ACCESSION   AX482700
VERSION     AX482700.1  GI:22317120
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Takenaka,S.
  TITLE     Gene detection method, detection device, and detection chip
  JOURNAL   Patent: WO 02057488-A 1 25-JUL-2002;
            TUM GENE INC (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
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    source          1. .20
                    /organism="Mus sp."
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:10095"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        820 GAACCCCACTGAGGTCT 836
              ||||||||| ||| |||
Db         17 GAACCCCACAGAGCTCT 1


RESULT 3312
AX355150
LOCUS       AX355150                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 178 from Patent WO0197843.
ACCESSION   AX355150
VERSION     AX355150.1  GI:18619817
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 178 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphodiester backbone"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        520 CGGGCGCCCGGCCGGCC 536
              ||| || ||||||||||
Db          2 CGGCCGGCCGGCCGGCC 18


RESULT 3313
AX355150/c
LOCUS       AX355150                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 178 from Patent WO0197843.
ACCESSION   AX355150
VERSION     AX355150.1  GI:18619817
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 178 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphodiester backbone"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        520 CGGGCGCCCGGCCGGCC 536
              ||| || ||||||||||
Db         19 CGGCCGGCCGGCCGGCC 3


RESULT 3314
AX356992
LOCUS       AX356992                 20 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 34 from Patent WO0206523.
ACCESSION   AX356992
VERSION     AX356992.1  GI:18674188
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Acuna,G., Foernzler,D. and Leong,D.U.
  TITLE     Method for detecting pre-disposition to hepatotoxicity
  JOURNAL   Patent: WO 0206523-A 34 24-JAN-2002;
            F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        894 CAGTGGCTGAAGTACAG 910
              |||| | ||||||||||
Db          1 CAGTTGATGAAGTACAG 17


RESULT 3315
AX376964
LOCUS       AX376964                 20 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 21 from Patent EP1180547.
ACCESSION   AX376964
VERSION     AX376964.1  GI:19573258
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Aotsuka,S.C.
  TITLE     Method for producing dna
  JOURNAL   Patent: EP 1180547-A 21 20-FEB-2002;
            NISSHINBO INDUSTRIES, INC. (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2120 TTAGGAAACTTGTAGAA 2136
              ||| ||||| |||||||
Db          2 TTAAGAAACATGTAGAA 18


RESULT 3316
AX397813/c
LOCUS       AX397813                 20 bp    DNA     linear   PAT 27-MAY-2002
DEFINITION  Sequence 47 from Patent WO0220852.
ACCESSION   AX397813
VERSION     AX397813.1  GI:21260687
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AX214231
LOCUS       AX214231                 20 bp    RNA     linear   PAT 06-SEP-2001
DEFINITION  Sequence 44 from Patent WO0159102.
ACCESSION   AX214231
VERSION     AX214231.1  GI:15524308
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Breaker,R. and Emilsson,G.
  TITLE     Nucleozymes with endonuclease activity
  JOURNAL   Patent: WO 0159102-A 44 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2537 AGGGTATTAAGAATTAA 2553
              ||||||||||| ||| ||
Db          2 AGGGTATTAATAATGAA 18


RESULT 3308
AX294287/c
LOCUS       AX294287                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 6049 from Patent WO0179548.
ACCESSION   AX294287
VERSION     AX294287.1  GI:17055970
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 6049 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        395 TCGCATCTGGGGGAAGC 411
              ||||||| |||| |||
Db         19 TCGCATCTAGGGGGAGC 3


RESULT 3309
AX295071
LOCUS       AX295071                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 6833 from Patent WO0179548.
ACCESSION   AX295071
VERSION     AX295071.1  GI:17056754
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 6833 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2299 GGGTAGGCACGAAGCAA 2315
              |||||| | ||||||||
Db          4 GGGTAGACCCGAAGCAA 20


RESULT 3310
AX295402
LOCUS       AX295402                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 7164 from Patent WO0179548.
ACCESSION   AX295402
VERSION     AX295402.1  GI:17057091
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 7164 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1356 CCCACGGGTTTGGCAGC 1372
              ||||||||| ||| |||
Db          2 CCCACGGGTCTGGTAGC 18


RESULT 3311
AX298595/c
LOCUS       AX298595                 20 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 229 from Patent WO0183749.
ACCESSION   AX298595
VERSION     AX298595.1  GI:17128585
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
            Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
  TITLE     Gene and sequence variation associated with sensing carbohydrate
            compounds and other sweeteners
  JOURNAL   Patent: WO 0183749-A 229 08-NOV-2001;
            WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
            (US)
FEATURES             Location/Qualifiers
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  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 139 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        520 CGGGCGCCCGGCCGGCC 536
              ||| || ||||||||||
Db         19 CGGCCGGCCGGCCGGCC 3


RESULT 3303
AX117022
LOCUS       AX117022                  20 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 2145 from Patent WO0129262.
ACCESSION   AX117022
VERSION     AX117022.1  GI:14033964
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 2145 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1442 TCCTACATGAACCCTGG 1458
              ||||| |||| ||||||
Db          1 TCCTAGATGACCCCTGG 17


RESULT 3304
AX117942/c
LOCUS       AX117942                  20 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 3065 from Patent WO0129262.
ACCESSION   AX117942
VERSION     AX117942.1  GI:14034893
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 3065 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        898 GGCTGAAGTACAGAGGC 914
              ||||| ||||||| |||
Db         20 GGCTGGAGTACAGTGGC 4


RESULT 3305
AX149223
LOCUS       AX149223                  20 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 425 from Patent WO0136625.
ACCESSION   AX149223
VERSION     AX149223.1  GI:14347747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 425 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| |||| ||||||
Db          1 TTTTTATTTTCAACTTT 17


RESULT 3306
AX166722/c
LOCUS       AX166722                  20 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 213 from Patent WO0138503.
ACCESSION   AX166722
VERSION     AX166722.1  GI:14546997
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
            Flanagan,P. and Clary,D.S.
  TITLE     Novel human protein kinases and protein kinase-like enzymes
  JOURNAL   Patent: WO 0138503-A 213 31-MAY-2001;
            Sugen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        704 GTCGACGACCAGCACCT 720
              ||||| ||||||||| |
Db         18 GTCGAAGACCAGCACGT 2


RESULT 3307
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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1855 CAGACCCACACACTTAG 1871
              ||||||| |||||| ||
Db          4 CAGACCCTCACACTCAG 20


RESULT 3298
AX003426
LOCUS       AX003426                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 6 from Patent WO9928439.
ACCESSION   AX003426
VERSION     AX003426.1  GI:9927230
KEYWORDS    .
SOURCE      B19 virus
  ORGANISM  B19 virus
            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.
REFERENCE   1
  AUTHORS   Auguste,V., Garbarg-Chenon,A. and Nguyen,Q.T.
  TITLE     Erythrovirus and its applications
  JOURNAL   Patent: WO 9928439-A 6 10-JUN-1999;
            ASSIST PUBL HOPITAUX DE PARIS (FR); AUGUSTE VERONIQUE (FR); GARBARG
            CHENON ANTOINE (FR); NGUYEN QUANG TRI (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="B19 virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10798"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        893 ACAGTGGCTGAAGTACA 909
              |||| |||||| |||||
Db          1 ACAGAGGCTGATGTACA 17


RESULT 3299
AX008654/c
LOCUS       AX008654                 20 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 7 from Patent WO9966037.
ACCESSION   AX008654
VERSION     AX008654.1  GI:9996178
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: WO 9966037-A 7 23-DEC-1999;
            RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide inhibiting the common
                     subunit of IL-4 and IL-13 human receptor"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              | ||||||||||| |||
Db         18 GGGGCGGGGGCGGGGGC 2


RESULT 3300
AX046104/c
LOCUS       AX046104                 20 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 15 from Patent WO0066619.
ACCESSION   AX046104
VERSION     AX046104.1  GI:11344208
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Roy,F. and Bonne,S.
  TITLE     Means and methods for altering the functional properties in
            eukaryotic cells
  JOURNAL   Patent: WO 0066619-A 15 09-NOV-2000;
            Vlaams Interuniversitair Instituut voor Biotechnologie vz; w. (BE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="reverse primer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         591 CCTACCGCCGCTCCGAC 607
               ||||||||| || ||||
Db          19 CCTACCGCCTCTACGAC 3


RESULT 3301
AX103947
LOCUS       AX103947                 20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 139 from Patent WO0122972.
ACCESSION   AX103947
VERSION     AX103947.1  GI:13920144
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 139 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         520 CGGGCGCCCGGCCGGCC 536
               ||| || ||||||||||
Db          2 CGGCCGGCCGGCCGGCC 18


RESULT 3302
AX103947/c
LOCUS       AX103947                 20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 139 from Patent WO0122972.
ACCESSION   AX103947
VERSION     AX103947.1  GI:13920144
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
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  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1590 ACTGGGAACCCCTCCTG 1606
              |||| ||||||||| ||
Db         17 ACTGCGAACCCCTCTTG 1


RESULT 3293
AR313789
LOCUS       AR313789                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4326 from patent US 6559294.
ACCESSION   AR313789
VERSION     AR313789.1  GI:31707215
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 4326 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1326 AGAACTGCTTGTCTCAT 1342
              |||||||||||  |||
Db          3 AGAACTGCTTGTGCCAT 19


RESULT 3294
AR337182
LOCUS       AR337182                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 107 from patent US 6566135.
ACCESSION   AR337182
VERSION     AR337182.1  GI:33723036
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Watt,A.T.
  TITLE     Antisense modulation of caspase 6 expression
  JOURNAL   Patent: US 6566135-A 107 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        540 TGCCCCACCTCTCCGGG 556
              \\\\\\ |||||| |||
Db          2 TGCCCCGCCTCTCTGGG 18


RESULT 3295
AR344858/c
LOCUS       AR344858                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 47 from patent US 6582920.
ACCESSION   AR344858
VERSION     AR344858.1  GI:33740939
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
  TITLE     Amplification of HIV-1 RT sequences for detection of sequences
            associated with drug-resistance mutations
  JOURNAL   Patent: US 6582920-A 47 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1729 ATTATCAGAAGGTGACA 1745
              ||||||||||||  | ||
Db         20 ATTATCAGAAGGAGCCA 4


RESULT 3296
AR373535/c
LOCUS       AR373535                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 105 from patent US 6602713.
ACCESSION   AR373535
VERSION     AR373535.1  GI:40075664
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of protein phosphatase 2 catalytic subunit
            beta expression
  JOURNAL   Patent: US 6602713-A 105 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGCAG 69
              ||||||| |||||| |
Db         20 GGCGGGGGAGGCGGCGG 4


RESULT 3297
AR438112
LOCUS       AR438112                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from patent US 6660906.
ACCESSION   AR438112
VERSION     AR438112.1  GI:40204574
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tsichlis,P.N.
  TITLE     Tpl2 transgenic knockout mice
  JOURNAL   Patent: US 6660906-A 5 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
```

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FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1199 ATGGCAGCTAGGAAGAA 1215
              ||||||  |||||||||
Db          4 ATGGCAAATAGGAAGAA 20


RESULT 3288
AR271203
LOCUS       AR271203                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 146 from patent US 6503152.
ACCESSION   AR271203
VERSION     AR271203.1  GI:29702506
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Pelz,D.T.
  TITLE     Putting trainer
  JOURNAL   Patent: US 6503152-A 146 07-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        624 CACACGCCCTGGATGCC 640
              ||||||  |||||||||
Db          1 CACACGATCTGGATGCC 17


RESULT 3289
AR274662/c
LOCUS       AR274662                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 46 from patent US 6506595.
ACCESSION   AR274662
VERSION     AR274662.1  GI:29707196
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sato,S., Higashikuni,N., Kudo,T. and Kondo,M.
  TITLE     DNAs encoding new fusion proteins and processes for preparing
            useful polypeptides through expression of the DNAs
  JOURNAL   Patent: US 6506595-A 46 14-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1934 GTTAAGGTAATGGTTGG 1950
              | |||||  |||||||||
Db         20 GATAAGGGAATGGTTGG 4


RESULT 3290
AR275179/c
```

```
LOCUS       AR275179                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 11 from patent US 6506889.
ACCESSION   AR275179
VERSION     AR275179.1  GI:29708163
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Han,M. and Sieburth,D.
  TITLE     Ras suppressor SUR-8 and related compositions and methods
  JOURNAL   Patent: US 6506889-A 11 14-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2210 ATGGGAGACTCTTTGAA 2226
              ||| |||||||||| |||
Db         17 ATGAGAGACTCTTGGAA 1


RESULT 3291
AR278913
LOCUS       AR278913                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 10 from patent US 6514690.
ACCESSION   AR278913
VERSION     AR278913.1  GI:29713547
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Li,F., Hui,Z., Anderson,D.A., Logarnini,S.A. and Torresi,J.
  TITLE     Immunoreactive antigens of Hepatitis E Virus
  JOURNAL   Patent: US 6514690-A 10 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2239 CTTAAGGTACTGAAGCT 2255
              |||||||  ||||||||
Db          2 CTTAAGGCGCTGAAGCT 18


RESULT 3292
AR312181/c
LOCUS       AR312181                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2718 from patent US 6559294.
ACCESSION   AR312181
VERSION     AR312181.1  GI:31705607
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2718 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
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  Query Match           0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2623 AACTTTGTCTCGTTCCT 2639
              |||| |||||| |||||
Db          4 AACTCTGTCTCCTTCCT 20


RESULT 3283
AR235921
LOCUS       AR235921                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 28 from patent US 6461863.
ACCESSION   AR235921
VERSION     AR235921.1  GI:27279287
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Jarvis,D.L.
  TITLE     Modifying insect cell gylcosylation pathways with baculovirus
            expression vectors
  JOURNAL   Patent: US 6461863-A 28 08-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2346 GTGGAGGTTCTGTATTT 2362
              ||| |||||||||| |||
Db          1 GTGTAGGTTCTGTGTTT 17


RESULT 3284
AR264956/c
LOCUS       AR264956                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 40 from patent US 6492121.
ACCESSION   AR264956
VERSION     AR264956.1  GI:29693343
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 40 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2519 TTTTATTCATATATATA 2535
              |||| || |||||||||
Db         18 TTTTTTTTATATATATA 2


RESULT 3285
AR264957/c
LOCUS       AR264957                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 41 from patent US 6492121.
ACCESSION   AR264957
VERSION     AR264957.1  GI:29693344
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 41 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2519 TTTTATTCATATATATA 2535
              |||| || |||||||||
Db         18 TTTTTTTTATATATATA 2


RESULT 3286
AR264958/c
LOCUS       AR264958                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 42 from patent US 6492121.
ACCESSION   AR264958
VERSION     AR264958.1  GI:29693345
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 42 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2519 TTTTATTCATATATATA 2535
              |||| || |||||||||
Db         18 TTTTTTTTATATATATA 2


RESULT 3287
AR268790
LOCUS       AR268790                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 22 from patent US 6500625.
ACCESSION   AR268790
VERSION     AR268790.1  GI:29699415
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mulshine,J.L. and Tockman,M.S.
  TITLE     Methods for diagnosing cancer or precancer based upon hnRNP protein
            expression
  JOURNAL   Patent: US 6500625-A 22 31-DEC-2002;
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  JOURNAL   Patent: US 6369208-A 2 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          3 TTTTTATTTTTAATTTT 19


RESULT 3278
AR207166
LOCUS       AR207166                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 60 from patent US 6372492.
ACCESSION   AR207166
VERSION     AR207166.1  GI:21505991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Cowsert,L.M.
  TITLE     Antisense modulation of talin expression
  JOURNAL   Patent: US 6372492-A 60 16-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        429 ACCCCCTGCACCAGCCG 445
              || |||||||||||| |
Db          3 ACGCCCTGCACCAGCAG 19


RESULT 3279
AR208724/c
LOCUS       AR208724                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 23 from patent US 6383808.
ACCESSION   AR208724
VERSION     AR208724.1  GI:21509954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P. and Freier,S.M.
  TITLE     Antisense inhibition of clusterin expression
  JOURNAL   Patent: US 6383808-A 23 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2545 AAGAATTAAGAGGATGC 2561
              |||||  ||||||||||
Db         19 AAGAAGAAAGAGGATGC 3


RESULT 3280
AR228938/c
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LOCUS       AR228938                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 38 from patent US 6448080.
ACCESSION   AR228938
VERSION     AR228938.1  GI:27268080
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ward,D.T. and Watt,A.T.
  TITLE     Antisense modulation of WRN expression
  JOURNAL   Patent: US 6448080-A 38 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2450 TGAGACATGGGATCCAA 2466
              ||| |||||||| ||||
Db         19 TGAAACATGGGACCCAA 3


RESULT 3281
AR230963/c
LOCUS       AR230963                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 223 from patent US 6451602.
ACCESSION   AR230963
VERSION     AR230963.1  GI:27271750
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Popoff,I. and Cowsert,L.M.
  TITLE     Antisense modulation of PARP expression
  JOURNAL   Patent: US 6451602-A 223 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 TCCAGTGACCCGGACAG 38
              |||||| | ||||||||
Db         17 TCCAGTAATCCGGACAG 1


RESULT 3282
AR231782
LOCUS       AR231782                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6455249.
ACCESSION   AR231782
VERSION     AR231782.1  GI:27273357
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hsu,I.-C., Highsmith,W.E. Jr. and Shih,J.
  TITLE     Method of amplifying DNA and RNA mismatch cleavage products
  JOURNAL   Patent: US 6455249-A 5 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
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```
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lohman,K.L., Ostrerova,N.V., Cleve,M.V. and Reid,R.A.
  TITLE     Detection of nucleic acids in cells by thermophilic strand
            displacement amplification
  JOURNAL   Patent: US 5631147-A 5 20-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1729 ATTATCAGAAGGTGACA 1745
              ||||||||||||  | ||
Db         19 ATTATCAGAAGGAGCCA 3


RESULT 3273
I46642/c
LOCUS       I46642                   20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 621 from patent US 5639612.
ACCESSION   I46642
VERSION     I46642.1  GI:2470607
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
            polynucleotide probes identified based on T.sub.m
  JOURNAL   Patent: US 5639612-A 621 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        353 CCCTACCAGCAGCTGGC 369
              |||||  |||||  |||||
Db         17 CCCTAGCAGCAACTGGC 1


RESULT 3274
I95826/c
LOCUS       I95826                   20 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 5 from patent US 5733752.
ACCESSION   I95826
VERSION     I95826.1  GI:3940296
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lohman,K.L., Ostrerova,N.V., Cleve,M.Van. and Reid,R.Alan.
  TITLE     Detection of nucleid acids in cells by thermophilic strand
            displacement amplification
  JOURNAL   Patent: US 5733752-A 5 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1729 ATTATCAGAAGGTGACA 1745
              ||||||||||||  | ||
Db         19 ATTATCAGAAGGAGCCA 3


RESULT 3275
AR182905
LOCUS       AR182905                 20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 77 from patent US 6339068.
ACCESSION   AR182905
VERSION     AR182905.1  GI:20226112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
  TITLE     Vectors and methods for immunization or therapeutic protocols
  JOURNAL   Patent: US 6339068-A 77 15-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        520 CGGGCGCCCGGCCGGCC 536
              |||  ||  ||||||||||
Db          2 CGGCCGGCCGGCCGGCC 18


RESULT 3276
AR182905/c
LOCUS       AR182905                 20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 77 from patent US 6339068.
ACCESSION   AR182905
VERSION     AR182905.1  GI:20226112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
  TITLE     Vectors and methods for immunization or therapeutic protocols
  JOURNAL   Patent: US 6339068-A 77 15-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        520 CGGGCGCCCGGCCGGCC 536
              |||  ||  ||||||||||
Db         19 CGGCCGGCCGGCCGGCC 3


RESULT 3277
AR205764
LOCUS       AR205764                 20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 2 from patent US 6369208.
ACCESSION   AR205764
VERSION     AR205764.1  GI:21503429
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
```

```
            TSURUOKA NOBUO,
            PI   YAMAGUCHI MARE
            PC   C07K15/14,A61K37/02,C12N5/10,C12N15/19,C12P21/02,(C12P21/02,
            PC   C12R1:91);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences' FT
            misc_feature    1. .20
            FT                   /note='PCR primer named lambda gt11-foward F1
            FT                   primer'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        803 CTGGTGGGGGCCGTAAT 819
              ||||||  |||||  ||||
Db         18 CTGGTGTGGGCCATAAT 2


RESULT 3269
E39195/c
LOCUS       E39195                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  DNA encoding novel fused protein and process for producing useful
            protein mediating the expression thereof DNA encoding novel fused
            protein and process for producing useful protein mediating the
            expression thereof.
ACCESSION   E39195
VERSION     E39195.1  GI:13019269
KEYWORDS    JP 1999341991-A/41.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Seiji,S., Masahiko,H., Toshiyuki,K. and Masaaki,K.
  TITLE     DNA encoding novel fused protein and process for producing useful
            protein mediating the expression thereof
  JOURNAL   Patent: JP 1999341991-A 41 14-DEC-1999;
            ITO HAM KK,JUZO UDAKA
COMMENT     OS   Artificial Sequence
            PN   JP 1999341991-A/41
            PD   14-DEC-1999
            PF   30-MAR-1999 JP 1999089488
            PR
            PI   SEIJI SATO,MASAHIKO HIGASHIKUJI,TOSHIYUKI KUDO,MASAAKI KONDO
            PC   C12N15/09,C12N1/21,C12P21/02,C12P21/02//C07K14/605,C07K14/62,
            PC   C07K14/655,
            PC   C07K19/00,(C12N15/09,C12R1:08),(C12N1/21,C12R1:08),(C12P21/02,
            PC   C12R1:08),
            PC   C12N15/00,(C12N15/00,C12R1:08)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1934 GTTAAGGTAATGGTTGG 1950
              | |||||  |||||||||
Db         20 GATAAGGGAATGGTTGG 4


RESULT 3270
I12653/c
LOCUS       I12653                    20 bp    DNA     linear   PAT 26-JUL-1995
DEFINITION  Sequence 63 from patent US 5427909.
ACCESSION   I12653
VERSION     I12653.1  GI:910035
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okamoto,H. and Nakamura,T.
  TITLE     Oligonucleotides and determination system of HCV genotypes
  JOURNAL   Patent: US 5427909-A 63 27-JUN-1995;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1421 GCCCTGATTGTCATAGA 1437
              |||||  ||||  ||||||
Db         20 GCCCTCATTGCCATAGA 4


RESULT 3271
I19623
LOCUS       I19623                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 4 from patent US 5510239.
ACCESSION   I19623
VERSION     I19623.1  GI:1599978
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baracchini,E. Jr. and Bennett,C.F.
  TITLE     Oligonucleotide modulation of multidrug resistance-associated
            protein
  JOURNAL   Patent: US 5510239-A 4 23-APR-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              | ||||  ||||||||||
Db          4 GTGGCGCGGGCGGCGGC 20


RESULT 3272
I43323/c
LOCUS       I43323                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 5 from patent US 5631147.
ACCESSION   I43323
VERSION     I43323.1  GI:2468567
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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DEFINITION  Sequence 26 from patent US 6306655.
ACCESSION   AR174366
VERSION     AR174366.1  GI:17914686
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP alpha expression
  JOURNAL   Patent: US 6306655-A 26 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        378 AGTCGGCCGACCCCTAC 394
              ||||||||||  ||||
Db         18 AGTCGGCCGACTTCTAC 2


RESULT 3266
BD227905/c
LOCUS       BD227905                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha).
ACCESSION   BD227905
VERSION     BD227905.1  GI:33037675
KEYWORDS    JP 2002526125-A/108.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,F.C., Butler,M.M. and Jr,W.J.S.
  TITLE     Antisense oligonucleotide regulation of expression of tumor
            necrosis factor-alpha (TNF-alpha)
  JOURNAL   Patent: JP 2002526125-A 108 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526125-A/108
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574737
            PR   05-OCT-1998 US    09/166186,18-MAY-1999 US    09/313932 PI
            BRENDA F BAKER,FRANK C BENNETT,MADELINE M BUTLER,WILLIAM J  PI
            SHANAHAN JR
            PC   C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/
            PC   00,A61P1/16,
            PC   A61P1/18,A61P3/10,A61P17/00,A61P17/04,A61P29/00,A61P31/00, PC
             C07H21/02,
            PC   C07H21/04,C12N15/00
            CC   Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        453 CAGGCAGCCAGCAGCAG 469
              |||  ||||||||||  ||
Db         20 CAGCCAGCCAGCAGAAG 4


RESULT 3267
BD241888/c
LOCUS       BD241888                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation.
ACCESSION   BD241888
VERSION     BD241888.1  GI:33051658
KEYWORDS    JP 2002518007-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Renzi,P.
  TITLE     Antisense oligonucleotides for treating or preventing atopic
            diseases and neoplastic cell proliferation
  JOURNAL   Patent: JP 2002518007-A 7 25-JUN-2002;
            RECHERCHES EXPERTISES ET DEVELOPPEMENT MEDICAUX PARENZ INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002518007-A/7
            PD   25-JUN-2002
            PF   17-JUN-1999 JP 2000554846
            PR   17-JUN-1998 CA      2235420
            PI   PAOLO RENZI
            PC   C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P11/06,A61P29/00,
            PC   A61P35/00,
            PC   A61P37/08,C12N15/00,A61K37/02
            CC   Antisense oligonucleotide inhibiting the common subunit of IL-
            CC            4 and IL-13
            CC   human receptor
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              | ||||||||||| |||
Db         18 GGGGCGGGGGCGGGGGC 2


RESULT 3268
E08391/c
LOCUS       E08391                    20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer for analyzing cDNA sequences of human megakaryocyte
            growth differentiating factor.
ACCESSION   E08391
VERSION     E08391.1  GI:2176508
KEYWORDS    JP 1994313000-A/15.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tsujimoto,M., Kurihara,T., Ishida,N., Iwasa,F., Nakazato,H.,
            Yamaichi,H., Miura,T., Tsuruoka,N. and Yamaguchi,M.
  TITLE     MEGAKARYOCYTE-PROLIFERATING AND DIFFERENTIATING FACTOR
  JOURNAL   Patent: JP 1994313000-A 15 08-NOV-1994;
            SUNTORY LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994313000-A/15
            PD   08-NOV-1994
            PF   16-JUL-1993 JP 1993197752
            PR   17-JUL-1992 JP 92P   212305, 04-MAR-1993 JP 93P    67339 PI
            TSUJIMOTO MASAFUMI, KURIHARA TATSUYA, ISHIDA NOBUHIRO, PI   IWASA
            FUYUKI,
            PI   NAKAZATO HIROSHI, YAMAICHI HIROZO, MIURA TAKEHISA, PI
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AR126737
LOCUS       AR126737                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 166 from patent US 6180353.
ACCESSION   AR126737
VERSION     AR126737.1  GI:14113330
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M. and Cowsert,L.M.
  TITLE     Antisense modulation of daxx expression
  JOURNAL   Patent: US 6180353-A 166 30-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2032 AGGCAAAGGTTCTATCT 2048
              ||||||||| ||| ||||
Db          1 AGGCAAAGCTTCCATCT 17


RESULT 3261
AR130999
LOCUS       AR130999                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 26 from patent US 6190905.
ACCESSION   AR130999
VERSION     AR130999.1  GI:14119324
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dalb.o slashed.ge,H., Christgau,S., Andersen,L.Nonboe.,
            Kofod,L.Venke., Kauppinen,M.Sakari., Nielsen,J.Bech. and
            Dambmann,C.
  TITLE     Enzyme with protease activity
  JOURNAL   Patent: US 6190905-A 26 20-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1255 AGAACTTCTCAGCCAAG 1271
              |||||||||| | ||||
Db          4 AGAACTTCTCCGTCAAG 20


RESULT 3262
AR150032/c
LOCUS       AR150032                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 108 from patent US 6228642.
ACCESSION   AR150032
VERSION     AR150032.1  GI:15114623
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-(.alpha.) (TNF-.alpha.) expression
  JOURNAL   Patent: US 6228642-A 108 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        453 CAGGCAGCCAGCAGCAG 469
              ||| |||||||||| ||
Db         20 CAGCCAGCCAGCAGAAG 4


RESULT 3263
AR158377
LOCUS       AR158377                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 22 from patent US 6251586.
ACCESSION   AR158377
VERSION     AR158377.1  GI:16220399
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mulshine,J.L. and Tockman,M.S.
  TITLE     Epithelial protein and DNA thereof for use in early cancer
            detection
  JOURNAL   Patent: US 6251586-A 22 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1199 ATGGCAGCTAGGAAGAA 1215
              ||||||  |||||||||
Db          4 ATGGCAAATAGGAAGAA 20


RESULT 3264
AR163975
LOCUS       AR163975                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 173 from patent US 6271030.
ACCESSION   AR163975
VERSION     AR163975.1  GI:16234857
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP beta expression
  JOURNAL   Patent: US 6271030-A 173 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        712 CCAGCACCTGTTGCTGC 728
              |||||||||  ||||||
Db          3 CCAGCACCTTGTGCTGC 19


RESULT 3265
AR174366/c
LOCUS       AR174366                 20 bp    DNA     linear   PAT 17-DEC-2001
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RESULT 3255
AR107643/c
LOCUS       AR107643                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 83 from patent US 6110664.
ACCESSION   AR107643
VERSION     AR107643.1  GI:12823130
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 83 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAA 1519
              ||||||| | |||||||
Db         17 AGAAACAAATGAAATAA 1

RESULT 3256
AR108815
LOCUS       AR108815                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 2 from patent US 6111095.
ACCESSION   AR108815
VERSION     AR108815.1  GI:12824302
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 2 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          3 TTTTTATTTTTAATTTT 19

RESULT 3257
AR109207/c
LOCUS       AR109207                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6114118.
ACCESSION   AR109207
VERSION     AR109207.1  GI:12825483
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Templeton,J.W., Feng,J., Adams,L.Garry., Schurr,E., Gros,P.,
            Davis,D.S. and Smith,R. III.
  TITLE     Method of identification of animals resistant or susceptible to
            disease such as ruminant brucellosis, tuberculosis,
            paratuberculosis and salmonellosis
  JOURNAL   Patent: US 6114118-A 4 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2650 ACCCTAAGGTGAGTGTG 2666
              ||||||||||||| ||
Db         18 ACCCTAAGGTGAGCTTG 2

RESULT 3258
AR116574
LOCUS       AR116574                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 155 from patent US 6133246.
ACCESSION   AR116574
VERSION     AR116574.1  GI:14096896
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of JNK proteins
  JOURNAL   Patent: US 6133246-A 155 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1457 GGAGACCAGAGTCCAGC 1473
              |||||||| |||| |||
Db          3 GGAGACCAAAGTCGAGC 19

RESULT 3259
AR124483/c
LOCUS       AR124483                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 52 from patent US 6171860.
ACCESSION   AR124483
VERSION     AR124483.1  GI:14109844
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense inhibition of rank expression
  JOURNAL   Patent: US 6171860-A 52 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1457 GGAGACCAGAGTCCAGC 1473
              |||| |||||| |||||
Db         20 GGAGGCCAGAGACCAGC 4

RESULT 3260
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RESULT 3250
AR082428/c
LOCUS       AR082428                 20 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 25 from patent US 5972886.
ACCESSION   AR082428
VERSION     AR082428.1  GI:10009154
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tsujimoto,M., Iwasa,F., Tsuruoka,N., Nakazato,H., Miura,K.,
            Ishida,N., Kurihara,T., Yamaichi,K. and Yamaguchi,N.
  TITLE     Megakaryocyte differentiation factor
  JOURNAL   Patent: US 5972886-A 25 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        803 CTGGTGGGGGCCGTAAT 819
              ||||||  |||||  ||||
Db         18 CTGGTGTGGGCCATAAT 2


RESULT 3251
AR089233
LOCUS       AR089233                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 22 from patent US 5994062.
ACCESSION   AR089233
VERSION     AR089233.1  GI:10015990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mulshine,J.L. and Tockman,M.S.
  TITLE     Epithelial protein and DNA thereof for use in early cancer
            detection
  JOURNAL   Patent: US 5994062-A 22 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1199 ATGGCAGCTAGGAAGAA 1215
              ||||||  |||||||||
Db          4 ATGGCAAATAGGAAGAA 20


RESULT 3252
AR092669
LOCUS       AR092669                 20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 26 from patent US 5998190.
ACCESSION   AR092669
VERSION     AR092669.1  GI:10019421
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dalb.o slashed.ge,H., Christgau,S., Andersen,L.Nonboe.,
            Kofod,L.Venke., Kauppinen,M.Sakari., Nielsen,J.Bech. and
            Dambmann,C.
  TITLE     Enzyme with protease activity
  JOURNAL   Patent: US 5998190-A 26 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1255 AGAACTTCTCAGCCAAG 1271
              |||||||||| | ||||
Db          4 AGAACTTCTCCGTCAAG 20


RESULT 3253
AR100377/c
LOCUS       AR100377                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 108 from patent US 6080580.
ACCESSION   AR100377
VERSION     AR100377.1  GI:12810825
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
  TITLE     Antisense oligonucleotide modulation of tumor necrosis
            factor-.alpha. (TNF-.alpha.) expression
  JOURNAL   Patent: US 6080580-A 108 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        453 CAGGCAGCCAGCAGCAG 469
              ||| ||||||||||| ||
Db         20 CAGCCAGCCAGCAGAAG 4


RESULT 3254
AR103911
LOCUS       AR103911                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 23 from patent US 6087489.
ACCESSION   AR103911
VERSION     AR103911.1  GI:12815499
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M.
  TITLE     Antisense oligonucleotide modulation of human thymidylate synthase
            expression
  JOURNAL   Patent: US 6087489-A 23 11-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        370 CTACTCCCAGTCGGCCG 386
              | ||||||| ||||||
Db          2 CAACTCCCAGGCGGCCG 18
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RESULT 3245
AR037329
LOCUS       AR037329                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5801154.
ACCESSION   AR037329
VERSION     AR037329.1  GI:5955185
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baracchini,E., Bennett,C.Frank. and Dean,N.M.
  TITLE     Antisense oligonucleotide modulation of multidrug
            resistance-associated protein
  JOURNAL   Patent: US 5801154-A 4 01-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              | |||| ||||||||||
Db          4 GTGGCGCGGGCGGCGGC 20


RESULT 3246
AR040612
LOCUS       AR040612                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5807838.
ACCESSION   AR040612
VERSION     AR040612.1  GI:5959975
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baracchini,E. Jr. and Bennett,C.Frank.
  TITLE     Oligonucleotide modulation of multidrug resistance-associated
            protein
  JOURNAL   Patent: US 5807838-A 4 15-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              | |||| ||||||||||
Db          4 GTGGCGCGGGCGGCGGC 20


RESULT 3247
AR052440/c
LOCUS       AR052440                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 25 from patent US 5831030.
ACCESSION   AR052440
VERSION     AR052440.1  GI:5975804
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tsujimoto,M., Iwasa,F., Tsuruoka,N., Nakazato,H., Miura,K.,
            Ishida,N., Kurihara,T., Yamaichi,K. and Yamaguchi,N.
  TITLE     Antibodies specific for megakaryocyte differentiation factor
  JOURNAL   Patent: US 5831030-A 25 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        803 CTGGTGGGGGCCGTAAT 819
              |||||| ||||| ||||
Db         18 CTGGTGTGGGCCATAAT 2


RESULT 3248
AR068795
LOCUS       AR068795                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 26 from patent US 5854050.
ACCESSION   AR068795
VERSION     AR068795.1  GI:6001002
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dalb.o slashed.ge,H., Christgau,S., Andersen,L.Nonboe.,
            Kofod,L.Venke., Kauppinen,M.Sakari., Nielsen,J.Bech. and
            Dambmann,C.
  TITLE     Enzyme with protease activity
  JOURNAL   Patent: US 5854050-A 26 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        1255 AGAACTTCTCAGCCAAG 1271
               |||||||||| | ||||
Db          4 AGAACTTCTCCGTCAAG 20


RESULT 3249
AR075147
LOCUS       AR075147                  20 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 5 from patent US 5955322.
ACCESSION   AR075147
VERSION     AR075147.1  GI:10001899
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Guarnieri,F. and Bancroft,F.Carter.
  TITLE     DNA-based computer
  JOURNAL   Patent: US 5955322-A 5 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        252 TCCCCCACCTCTCCTCC 268
              ||||| ||||||||||
Db          4 TCCCCTTCCTCTCCTCC 20
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                  ||||||||| ||||||
Db          1 TTTATTTCATTTGTTTC 17


RESULT 3240
A40401
LOCUS       A40401                    20 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 28 from Patent WO9425606.
ACCESSION   A40401
VERSION     A40401.1  GI:2296441
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kocher,H.P., Schneider-Scherzer,E., Schoergendorfer,K. and Weber,G.
  TITLE     RECOMBINANT ALANINE RACEMASE AND GAPDH FROM TOLYPOCLADIUM
  JOURNAL   Patent: WO 9425606-A 28 10-NOV-1994;
            SANDOZ AG (AT)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1319 AACATACAGAACTGCTT 1335
              |||| ||||| ||||||
Db          3 AACAAACAGAGCTGCTT 19


RESULT 3241
AR010207/c
LOCUS       AR010207                  20 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5756702.
ACCESSION   AR010207
VERSION     AR010207.1  GI:3969012
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lohman,K.L., Ostrerova,N.V., Van Cleve,M. and Reid,R.Alan.
  TITLE     Detection of nucleic acids in cells by thermophilic strand
            displacement amplification
  JOURNAL   Patent: US 5756702-A 5 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1729 ATTATCAGAAGGTGACA 1745
              ||||||||||||| | ||
Db         19 ATTATCAGAAGGAGCCA 3


RESULT 3242
AR011627
LOCUS       AR011627                  20 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 36 from patent US 5763159.
ACCESSION   AR011627
VERSION     AR011627.1  GI:3969617
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Simmonds,P., Chan,S.-W. and Yap,P.Lee.
  TITLE     Hepatitis-C virus testing
  JOURNAL   Patent: US 5763159-A 36 09-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        250 GGTCCCCCACCTCTCCT 266
              |||||| | ||||||||
Db          1 GGTCCCACCCCTCTCCT 17


RESULT 3243
AR030970
LOCUS       AR030970                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5861501.
ACCESSION   AR030970
VERSION     AR030970.1  GI:5944184
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 2 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          3 TTTTTATTTTAATTTT 19


RESULT 3244
AR031542/c
LOCUS       AR031542                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5866374.
ACCESSION   AR031542
VERSION     AR031542.1  GI:5945831
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kobayashi,O., Hayashi,N. and Sone,H.
  TITLE     Gene conferring flocculating property on yeast and gene product
            thereof
  JOURNAL   Patent: US 5866374-A 8 02-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        160 GGACGCCATGTTGTGGA 176
              |||| |||||||||| |
Db         19 GGACACCATGTTGTGTA 3
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            FT   primer_bind     1. .19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1920 CCTTTTTTTTCAGTGTT 1936
              ||||||| |||| ||||
Db          2 CCTTTTTCTTCACTGTT 18


RESULT 3236
BD196765
LOCUS       BD196765                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Prostatic cancer gene.
ACCESSION   BD196765
VERSION     BD196765.1  GI:33006535
KEYWORDS    JP 2002516657-A/354.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
  TITLE     Prostatic cancer gene
  JOURNAL   Patent: JP 2002516657-A 354 11-JUN-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002516657-A/354
            PD   11-JUN-2002
            PF   22-DEC-1998 JP 2000525562
            PR   22-DEC-1997 US    08/996306,09-SEP-1998 US    60/099658 PI
            DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
            C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
            C12N1/19,
            PC   C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
            ,C12N15/00,C12N5/00,
            PC   C12N5/00,C12N15/00
            CC   upstream amplification primer for SEQ 260, SEQ 337 FH   Key
                 Location/Qualifiers
            FT   primer_bind     1. .19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1920 CCTTTTTTTTCAGTGTT 1936
              ||||||| |||| ||||
Db          2 CCTTTTTCTTCACTGTT 18


RESULT 3237
AR107647/c
LOCUS       AR107647                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 87 from patent US 6110664.
ACCESSION   AR107647
VERSION     AR107647.1  GI:12823134
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 87 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1504 GAAACACAGGAAATAAA 1520
              |||||| | ||||||||
Db         20 GAAACAAATGAAATAAA 4


RESULT 3238
AX048444/c
LOCUS       AX048444                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 43 from Patent WO0071747.
ACCESSION   AX048444
VERSION     AX048444.1  GI:12225608
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 43 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1974 CCTTGAAAAAAAGAAAA 1990
              |||| ||||||| ||||
Db         17 CCTTAAAAAAAAAAAAA 1


RESULT 3239
AR107644
LOCUS       AR107644                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 84 from patent US 6110664.
ACCESSION   AR107644
VERSION     AR107644.1  GI:12823131
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 84 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2267 TTTATTTCAGATGTTTC 2283
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            Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
REFERENCE   1
  AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
  TITLE     Verification of food origin based on nucleic acid pattern
            recognition
  JOURNAL   Patent: WO 03060160-A 144 24-JUL-2003;
            Genomar ASA (NO)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Salmo salar"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:8030"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        269 GCCGGGCAGCACCTCTA 285
              ||| ||||||| |||||
Db          2 GCCAGGCAGCAGCTCTA 18


RESULT 3233
BD103645
LOCUS       BD103645                  19 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An ex vivo animal or challenge model as method to measure
            protective immunity directed against parasites and vaccines shown
            to be protective in said method.
ACCESSION   BD103645
VERSION     BD103645.1  GI:22649219
KEYWORDS    JP 2001527391-A/9.
SOURCE      Fasciola hepatica (liver fluke)
  ORGANISM  Fasciola hepatica
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Echinostomida; Echinostomata; Fascioloidea; Fasciolidae; Fasciola.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Milligen,F.J.V., Cornelissen,J.B.W.J. and Bokhout,B.A.
  TITLE     An ex vivo animal or challenge model as method to measure
            protective immunity directed against parasites and vaccines shown
            to be protective in said method
  JOURNAL   Patent: JP 2001527391-A 9 25-DEC-2001;
            STICHTING DIENST LANDBOUWKUNDING ONDERZOEK
COMMENT     OS   Fasciola hepatica
            PN   JP 2001527391-A/9
            PD   25-DEC-2001
            PF   11-MAR-1998 JP 1998539474
            PR   11-MAR-1997 EP   97200730.6
            PI   FLORINE JOHANNA VAN MILLIGEN,
            PI   JOHANNES BERNARDUS WILHELMUS JOSEPH CORNELISSEN,BERNARD ADRI
            PI   BOKHOUT
            PC   C12N15/57,C12N9/64,C12Q1/68,C07K16/40,A01K67/027,A61K31/70, PC
              A61K38/48,
            PC   G01N33/573,G01N33/68
            CC   /Note='primer forward Adult, pos. 407-425'
            FH   Key             Location/Qualifiers
            FT   primer bind     (). .().
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Fasciola hepatica"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6192"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2630 TCTCGTTCCTGTTGGGC 2646
              | | |||||||||||||
Db          3 TGTGGTTCCTGTTGGGC 19


RESULT 3234
BD107601
LOCUS       BD107601                  19 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel microsatellite DNA derived from pear plants and method for
            discriminating pear plants using the same.
ACCESSION   BD107601
VERSION     BD107601.1  GI:23202419
KEYWORDS    JP 2002034597-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Yamamoto,T., Sawamura,Y., Imai,T., Matsuda,N., Saito,T., Shoda,M.,
            Kotobuki,K., Hayashi,K., Ba,Y., Kozono,M. and Kimura,T.
  TITLE     Novel microsatellite DNA derived from pear plants and method for
            discriminating pear plants using the same
  JOURNAL   Patent: JP 2002034597-A 10 05-FEB-2002;
            FRUIT TREE RES STATION
COMMENT     OS   Artificial Sequence
            PN   JP 2002034597-A/10
            PD   05-FEB-2002
            PF   21-JUL-2000 JP 2000220339
            PI   TOSHIYA YAMAMOTO,YUTAKA SAWAMURA,TSUYOSHI IMAI,NAGAO MATSUDA,
            PI   TOSHIHIRO SAITO,MORIYUKI SHODA,KAZUO KOTOBUKI,KENKI HAYASHI,
            PI   YOSHIYUKI BAN,
            PI   MASANORI KOZONO,TETSUYA KIMURA
            PC   C12Q1/68,A01H1/00,C12N15/09,C12N15/00
            CC   Description of Artificial Sequence:Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        173 TGGAAAATAACCGATAA 189
              |||| |||||| |||||
Db          2 TGGAGAATAACTGATAA 18


RESULT 3235
BD196445
LOCUS       BD196445                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Prostatic cancer gene.
ACCESSION   BD196445
VERSION     BD196445.1  GI:33006215
KEYWORDS    JP 2002516657-A/34.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
  TITLE     Prostatic cancer gene
  JOURNAL   Patent: JP 2002516657-A 34 11-JUN-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002516657-A/34
            PD   11-JUN-2002
            PF   22-DEC-1998 JP 2000525562
            PR   22-DEC-1997 US    08/996306,09-SEP-1998 US    60/099658 PI
            DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
            C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
            C12N1/19,
            PC   C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
            ,C12N15/00,C12N5/00,
            PC   C12N5/00,C12N15/00
            CC   upstream amplification primer 99-221-PU
            FH   Key             Location/Qualifiers
```

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Db         19 GGCCAGGGGGAAGACTT 3


RESULT 3228
AX131091/c
LOCUS       AX131091                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2309 from Patent WO0130362.
ACCESSION   AX131091
VERSION     AX131091.1  GI:14137396
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 2309 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin E ribozyme binding site"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        208 CTGCGAGGATCGCCACG 224
              |||||||||  ||||||
Db         17 CTGCGAGGAGAGCCACG 1


RESULT 3229
AX132837/c
LOCUS       AX132837                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 4055 from Patent WO0130362.
ACCESSION   AX132837
VERSION     AX132837.1  GI:14139147
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 4055 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="PCNA HH ribozyme binding site"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAA 2795
              |||||  ||  ||||||||
Db         18 AGAATAGAGAAAAAAAA 2


RESULT 3230
AX132840/c
LOCUS       AX132840                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 4058 from Patent WO0130362.
ACCESSION   AX132840
VERSION     AX132840.1  GI:14139150
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 4058 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="PCNA HH ribozyme binding site"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1491 TGGAGAAAATGGAGAAA 1507
              ||||||  |||  ||||||
Db         17 TGGAGAGAATAGAGAAA 1


RESULT 3231
AX378760
LOCUS       AX378760                  19 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 549 from Patent WO0206525.
ACCESSION   AX378760
VERSION     AX378760.1  GI:19574613
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I., Abderrahim,H. and Bihain,B.
  TITLE     Obesity associated biallelic marker maps
  JOURNAL   Patent: WO 0206525-A 549 24-JAN-2002;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     primer_bind     1. .19
                     /note="upstream amplification primer 99-221 for SEQ 527"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1920 CCTTTTTTTTCAGTGTT 1936
              |||||||  ||||  ||||
Db          2 CCTTTTTCTTCACTGTT 18


RESULT 3232
AX803976
LOCUS       AX803976                  19 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 144 from Patent WO03060160.
ACCESSION   AX803976
VERSION     AX803976.1  GI:38521111
KEYWORDS    .
SOURCE      Salmo salar (Atlantic salmon)
  ORGANISM  Salmo salar
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4936 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2709 TCTCTGCCTGTAAATGT 2725
              | ||||| |||||||||
Db          2 TATCTGCTTGTAAATGT 18


RESULT 3224
AR296121
LOCUS       AR296121                  19 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 7856 from patent US 6537751.
ACCESSION   AR296121
VERSION     AR296121.1  GI:31683405
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 7856 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1920 CCTTTTTTTTCAGTGTT 1936
              ||||||| |||| ||||
Db          2 CCTTTTTCTTCACTGTT 18


RESULT 3225
AR307194
LOCUS       AR307194                  19 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 15 from patent US 6551594.
ACCESSION   AR307194
VERSION     AR307194.1  GI:31697668
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   van Milligen,F.J., Cornelissen,J.B.W.J. and Bokhout,B.A.
  TITLE     Ex vivo animal or challenge model as method to measure protective
            immunity directed against parasites and vaccines shown to be
            protective in said method
  JOURNAL   Patent: US 6551594-A 15 22-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2630 TCTCGTTCCTGTTGGGC 2646
              | | |||||||||||||||
Db          3 TGTGGTTCCTGTTGGGC 19


RESULT 3226
AX011598
LOCUS       AX011598                  19 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 11 from Patent WO9955860.
ACCESSION   AX011598
VERSION     AX011598.1  GI:9998122
KEYWORDS    .
SOURCE      Gallus sp.
  ORGANISM  Gallus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1
  AUTHORS   Burgess,S.C., Davison,T.F. and Ross,L.J.
  TITLE     Host-encoded protein expressed on marek's disease (mdv)-infected
            cells and antibody thereto
  JOURNAL   Patent: WO 9955860-A 11 04-NOV-1999;
            ANIMAL HEALTH INST (GB); BURGESS SHANE CAMPBELL (GB); DAVISON
            THORNTON FREDERICK (GB); ROSS LOUIS JOSEPH NORMAN (GB)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Gallus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9036"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1250 TTCACAGAACTTCTCAG 1266
              |||||| | ||||||||
Db          3 TTCACACACCTTCTCAG 19


RESULT 3227
AX130773/c
LOCUS       AX130773                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1991 from Patent WO0130362.
ACCESSION   AX130773
VERSION     AX130773.1  GI:14137078
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1991 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin D3 ribozyme binding site"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1606 GGCCTGGGGGAAGAGTT 1622
              |||| |||||||||| ||
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RESULT 3218
AR205775
LOCUS       AR205775                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 13 from patent US 6369208.
ACCESSION   AR205775
VERSION     AR205775.1  GI:21503443
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 13 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3219
AR205776
LOCUS       AR205776                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 14 from patent US 6369208.
ACCESSION   AR205776
VERSION     AR205776.1  GI:21503444
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 14 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3220
AR205777
LOCUS       AR205777                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 15 from patent US 6369208.
ACCESSION   AR205777
VERSION     AR205777.1  GI:21503445
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 15 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3221
AR205778
LOCUS       AR205778                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 16 from patent US 6369208.
ACCESSION   AR205778
VERSION     AR205778.1  GI:21503447
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 16 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3222
AR280183
LOCUS       AR280183                 19 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 21 from patent US 6518044.
ACCESSION   AR280183
VERSION     AR280183.1  GI:29715570
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Berka,R.M., Rey,M.W., Brown,K. and Brown,S.H.
  TITLE     Promoters for expressing genes in a fungal cell
  JOURNAL   Patent: US 6518044-A 21 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         19 GTGTCCAGTGACCCGGA 35
              |||| |||||||||| ||
Db          1 GTGTGCAGTGACCCAGA 17


RESULT 3223
AR293201
LOCUS       AR293201                 19 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4936 from patent US 6537751.
ACCESSION   AR293201
VERSION     AR293201.1  GI:31680485
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Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3213
AR205768
LOCUS       AR205768                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6369208.
ACCESSION   AR205768
VERSION     AR205768.1  GI:21503434
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 6 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3214
AR205769
LOCUS       AR205769                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 7 from patent US 6369208.
ACCESSION   AR205769
VERSION     AR205769.1  GI:21503435
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 7 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3215
AR205770
LOCUS       AR205770                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 8 from patent US 6369208.
ACCESSION   AR205770
VERSION     AR205770.1  GI:21503437
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 8 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3216
AR205771
LOCUS       AR205771                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 9 from patent US 6369208.
ACCESSION   AR205771
VERSION     AR205771.1  GI:21503438
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 9 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3217
AR205772
LOCUS       AR205772                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 10 from patent US 6369208.
ACCESSION   AR205772
VERSION     AR205772.1  GI:21503439
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 10 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18
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  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3208
I81331
LOCUS       I81331                 19 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 5 from patent US 5710032.
ACCESSION   I81331
VERSION     I81331.1  GI:3209621
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Piepersberg,W., Brau,B. and Sichel,P.
  TITLE     Secondary-metabolite biosynthesis genes from actinomycetes, method
            of isolating them and their use
  JOURNAL   Patent: US 5710032-A 5 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        243 ATCCGCGGGTCCCCCAC 259
              |||||| ||||| ||||
Db          1 ATCCGCAGGTCCACCAC 17


RESULT 3209
I88034
LOCUS       I88034                 19 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 12 from patent US 5716846.
ACCESSION   I88034
VERSION     I88034.1  GI:3407974
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Brown,S.Joel., Dattagupta,N. and Naidu,Y.M.
  TITLE     Method for inhibiting cellular proliferation using antisense
            oligonucleotides to interleukin-6 receptor mRNA
  JOURNAL   Patent: US 5716846-A 12 10-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        455 GGCAGCCAGCAGCAGGC 471
              ||||||||||||| ||
Db          2 GGCAGCCAGCAGCGCGC 18


RESULT 3210
AR202164
LOCUS       AR202164               19 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 21 from patent US 6361973.
ACCESSION   AR202164
VERSION     AR202164.1  GI:20256703
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Berka,R.M., Rey,M.W., Brown,K. and Brown,S.H.
  TITLE     Promoters for expressing genes in a fungal cell
  JOURNAL   Patent: US 6361973-A 21 26-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         19 GTGTCCAGTGACCCGGA 35
              |||| |||||||||| ||
Db          1 GTGTGCAGTGACCCAGA 17


RESULT 3211
AR205763
LOCUS       AR205763               19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 1 from patent US 6369208.
ACCESSION   AR205763
VERSION     AR205763.1  GI:21503428
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 1 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3212
AR205766
LOCUS       AR205766               19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 4 from patent US 6369208.
ACCESSION   AR205766
VERSION     AR205766.1  GI:21503432
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6369208-A 4 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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```
RESULT 3204
BD242593
LOCUS       BD242593                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Host-encoded protein expressed by Marek's disease virus
            (MDV)-infected cell, and antibody against it.
ACCESSION   BD242593
VERSION     BD242593.1  GI:33052363
KEYWORDS    JP 2002518995-A/7.
SOURCE      Gallus sp.
  ORGANISM  Gallus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Burgess,S.C., Davison,T.F. and Ross,L.J.N.
  TITLE     Host-encoded protein expressed by Marek's disease virus
            (MDV)-infected cell, and antibody against it
  JOURNAL   Patent: JP 2002518995-A 7 02-JUL-2002;
            INSTITUTE FOR ANIMAL HEALTH LTD
COMMENT     OS   Gallus sp. (chicken)
            PN   JP 2002518995-A/7
            PD   02-JUL-2002
            PF   22-APR-1999 JP 2000546004
            PR   29-APR-1998 GB    9809070.7
            PI   SHANE CAMPBELL BURGESS,THORNTON FREDERICK
            DAVISON,LOUIS JOSEPH
            PI   NORMAN ROSS
            PC   C12N15/09,A61K38/00,A61K39/395,A61P31/12,C07K14/055,C07K16/08,
            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08//(C12P21/08, PC
              C12R1:91),
            PC   C12N15/00,A61K37/02,C12N5/00
            CC   Host-encoded protein expressed by Marek's disease virus (MDV)-
            CC            infected
            CC   cell, and antibody against it
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Gallus sp. (chicken)'.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Gallus sp."
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9036"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1250 TTCACAGAACTTCTCAG 1266
              |||||| | ||||||||
Db          3 TTCACACACCTTCTCAG 19


RESULT 3205
BD269034
LOCUS       BD269034                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Promoters for expressing genes in a fungal cell.
ACCESSION   BD269034
VERSION     BD269034.1  GI:33078802
KEYWORDS    JP 2002539793-A/18.
SOURCE      Fusarium
  ORGANISM  Fusarium
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; mitosporic Hypocreales.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Berka,R.M., Rey,M.W., Brown,K. and Brown,S.H.
  TITLE     Promoters for expressing genes in a fungal cell
  JOURNAL   Patent: JP 2002539793-A 18 26-NOV-2002;
            NOVOZYMES BIOTECH INC
COMMENT     OS   Fusarium
            PN   JP 2002539793-A/18
            PD   26-NOV-2002
            PF   22-MAR-2000 JP 2000606759
            PR   22-MAR-1999 US    09/274449
            PI   RANDY M BERKA,MICHAEL W REY,KIMBERLY BROWN,STEPHEN H BROWN PC
             C12N15/09,C07K14/37,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
            ,C12N9/00,C12P21/02,
            PC   C12N15/00,C12N5/00
            CC   Promoters for expressing genes in a fungal cell FH   Key
                  Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Fusarium'.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Fusarium"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:5506"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         19 GTGTCCAGTGACCCGGA 35
              |||| |||||||||| ||
Db          1 GTGTGCAGTGACCCAGA 17


RESULT 3206
I38722
LOCUS       I38722                   19 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 5 from patent US 5614619.
ACCESSION   I38722
VERSION     I38722.1  GI:2084776
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Piepersberg,W., Stockmann,M., Taleghani,K.M., Distler,Jurgen.,
            Grabley,S., Sichel,P. and Br au,B.
  TITLE     Secondary-metabolite biosynthesis genes from actinomycetes, method
            of isolating them and their use
  JOURNAL   Patent: US 5614619-A 5 25-MAR-1997;
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        243 ATCCGCGGGTCCCCCAC 259
              |||||| ||||| ||||
Db          1 ATCCGCAGGTCCACCAC 17


RESULT 3207
I62823
LOCUS       I62823                   19 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5660989.
ACCESSION   I62823
VERSION     I62823.1  GI:2480531
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cole,J.L., Kuo,L.C. and Olsen,D.B.
  TITLE     DNA polymerase extension assay for influenza virus endonuclease
  JOURNAL   Patent: US 5660989-A 1 26-AUG-1997;
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="unassigned DNA"
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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3199
AR108823
LOCUS       AR108823                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 10 from patent US 6111095.
ACCESSION   AR108823
VERSION     AR108823.1  GI:12824310
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 10 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3200
AR108826
LOCUS       AR108826                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 13 from patent US 6111095.
ACCESSION   AR108826
VERSION     AR108826.1  GI:12824313
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 13 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3201
AR108827
LOCUS       AR108827                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 14 from patent US 6111095.
ACCESSION   AR108827
VERSION     AR108827.1  GI:12824314
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 14 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3202
AR108828
LOCUS       AR108828                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 15 from patent US 6111095.
ACCESSION   AR108828
VERSION     AR108828.1  GI:12824315
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 15 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3203
AR108829
LOCUS       AR108829                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 16 from patent US 6111095.
ACCESSION   AR108829
VERSION     AR108829.1  GI:12824316
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 16 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18
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     source          i. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3194
AR108817
LOCUS       AR108817                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6111095.
ACCESSION   AR108817
VERSION     AR108817.1  GI:12824304
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 4 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3195
AR108819
LOCUS       AR108819                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 6 from patent US 6111095.
ACCESSION   AR108819
VERSION     AR108819.1  GI:12824306
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 6 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3196
AR108820
LOCUS       AR108820                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 7 from patent US 6111095.
ACCESSION   AR108820
VERSION     AR108820.1  GI:12824307
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 7 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3197
AR108821
LOCUS       AR108821                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 8 from patent US 6111095.
ACCESSION   AR108821
VERSION     AR108821.1  GI:12824308
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 8 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3198
AR108822
LOCUS       AR108822                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 9 from patent US 6111095.
ACCESSION   AR108822
VERSION     AR108822.1  GI:12824309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 9 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
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```
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 10 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3189
AR030981
LOCUS       AR030981                19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 13 from patent US 5861501.
ACCESSION   AR030981
VERSION     AR030981.1  GI:5944195
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 13 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3190
AR030982
LOCUS       AR030982                19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5861501.
ACCESSION   AR030982
VERSION     AR030982.1  GI:5944196
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 14 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3191
AR030983
LOCUS       AR030983                19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5861501.
ACCESSION   AR030983
VERSION     AR030983.1  GI:5944197
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 15 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3192
AR030984
LOCUS       AR030984                19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5861501.
ACCESSION   AR030984
VERSION     AR030984.1  GI:5944198
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 16 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3193
AR108814
LOCUS       AR108814                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 1 from patent US 6111095.
ACCESSION   AR108814
VERSION     AR108814.1  GI:12824301
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 6111095-A 1 29-AUG-2000;
FEATURES             Location/Qualifiers
```

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DEFINITION  Sequence 4 from patent US 5861501.
ACCESSION   AR030972
VERSION     AR030972.1  GI:5944186
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 4 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3184
AR030974
LOCUS       AR030974                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5861501.
ACCESSION   AR030974
VERSION     AR030974.1  GI:5944188
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 6 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3185
AR030975
LOCUS       AR030975                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 7 from patent US 5861501.
ACCESSION   AR030975
VERSION     AR030975.1  GI:5944189
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 7 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3186
AR030976
LOCUS       AR030976                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5861501.
ACCESSION   AR030976
VERSION     AR030976.1  GI:5944190
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 8 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3187
AR030977
LOCUS       AR030977                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 9 from patent US 5861501.
ACCESSION   AR030977
VERSION     AR030977.1  GI:5944191
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 9 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTTAATTTT 18


RESULT 3188
AR030978
LOCUS       AR030978                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 10 from patent US 5861501.
ACCESSION   AR030978
VERSION     AR030978.1  GI:5944192
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAA 2794
              | ||||| |||||||||
Db         17 TTGAATTAAAAAAAAAA 1


RESULT 3179
BD089251
LOCUS       BD089251                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089251
VERSION     BD089251.1  GI:22634861
KEYWORDS    JP 2001321190-A/1495.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 1495 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/1495
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
              Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        607 CCTGCTGCTGCCCCACG 623
              |||||| |||||| |||
Db          2 CCTGCTTCTGCCCTACG 18


RESULT 3180
A25084
LOCUS       A25084                   19 bp    DNA     linear   PAT 27-FEB-1995
DEFINITION  Synthetic Streptomyces nodosus sequencing primer P91.
ACCESSION   A25084
VERSION     A25084.1  GI:833536
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   .
  TITLE     SECONDARY-METABOLITE BIOSYNTHESIS GENES FROM ACTINOMYCETES, METHOD
            OF ISOLATING THEM, AND THEIR USE
  JOURNAL   Patent: WO 9306219-A 5 01-APR-1993;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        243 ATCCGCGGGTCCCCCAC 259
              |||||| ||||| ||||
Db          1 ATCCGCAGGTCCACCAC 17


RESULT 3181
A85285
LOCUS       A85285                   19 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 15 from Patent WO9840497.
ACCESSION   A85285
VERSION     A85285.1  GI:6733905
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bokhout,B.A. and Cornelissen,J.B.
  TITLE     AN EX VIVO ANIMAL OR CHALLENGE MODEL AS METHOD TO MEASURE
            PROTECTIVE IMMUNITY DIRECTED AGAINST PARASITES AND VACCINES SHOWN
            TO BE PROTECTIVE IN SAID METHOD
  JOURNAL   Patent: WO 9840497-A 15 17-SEP-1998;
            BOKHOUT BERNARD ADRI (NL); CORNELISSEN JOHANNES BERNARDUS (NL)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2630 TCTCGTTCCTGTTGGGC 2646
              | | ||||||||||||||
Db          3 TGTGGTTCCTGTTGGGC 19


RESULT 3182
AR030969
LOCUS       AR030969                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5861501.
ACCESSION   AR030969
VERSION     AR030969.1  GI:5944183
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
  TITLE     Capped synthetic RNA, analogs, and aptamers
  JOURNAL   Patent: US 5861501-A 1 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTAACTTT 2192
              ||||| ||||||| |||
Db          2 TTTTTATTTTAATTTT 18


RESULT 3183
AR030972
LOCUS       AR030972                 19 bp    DNA     linear   PAT 29-SEP-1999
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```
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
            Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
  TITLE     Gene and sequence variation associated with sensing carbohydrate
            compounds and other sweeteners
  JOURNAL   Patent: WO 0183749-A 215 08-NOV-2001;
            WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
            (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Mus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10095"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        575 AGCGCCCGCAGGGATGC 591
              || ||| ||||||||||
Db          2 AGTGCCTGCAGGGATGC 18


RESULT 3175
AX301867
LOCUS       AX301867                 18 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 22 from Patent WO0185944.
ACCESSION   AX301867
VERSION     AX301867.1  GI:17382924
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Anderson,C.M., Davis,R.E., Clevenger,W., Wiley,S.E., Miller,S.W.,
            Szabo,T.R., Ghosh,S.S., Moos,W.H., Pei,Y. and Carroll,A.K.
  TITLE     Production of adenine nucleotide translocator (ant), novel ant
            ligands and screening assays therefor
  JOURNAL   Patent: WO 0185944-A 22 15-NOV-2001;
            MITOKOR (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR Primer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1129 TGAAGCCGAATTTCCTA 1145
              |||||| ||| ||||||
Db          1 TGAAGCGGAAGTTCCTA 17


RESULT 3176
AX327038/c
LOCUS       AX327038                 18 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 234 from Patent WO0178894.
ACCESSION   AX327038
VERSION     AX327038.1  GI:18097749
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Keith,T.
  TITLE     Novel human gene relating to respiratory diseases, obesity, and
            inflammatory bowel disease
  JOURNAL   Patent: WO 0178894-A 234 25-OCT-2001;
            Genome Therapeutics Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2322 GCTGCTTGTCACCCCCA 2338
              ||||||| ||| |||||
Db         18 GCTGCTTCTCATCCCCA 2


RESULT 3177
AX404240
LOCUS       AX404240                 18 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 66 from Patent WO0224747.
ACCESSION   AX404240
VERSION     AX404240.1  GI:21437521
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U. and Hoffmeyer,S.
  TITLE     Polymorphisms in human genes of cardiovascular regulators and their
            use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 0224747-A 66 28-MAR-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         63 GCGGCAGACGCCTGGTC 79
              ||  ||||||||||||
Db          1 GCCCCAGACGCCTGGTC 17


RESULT 3178
AX662307/c
LOCUS       AX662307                 18 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 46 from Patent WO02059293.
ACCESSION   AX662307
VERSION     AX662307.1  GI:29163190
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Forster,A.C. and Blacklow,S.C.
  TITLE     Process and compositions for peptide, protein and peptidomimetic
            synthesis
  JOURNAL   Patent: WO 02059293-A 46 01-AUG-2002;
            Forster, Anthony C. (US) ; Blacklow, Stephen C. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="FROM SYNTHETIC DNA"
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    source          1. .18
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Sequencing primer"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1129 TGAAGCCGAATTTCCTA 1145
              ||||||  |||  ||||||
Db          1 TGAAGCGGAAGTTCCTA 17


RESULT 3170
AX135661
LOCUS       AX135661                 18 bp    DNA     linear   PAT 29-MAY-2001
DEFINITION  Sequence 2 from Patent WO0132922.
ACCESSION   AX135661
VERSION     AX135661.1  GI:14271931
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sorge,J.A.
  TITLE     Methods for detection of a target nucleic acid sequence
  JOURNAL   Patent: WO 0132922-A 2 10-MAY-2001;
            STRATAGENE (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="FEN nuclease cleavage product"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              ||||  |||  ||||||||
Db          1 AAAATAAATAAAAAAAA 17


RESULT 3171
AX135661/c
LOCUS       AX135661                 18 bp    DNA     linear   PAT 29-MAY-2001
DEFINITION  Sequence 2 from Patent WO0132922.
ACCESSION   AX135661
VERSION     AX135661.1  GI:14271931
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Sorge,J.A.
  TITLE     Methods for detection of a target nucleic acid sequence
  JOURNAL   Patent: WO 0132922-A 2 10-MAY-2001;
            STRATAGENE (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="FEN nuclease cleavage product"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||  |||  ||||
Db         17 TTTTTTTTATTTATTTT 1


RESULT 3172
AX149024
LOCUS       AX149024                 18 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 226 from Patent WO0136625.
ACCESSION   AX149024
VERSION     AX149024.1  GI:14347548
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 226 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense oligonucleotide"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTT 2178
              ||||||||  |  ||||||
Db          2 CTCCTTTTGTGTTTTT 18


RESULT 3173
AX207025/c
LOCUS       AX207025                 18 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 48 from Patent WO0155214.
ACCESSION   AX207025
VERSION     AX207025.1  GI:15394801
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Whittaker,P.A., Jones,S.J. and Hanley,M.T.
  TITLE     Disease-associated gene
  JOURNAL   Patent: WO 0155214-A 48 02-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2633 CGTTCCTGTTGGGCTGA 2649
              |||  ||||||||||  |
Db         18 CGTGCCTGTTGGGCTCA 2


RESULT 3174
AX298581
LOCUS       AX298581                 18 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 215 from Patent WO0183749.
ACCESSION   AX298581
VERSION     AX298581.1  GI:17128571
KEYWORDS    .
```

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  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        932 TGCTTAAATGCCTCGTT 948
              || | ||||||||||||
Db         17 TGGTGAAATGCCTCGTT 1


RESULT 3165
AR316676
LOCUS       AR316676                  18 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 22 from patent US 6562563.
ACCESSION   AR316676
VERSION     AR316676.1  GI:33695622
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Murphy,A.N., Clevenger,W., Wiley,S.E., Andreyev,A.Y., Frigeri,L.G.,
            Velecelebi,G. and Davis,R.E.
  TITLE     Compositions and mehtods for determining interactions of
            mitochondrial components, and for identifying agents that alter
            such interactions
  JOURNAL   Patent: US 6562563-A 22 13-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1129 TGAAGCCGAATTTCCTA 1145
              |||||| ||| ||||||
Db          1 TGAAGCGGAAGTTCCTA 17


RESULT 3166
AR324769/c
LOCUS       AR324769                  18 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 2171 from patent US 6566127.
ACCESSION   AR324769
VERSION     AR324769.1  GI:33710577
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 2171 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2687 AAATGGAGATTTGGAAT 2703
              |||||||||| || |||
Db         18 AAATGGAGATCTGTAAT 2


RESULT 3167
AR352433
LOCUS       AR352433                  18 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 2 from patent US 6589743.
ACCESSION   AR352433
VERSION     AR352433.1  GI:33757570
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Sorge,J.A.
  TITLE     Methods for detection of a target nucleic acid using a probe
            comprising secondary structure
  JOURNAL   Patent: US 6589743-A 2 08-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||| ||| ||||||||
Db          1 AAAATAAATAAAAAAAA 17


RESULT 3168
AR352433/c
LOCUS       AR352433                  18 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 2 from patent US 6589743.
ACCESSION   AR352433
VERSION     AR352433.1  GI:33757570
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Sorge,J.A.
  TITLE     Methods for detection of a target nucleic acid using a probe
            comprising secondary structure
  JOURNAL   Patent: US 6589743-A 2 08-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||||||| ||| ||||
Db         17 TTTTTTTTATTTATTTT 1


RESULT 3169
AX134739
LOCUS       AX134739                  18 bp    DNA     linear   PAT 29-MAY-2001
DEFINITION  Sequence 22 from Patent WO0132876.
ACCESSION   AX134739
VERSION     AX134739.1  GI:14271256
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Murphy,A.N., Clevenger,W., Wiley,S.E., Andreyev,A.Y., Frigeri,L.G.,
            Velicelebi,G. and Davis,R.E.
  TITLE     Compositions and methods for determining interactions of
            mitochondrial components, and for identifying agents that alter
            such interactions
  JOURNAL   Patent: WO 0132876-A 22 10-MAY-2001;
            MITOKOR (US)
FEATURES             Location/Qualifiers
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FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              || |||| |||||||||
Db         18 GCTGCGGCGGCGGCGGC 2


RESULT 3160
AR211744
LOCUS       AR211744                  18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 13 from patent US 6399358.
ACCESSION   AR211744
VERSION     AR211744.1  GI:21515148
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Williams,K.Jon. and Tabas,I.
  TITLE     Human gene encoding human chondroitin 6-sulfotransferase
  JOURNAL   Patent: US 6399358-A 13 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        998 TTGCGGGAGAAGTTGGA 1014
              |||||||||| |||| |
Db          1 TTGCGGGAGAGGTTGTA 17


RESULT 3161
AR215616
LOCUS       AR215616                  18 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 164 from patent US 6410323.
ACCESSION   AR215616
VERSION     AR215616.1  GI:23313872
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Roberts,M.L. and Cowsert,L.M.
  TITLE     Antisense modulation of human Rho family gene expression
  JOURNAL   Patent: US 6410323-A 164 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1498 AATGGAGAAACACAGGA 1514
              |||||||||||| | ||
Db          2 AATGGAGAAACAGATGA 18


RESULT 3162
AR229578
LOCUS       AR229578                  18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 23 from patent US 6449562.
ACCESSION   AR229578
VERSION     AR229578.1  GI:27269205
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chandler,V.S., Fulton,J.R. and Chandler,M.B.
  TITLE     Multiplexed analysis of clinical specimens apparatus and method
  JOURNAL   Patent: US 6449562-A 23 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1489 CCTGGAGAAAATGGAGA 1505
              ||||||||| | |||||
Db          2 CCTGGAGAAGAAGGAGA 18


RESULT 3163
AR229579/c
LOCUS       AR229579                  18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 24 from patent US 6449562.
ACCESSION   AR229579
VERSION     AR229579.1  GI:27269206
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chandler,V.S., Fulton,J.R. and Chandler,M.B.
  TITLE     Multiplexed analysis of clinical specimens apparatus and method
  JOURNAL   Patent: US 6449562-A 24 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1489 CCTGGAGAAAATGGAGA 1505
              ||||||||| | |||||
Db         17 CCTGGAGAAGAAGGAGA 1


RESULT 3164
AR297815/c
LOCUS       AR297815                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 9550 from patent US 6537751.
ACCESSION   AR297815
VERSION     AR297815.1  GI:31685099
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 9550 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"
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            specific hybridization and crosslinking agents for nucleic acids
  JOURNAL   Patent: US 5659022-A 7 19-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        165 CCATGTTGTGGAAAATA 181
              ||||||||||| |||| |
Db         17 CCATGTTGTGCAAAAAA 1


RESULT 3155
I64429/c
LOCUS       I64429                  18 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 51 from patent US 5665355.
ACCESSION   I64429
VERSION     I64429.1  GI:2481323
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Primi,D.
  TITLE     Diagnosis and treatment of AIDS onset
  JOURNAL   Patent: US 5665355-A 51 09-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        793 TCAGAAGGAGCTGGTGG 809
              ||||||||| |||| ||
Db         17 TCAGAAGGAACTGGAGG 1


RESULT 3156
AR188970/c
LOCUS       AR188970                18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 4458 from patent US 6346398.
ACCESSION   AR188970
VERSION     AR188970.1  GI:20234935
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 4458 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2687 AAATGGAGATTTGGAAT 2703
              |||||||||| || |||
Db         18 AAATGGAGATCTGTAAT 2


RESULT 3157
AR195017
LOCUS       AR195017                18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2 from patent US 6350580.
ACCESSION   AR195017
VERSION     AR195017.1  GI:20244454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Sorge,J.A.
  TITLE     Methods for detection of a target nucleic acid using a probe
            comprising secondary structure
  JOURNAL   Patent: US 6350580-A 2 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||| ||| ||||||||
Db          1 AAAATAAATAAAAAAAA 17


RESULT 3158
AR195017/c
LOCUS       AR195017                18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2 from patent US 6350580.
ACCESSION   AR195017
VERSION     AR195017.1  GI:20244454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Sorge,J.A.
  TITLE     Methods for detection of a target nucleic acid using a probe
            comprising secondary structure
  JOURNAL   Patent: US 6350580-A 2 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||| ||| ||||
Db         17 TTTTTTTTATTTATTTT 1


RESULT 3159
AR196702/c
LOCUS       AR196702                18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1167 from patent US 6350934.
ACCESSION   AR196702
VERSION     AR196702.1  GI:20246139
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 1167 26-FEB-2002;
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REFERENCE   1  (bases 1 to 18)
  AUTHORS   Anderson,C.M., Davis,R.E., Clevenger,W., Wiley,S.E., Miller,S.W.,
            Szabo,T.R. and Ghosh,S.S.
  TITLE     Production of adenine nucleotide translocator (ANT), novel ANT
            ligand, and screening assay thereof
  JOURNAL   Patent: JP 2002539761-A 22 26-NOV-2002;
            MITOKOR
COMMENT     OS   Artificial Sequence
            PN   JP 2002539761-A/22
            PD   26-NOV-2002
            PF   03-NOV-1999 JP 2000579742
            PR   03-NOV-1998 US    09/185904,08-SEP-1999 US    09/393441 PI
            CHRISTEN M ANDERSON,ROBERT E DAVIS,WILLIAM CLEVENGER,SANDRA  PI
            EILEEN WILEY,
            PI   SCOTT W MILLER,TOMAS R SZABO,SOUMITRA S GHOSH PC
            C12N15/09,A61K31/704,A61K31/7048,A61K31/7056,A61K31/7064, PC
            A61K45/00,
            PC   A61P3/00,A61P3/10,A61P17/06,A61P25/08,A61P25/14,A61P25/16, PC
             A61P25/18,
            PC   A61P25/28,A61P27/16,A61P35/00,A61P43/00,C07H15/256,C07H15/26,
            PC   C07K1/22,
            PC   C07K14/47,C07K19/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
            ,C12P21/02,C12Q1/02,
            PC   G01N33/15,G01N33/50,C12N15/00,C12N5/00
            CC   Sequencing primer
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1129 TGAAGCCGAATTTCCTA 1145
              ||||||  |||  ||||||
Db          1 TGAAGCGGAAGTTCCTA 17


RESULT 3151
I25305
LOCUS       I25305                   18 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 92 from patent US 5550020.
ACCESSION   I25305
VERSION     I25305.1  GI:1605175
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Gallie,B.L., Dunn,J.M. and Stevens,J.K.
  TITLE     Method, reagents and kit for diagnosis and targeted screening for
            retinoblastoma
  JOURNAL   Patent: US 5550020-A 92 27-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2074 ATCTGACACACTCTAAA 2090
              ||||||  |||||  ||||
Db          2 ATCTGAAACACTATAAA 18


RESULT 3152
I62390/c
LOCUS       I62390                   18 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2 from patent US 5659022.
ACCESSION   I62390
VERSION     I62390.1  GI:2480338
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B., Meyer,R.B. Jr. and
            Gall,A.
  TITLE     Oligonucleotide-cyclopropapyrroloindole conjugates as sequence
            specific hybridization and crosslinking agents for nucleic acids
  JOURNAL   Patent: US 5659022-A 2 19-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       165 CCATGTTGTGGAAAATA 181
             ||||||||||  ||||  |
Db        17 CCATGTTGTGCAAAAAA 1


RESULT 3153
I62393/c
LOCUS       I62393                   18 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 5 from patent US 5659022.
ACCESSION   I62393
VERSION     I62393.1  GI:2480341
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B., Meyer,R.B. Jr. and
            Gall,A.
  TITLE     Oligonucleotide-cyclopropapyrroloindole conjugates as sequence
            specific hybridization and crosslinking agents for nucleic acids
  JOURNAL   Patent: US 5659022-A 5 19-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       165 CCATGTTGTGGAAAATA 181
             ||||||||||  ||||  |
Db        17 CCATGTTGTGCAAAAAA 1


RESULT 3154
I62395/c
LOCUS       I62395                   18 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 7 from patent US 5659022.
ACCESSION   I62395
VERSION     I62395.1  GI:2480343
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B., Meyer,R.B. Jr. and
            Gall,A.
  TITLE     Oligonucleotide-cyclopropapyrroloindole conjugates as sequence
```

```
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense modulation of RhoG expression
  JOURNAL   Patent: US 5965370-A 21 12-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1498 AATGGAGAAACACAGGA 1514
              ||||||||||||  | ||
Db          2 AATGGAGAAACAGATGA 18


RESULT 3146
AR089726
LOCUS       AR089726                  18 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 8 from patent US 5994075.
ACCESSION   AR089726
VERSION     AR089726.1  GI:10016481
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Goodfellow,P.N.
  TITLE     Methods for identifying a mutation in a gene of interest without a
            phenotypic guide
  JOURNAL   Patent: US 5994075-A 8 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              ||||||| | |||||||
Db          1 GCGGCGGCGACGGCGGC 17


RESULT 3147
AR096293
LOCUS       AR096293                  18 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 14 from patent US 6007231.
ACCESSION   AR096293
VERSION     AR096293.1  GI:10024971
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Vijg,J. and Bishop,R.
  TITLE     Method of computer aided automated diagnostic DNA test design, and
            apparatus therefor
  JOURNAL   Patent: US 6007231-A 14 28-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2623 AACTTTGTCTCGTTCCT 2639
              ||||  ||||||  |||||
Db          2 AACTCTGTCTCCTTCCT 18


RESULT 3148
AR098755/c
LOCUS       AR098755                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 10 from patent US 6077672.
ACCESSION   AR098755
VERSION     AR098755.1  GI:12808521
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of TRADD expression
  JOURNAL   Patent: US 6077672-A 10 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1191 GAAATGAGATGGCAGCT 1207
              ||  |||||||||||||
Db         17 GAGGTGAGATGGCAGCT 1


RESULT 3149
AR098790
LOCUS       AR098790                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 45 from patent US 6077672.
ACCESSION   AR098790
VERSION     AR098790.1  GI:12808556
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of TRADD expression
  JOURNAL   Patent: US 6077672-A 45 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              | |||||  |||||||||
Db          2 GTGGCGGCGGCGGCGGC 18


RESULT 3150
BD249716
LOCUS       BD249716                  18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Production of adenine nucleotide translocator (ANT), novel ANT
            ligand, and screening assay thereof.
ACCESSION   BD249716
VERSION     BD249716.1  GI:33059486
KEYWORDS    JP 2002539761-A/22.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
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AR009718
LOCUS       AR009718                 18 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5756341.
ACCESSION   AR009718
VERSION     AR009718.1  GI:3968523
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kistner,O., Barrett,N., Mundt,W. and Dorner,F.
  TITLE     Method for controlling the infectivity of viruses
  JOURNAL   Patent: US 5756341-A 5 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||| | |||||
Db          2 CTTTTTTTTCTCTTTTT 18


RESULT 3141
AR009719/c
LOCUS       AR009719                 18 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5756341.
ACCESSION   AR009719
VERSION     AR009719.1  GI:3968524
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kistner,O., Barrett,N., Mundt,W. and Dorner,F.
  TITLE     Method for controlling the infectivity of viruses
  JOURNAL   Patent: US 5756341-A 6 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||| | |||||
Db         17 CTTTTTTTTCTCTTTTT 1


RESULT 3142
AR063241/c
LOCUS       AR063241                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5844110.
ACCESSION   AR063241
VERSION     AR063241.1  GI:5990932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Gold,B.I.
  TITLE     Synthetic triple helix-forming compound precursors
  JOURNAL   Patent: US 5844110-A 2 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              ||||| |||||| ||||
Db         17 GAAAAGAAAAAAGAAAA 1


RESULT 3143
AR063243
LOCUS       AR063243                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5844110.
ACCESSION   AR063243
VERSION     AR063243.1  GI:5990934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Gold,B.I.
  TITLE     Synthetic triple helix-forming compound precursors
  JOURNAL   Patent: US 5844110-A 4 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              |||| |||||||| |||
Db          2 CTTTCTTTTTTTCTTT 18


RESULT 3144
AR069211/c
LOCUS       AR069211                 18 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 51 from patent US 5891623.
ACCESSION   AR069211
VERSION     AR069211.1  GI:7220099
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Primi,D.
  TITLE     Diagnosis and treatment of AIDS onset
  JOURNAL   Patent: US 5891623-A 51 06-APR-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        793 TCAGAAGGAGCTGGTGG 809
              ||||||||| |||| ||
Db         17 TCAGAAGGAACTGGAGG 1


RESULT 3145
AR078877
LOCUS       AR078877                 18 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 21 from patent US 5965370.
ACCESSION   AR078877
VERSION     AR078877.1  GI:10005623
KEYWORDS    .
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  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTT 2179
              ||||||||| ||| |||
Db          1 TCCTTTTTTCTTTCTTT 17


RESULT 3136
BD203175/c
LOCUS       BD203175                 17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD203175
VERSION     BD203175.1  GI:33012945
KEYWORDS    JP 2002509721-A/6201.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 6201 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/6201
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              |||||||||  ||||||
Db         17 TTTTTTTTTAATTTTA 1


RESULT 3137
A67588
LOCUS       A67588                   18 bp    DNA     linear   PAT 05-MAY-1999
DEFINITION  Sequence 8 from Patent WO9744485.
ACCESSION   A67588
VERSION     A67588.1  GI:4756451
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Goodfellow,P.N.
  TITLE     METHODS FOR IDENTIFYING A MUTATION IN A GENE OF INTEREST
  JOURNAL   Patent: WO 9744485-A 8 27-NOV-1997;
            HEXAGEN TECHNOLOGY LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              ||||||| | |||||||
Db          1 GCGGCGGCGACGGCGGC 17


RESULT 3138
AR008470
LOCUS       AR008470                 18 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5753489.
ACCESSION   AR008470
VERSION     AR008470.1  GI:3967579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kistner,O., Barrett,N., Mundt,W. and Dorner,F.
  TITLE     Method for producing viruses and vaccines in serum-free culture
  JOURNAL   Patent: US 5753489-A 5 19-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||| | |||||
Db          2 CTTTTTTTTCTCTTTTT 18


RESULT 3139
AR008471/c
LOCUS       AR008471                 18 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5753489.
ACCESSION   AR008471
VERSION     AR008471.1  GI:3967580
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kistner,O., Barrett,N., Mundt,W. and Dorner,F.
  TITLE     Method for producing viruses and vaccines in serum-free culture
  JOURNAL   Patent: US 5753489-A 6 19-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||| | |||||
Db         17 CTTTTTTTTCTCTTTTT 1


RESULT 3140
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RESULT 3133
BD201337/c
LOCUS       BD201337                17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD201337
VERSION     BD201337.1  GI:33011107
KEYWORDS    JP 2002509721-A/4363.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 4363 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/4363
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2208 AAATGGGAGACTCTTTG 2224
              ||| ||||||||||||
Db         17 AAACTGGAGACTCTTTG 1


RESULT 3134
BD202793
LOCUS       BD202793                17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD202793
VERSION     BD202793.1  GI:33012563
KEYWORDS    JP 2002509721-A/5819.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 5819 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/5819
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTT 2171
              ||||| | |||||||||
Db          1 TTTTTCTTTCCTTTTTT 17


RESULT 3135
BD202799
LOCUS       BD202799                17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD202799
VERSION     BD202799.1  GI:33012569
KEYWORDS    JP 2002509721-A/5825.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 5825 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/5825
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
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VERSION     BD199240.1  GI:33009010
KEYWORDS    JP 2002509721-A/2266.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 2266 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/2266
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2353 TTCTGTATTTTAAGAAA 2369
              || | ||||||||||||
Db          1 TTGTATATTTTAAGAAA 17


RESULT 3131
BD200714
LOCUS       BD200714                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD200714
VERSION     BD200714.1  GI:33010484
KEYWORDS    JP 2002509721-A/3740.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 3740 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/3740
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1095 CTGTTCATTTGGCTAGG 1111
              || |||||||||||| |
Db          1 CTCTTCATTTGGCTATG 17


RESULT 3132
BD200955/c
LOCUS       BD200955                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD200955
VERSION     BD200955.1  GI:33010725
KEYWORDS    JP 2002509721-A/3981.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 3981 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/3981
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        879 CTAAATACAAAGTGACA 895
              | ||||| |||||||||
Db         17 CCAAATAAAAAGTGACA 1
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DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104925
VERSION     BD104925.1  GI:22650499
KEYWORDS    WO 0192572-A/1029.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1029 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1029
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1376 GCCATCTGTGCCGCGGT 1392
              ||||| | |||||||||
Db         17 GCCATGTCTGCCGCGGT 1


RESULT 3128
BD105168/c
LOCUS       BD105168                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD105168
VERSION     BD105168.1  GI:22650742
KEYWORDS    WO 0192572-A/1272.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 1272 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/1272
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1382 TGTGCCGCGGTGTCTGC 1398
              || |||||||||| ||
Db         17 TGAGCCGCGGTGTCCGC 1


RESULT 3129
BD198661
LOCUS       BD198661                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD198661
VERSION     BD198661.1  GI:33008431
KEYWORDS    JP 2002509721-A/1687.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 1687 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/1687
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                 concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1117 TGCCTATGTCTGTGAAG 1133
              ||| ||| |||||||||
Db          1 TGCTTATTTCTGTGAAG 17


RESULT 3130
BD199240
LOCUS       BD199240                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD199240
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Qy       2682 GGGTGAAATGGAGATTT 2698
              ||||||||||||  |||
Db          1 GGGTGAAATGGAATTTT 17


RESULT 3124
BD067822
LOCUS       BD067822                  17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067822
VERSION     BD067822.1  GI:22613425
KEYWORDS    JP 2001511003-A/662.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 662 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/662
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTT 2169
              |||  ||||||||||||
Db          1 GATAGTTTTCTCCTTTT 17


RESULT 3125
BD075191
LOCUS       BD075191                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Methods for assessing cardiovascular status and compositions for
            use thereof.
ACCESSION   BD075191
VERSION     BD075191.1  GI:22620794
KEYWORDS    JP 2001519660-A/64.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Norberg,L.T., Andersson,M.K. and Lindstrom,P.H.R.
  TITLE     Methods for assessing cardiovascular status and compositions for
            use thereof
  JOURNAL   Patent: JP 2001519660-A 64 23-OCT-2001;
            EURONA MEDICAL AB
COMMENT     OS   Artificial Sequence
            PN   JP 2001519660-A/64
            PD   23-OCT-2001
            PF   01-APR-1998 JP 1998542530
            PR   04-APR-1997 US    60/042930
            PI   LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY  PI
            RUTGER LINDSTROM
            PC   C12Q1/68,C07K14/72,C07K14/575,C12N9/48
            CC   Description of Artificial Sequence: PCR PRIMER FH   Key
                 Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        483 GCCAGAGCCAGGAGGGA 499
              |||||||||||  || ||
Db          1 GCCAGAGCCAGCAGAGA 17


RESULT 3126
BD104780
LOCUS       BD104780                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104780
VERSION     BD104780.1  GI:22650354
KEYWORDS    WO 0192572-A/884.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 884 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/884
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:capture
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1004 GAGAAGTTGGACAAGAT 1020
              ||||||  |||||||||
Db          1 GAGAAGCGGGACAAGAT 17


RESULT 3127
BD104925/c
LOCUS       BD104925                  17 bp    DNA     linear   PAT 27-AUG-2002
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```
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 1328 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATATT 2476
              |||| ||||||||| ||
Db          1 GATCAAATTTTAATCTT 17


RESULT 3120
AX759686
LOCUS       AX759686                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 3007 from Patent WO03040369.
ACCESSION   AX759686
VERSION     AX759686.1  GI:32254302
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 3007 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        752 GGTCCCATTTCCATGAC 768
              | |||||| ||||||||
Db          1 GATCCCATCTCCATGAC 17


RESULT 3121
AX761264/c
LOCUS       AX761264                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 4585 from Patent WO03040369.
ACCESSION   AX761264
VERSION     AX761264.1  GI:32255880
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 4585 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        202 AGAGGACTGCGAGGATC 218
              |||||||||| |||||
Db         17 AGAGGACTGCTCGGATC 1


RESULT 3122
AX761779/c
LOCUS       AX761779                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 5100 from Patent WO03040369.
ACCESSION   AX761779
VERSION     AX761779.1  GI:32256395
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 5100 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        202 AGAGGACTGCGAGGATC 218
              | | ||||||||||||||
Db         17 ATATGACTGCGAGGATC 1


RESULT 3123
AX796710
LOCUS       AX796710                  17 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 84 from Patent EP1323835.
ACCESSION   AX796710
VERSION     AX796710.1  GI:37517365
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Yano,H., Nishida,M. and Suzuki,O.
  TITLE     Method for determining biospecies contained in test specimen and
            kit used for the same
  JOURNAL   Patent: EP 1323835-A 84 02-JUL-2003;
            Nisshinbo Industries, Inc. (JP)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer: amplify cytochrome B gene"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTT 2121
              |||| |||||||||| ||
Db          1 GGGGACCTTCTGGTCTT 17


RESULT 3115
AX744256
LOCUS       AX744256                  17 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 221 from Patent WO03031621.
ACCESSION   AX744256
VERSION     AX744256.1  GI:30722923
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 221 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2106 GGGGCCTTCTGGTTTTA 2122
              ||| |||||||||| |||
Db          1 GGGACCTTCTGGTCTTA 17


RESULT 3116
AX744257
LOCUS       AX744257                  17 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 222 from Patent WO03031621.
ACCESSION   AX744257
VERSION     AX744257.1  GI:30722924
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 222 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2107 GGGCCTTCTGGTTTTAG 2123
              || |||||||||| ||||
Db          1 GGACCTTCTGGTCTTAG 17


RESULT 3117
AX744258
LOCUS       AX744258                  17 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 223 from Patent WO03031621.
ACCESSION   AX744258
VERSION     AX744258.1  GI:30722925
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 223 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2108 GGCCTTCTGGTTTTAGG 2124
              | |||||||||| |||||
Db          1 GACCTTCTGGTCTTAGG 17


RESULT 3118
AX751001/c
LOCUS       AX751001                  17 bp    DNA     linear   PAT 20-JUN-2003
DEFINITION  Sequence 217 from Patent WO03033703.
ACCESSION   AX751001
VERSION     AX751001.1  GI:32133329
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human gtp-activator protein for rab-like gtpase
  JOURNAL   Patent: WO 03033703-A 217 24-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        430 CCCCCTGCACCAGCCGG 446
              | ||||||| |||||||
Db         17 CGCCCTGCAGCAGCCGG 1


RESULT 3119
AX758007
LOCUS       AX758007                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 1328 from Patent WO03040369.
ACCESSION   AX758007
VERSION     AX758007.1  GI:32252623
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3883 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATATT 2476
              ||||| |||||| ||||
Db          1 GATCCTATTTTAGTATT 17


RESULT 3111
AX738337/c
LOCUS       AX738337                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3927 from Patent WO03025177.
ACCESSION   AX738337
VERSION     AX738337.1  GI:30517625
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3927 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2447 TTTTGAGACATGGGATC 2463
              |||| ||| ||||||||
Db         17 TTTTAAGAGATGGGATC 1


RESULT 3112
AX739654
LOCUS       AX739654                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5244 from Patent WO03025177.
ACCESSION   AX739654
VERSION     AX739654.1  GI:30518951
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 5244 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              ||  |||||||||||||
Db          1 GATCAAAAAAAAAAAAA 17


RESULT 3113
AX739654/c
LOCUS       AX739654                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5244 from Patent WO03025177.
ACCESSION   AX739654
VERSION     AX739654.1  GI:30518951
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 5244 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAAC 2189
              ||||||||||||| | |
Db         17 TTTTTTTTTTTTTGATC 1


RESULT 3114
AX744255
LOCUS       AX744255                 17 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 220 from Patent WO03031621.
ACCESSION   AX744255
VERSION     AX744255.1  GI:30722922
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 220 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1256 GAACTTCTCAGCCAAGA 1272
              || |||||||||||  ||
Db          1 GATCTTCTCAGCCAGGA 17


RESULT 3106
AX734519/c
LOCUS       AX734519                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 109 from Patent WO03025177.
ACCESSION   AX734519
VERSION     AX734519.1  GI:30513796
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 109 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        768 CCAAGAACCCTCTGAAC 784
              ||| |||||||||||  |
Db         17 CCATGAACCCTCTGATC 1


RESULT 3107
AX736769
LOCUS       AX736769                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2359 from Patent WO03025177.
ACCESSION   AX736769
VERSION     AX736769.1  GI:30516057
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 2359 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        215 GATCGCCACGACGGGAG 231
              |||| ||||||| ||||
Db          1 GATCCCCACGACTGGAG 17


RESULT 3108
AX736899
LOCUS       AX736899                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2489 from Patent WO03025177.
ACCESSION   AX736899
VERSION     AX736899.1  GI:30516187
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 2489 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATATT 2476
              ||||| |||||||| ||
Db          1 GATCCTATTTTAATTTT 17


RESULT 3109
AX738194
LOCUS       AX738194                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3784 from Patent WO03025177.
ACCESSION   AX738194
VERSION     AX738194.1  GI:30517482
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3784 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        122 GATCCTGGATTTAACTG 138
              ||||||||||  |||||
Db          1 GATCCTGGATGGAACTG 17


RESULT 3110
AX738293
LOCUS       AX738293                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3883 from Patent WO03025177.
ACCESSION   AX738293
VERSION     AX738293.1  GI:30517581
KEYWORDS    .
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  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 1336 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        202 AGAGGACTGCGAGGATC 218
              ||||||||||| |||||
Db         17 AGAGGACTGCTCGGATC 1


RESULT 3102
AX733126/c
LOCUS       AX733126                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4760 from Patent WO03025175.
ACCESSION   AX733126
VERSION     AX733126.1  GI:30512469
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 4760 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2447 TTTTGAGACATGGGATC 2463
              |||| ||| ||||||||
Db         17 TTTTAAGAGATGGGATC 1


RESULT 3103
AX733234
LOCUS       AX733234                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4868 from Patent WO03025175.
ACCESSION   AX733234
VERSION     AX733234.1  GI:30512577
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 4868 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATATT 2476
              ||||||| ||||| |||
Db          1 GATCCAAGTTTAAAATT 17


RESULT 3104
AX734171
LOCUS       AX734171                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5805 from Patent WO03025175.
ACCESSION   AX734171
VERSION     AX734171.1  GI:30513514
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 5805 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATATT 2476
              ||||||  |||||||||
Db          1 GATCCATCTTTAATATT 17


RESULT 3105
AX734204
LOCUS       AX734204                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5838 from Patent WO03025175.
ACCESSION   AX734204
VERSION     AX734204.1  GI:30513547
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 5838 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
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RESULT 3097
AX724865
LOCUS       AX724865                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2552 from Patent WO03025176.
ACCESSION   AX724865
VERSION     AX724865.1  GI:30504208
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 2552 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2013 GATCAAGTCCTCTGGTA 2029
              ||||||||||| ||| |
Db          1 GATCAAGTCCTTTGGGA 17


RESULT 3098
AX726582
LOCUS       AX726582                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4269 from Patent WO03025176.
ACCESSION   AX726582
VERSION     AX726582.1  GI:30505925
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 4269 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        122 GATCCTGGATTTAACTG 138
              ||||||||||||  ||
Db          1 GATCCTGGATTTACATG 17


RESULT 3099
AX728110
LOCUS       AX728110                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5797 from Patent WO03025176.
ACCESSION   AX728110
VERSION     AX728110.1  GI:30507453
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 5797 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2013 GATCAAGTCCTCTGGTA 2029
              ||||||||||| || ||
Db          1 GATCAAGTCCTTTGTTA 17


RESULT 3100
AX729216/c
LOCUS       AX729216                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 850 from Patent WO03025175.
ACCESSION   AX729216
VERSION     AX729216.1  GI:30508559
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 850 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1437 ACAAATCCTACATGAAC 1453
              |||||| ||||||||  |
Db         17 ACAAATACTACATGATC 1


RESULT 3101
AX729702/c
LOCUS       AX729702                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1336 from Patent WO03025175.
ACCESSION   AX729702
VERSION     AX729702.1  GI:30509045
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
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            medicines
  JOURNAL   Patent: WO 03004526-A 1026 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1983 AAAGAAAAGTGTGTATC 1999
              ||||||| ||||| |||
Db         17 AAAGAAATGTGTGGATC 1


RESULT 3093
AX672996/c
LOCUS       AX672996                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1441 from Patent WO03004526.
ACCESSION   AX672996
VERSION     AX672996.1  GI:29331344
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 1441 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2447 TTTTGAGACATGGGATC 2463
              |||| ||| ||||||||
Db         17 TTTTAAGAGATGGGATC 1


RESULT 3094
AX674166
LOCUS       AX674166                 17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 2611 from Patent WO03004526.
ACCESSION   AX674166
VERSION     AX674166.1  GI:29332514
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
  JOURNAL   Patent: WO 03004526-A 2611 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAA 2796
              ||  |||||||||||||
Db          1 GATCTGAAAAAAAAAAA 17


RESULT 3095
AX687461
LOCUS       AX687461                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 193 from Patent EP1281758.
ACCESSION   AX687461
VERSION     AX687461.1  GI:29410155
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 193 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1491 TGGAGAAAATGGAGAAA 1507
              ||| |||| ||||||||
Db          1 TGGTGAAACTGGAGAAA 17


RESULT 3096
AX688046
LOCUS       AX688046                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 778 from Patent EP1281758.
ACCESSION   AX688046
VERSION     AX688046.1  GI:29410744
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 778 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1194 ATGAGATGGCAGCTAGG 1210
              | |||||||||||| ||
Db          1 AAGAGATGGCAGCTGGG 17
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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        464 CAGCAGGCCTGGCCCGG 480
              ||||| ||||||||||
Db         17 CAGCATCCCTGGCCCGG 1


RESULT 3088
AX475826/c
LOCUS       AX475826                  17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1047 from Patent WO0224750.
ACCESSION   AX475826
VERSION     AX475826.1  GI:22215111
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 1047 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        463 GCAGCAGGCCTGGCCCG 479
              ||||||  |||||||||
Db         17 GCAGCATCCCTGGCCCG 1


RESULT 3089
AX475827/c
LOCUS       AX475827                  17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1048 from Patent WO0224750.
ACCESSION   AX475827
VERSION     AX475827.1  GI:22215112
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 1048 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        462 AGCAGCAGGCCTGGCCC 478
              ||||||| ||||||||
Db         17 AGCAGCATCCCTGGCCC 1


RESULT 3090
AX503011
LOCUS       AX503011                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 4318 from Patent EP1229046.
ACCESSION   AX503011
VERSION     AX503011.1  GI:23385304
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 4318 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2250 GAAGCTTTATTTGCATA 2266
              |||| |||||||| |||
Db          1 GAAGGTTTATTTGAATA 17


RESULT 3091
AX503012
LOCUS       AX503012                  17 bp    DNA     linear   PAT 27-SEP-2002
DEFINITION  Sequence 4319 from Patent EP1229046.
ACCESSION   AX503012
VERSION     AX503012.1  GI:23385305
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhan,J.
  TITLE     Human testis expressed patched like protein
  JOURNAL   Patent: EP 1229046-A 4319 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2251 AAGCTTTATTTGCATAT 2267
              ||| |||||||| ||||
Db          1 AAGGTTTATTTGAATAT 17


RESULT 3092
AX672581/c
LOCUS       AX672581                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 1026 from Patent WO03004526.
ACCESSION   AX672581
VERSION     AX672581.1  GI:29330929
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
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ACCESSION   AX422230
VERSION     AX422230.1  GI:21525612
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 566 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        557 CTGGAGGCGGGCGCGGT 573
              ||||||| || ||||||
Db         17 CTGGAGGAGGACGCGGT 1


RESULT 3084
AX422231/c
LOCUS       AX422231                 17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 567 from Patent WO0188124.
ACCESSION   AX422231
VERSION     AX422231.1  GI:21525613
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and
            Randi,A.M.
  TITLE     Method and reagent for the inhibition of erg
  JOURNAL   Patent: WO 0188124-A 567 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        556 GCTGGAGGCGGGCGCGG 572
              |||||||| || |||||
Db         17 GCTGGAGGAGGACGCGG 1


RESULT 3085
AX474922
LOCUS       AX474922                 17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 143 from Patent WO0224750.
ACCESSION   AX474922
VERSION     AX474922.1  GI:22214207
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 143 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        160 GGACGCCATGTTGTGGA 176
              |||| || |||||||||
Db          1 GGACTCCCTGTTGTGGA 17


RESULT 3086
AX474923
LOCUS       AX474923                 17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 144 from Patent WO0224750.
ACCESSION   AX474923
VERSION     AX474923.1  GI:22214208
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 144 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        161 GACGCCATGTTGTGGAA 177
              ||| || ||||||||||
Db          1 GACTCCCTGTTGTGGAA 17


RESULT 3087
AX475825/c
LOCUS       AX475825                 17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1046 from Patent WO0224750.
ACCESSION   AX475825
VERSION     AX475825.1  GI:22215110
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 1046 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
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                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2568 CTGTTCTTGGCTTGGAA 2584
              || ||||||| ||||||
Db         17 CTCTTCTTGGATTGGAA 1


RESULT 3079
AX266071/c
LOCUS       AX266071                  17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 3462 from Patent WO0173002.
ACCESSION   AX266071
VERSION     AX266071.1  GI:16514870
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 3462 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1297 GCTCGCCCCAGTCTTGG 1313
              ||||||||||| | |||
Db         17 GCTCGCCCCAGGCCTGG 1


RESULT 3080
AX266072
LOCUS       AX266072                  17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 3463 from Patent WO0173002.
ACCESSION   AX266072
VERSION     AX266072.1  GI:16514871
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 3463 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1297 GCTCGCCCCAGTCTTGG 1313
              ||||||||||| | |||
Db          1 GCTCGCCCCAGGCCTGG 17


RESULT 3081
AX326501
LOCUS       AX326501                  17 bp    DNA     linear   PAT 02-SEP-2002
DEFINITION  Sequence 2639 from Patent WO0192512.
ACCESSION   AX326501
VERSION     AX326501.1  GI:18097265
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
  TITLE     Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
  JOURNAL   Patent: WO 0192512-A 2639 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Zea mays"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:4577"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        566 GGCGCGGTGAGCGCCCG 582
              ||||||||||| | ||||
Db          1 GGCGCGGTGACCCCCCG 17


RESULT 3082
AX326502/c
LOCUS       AX326502                  17 bp    DNA     linear   PAT 02-SEP-2002
DEFINITION  Sequence 2640 from Patent WO0192512.
ACCESSION   AX326502
VERSION     AX326502.1  GI:18097266
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
  TITLE     Targeted chromosomal genomic alterations in plants using modified
            single stranded oligonucleotides
  JOURNAL   Patent: WO 0192512-A 2640 06-DEC-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Zea mays"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:4577"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        566 GGCGCGGTGAGCGCCCG 582
              ||||||||||| | ||||
Db         17 GGCGCGGTGACCCCCCG 1


RESULT 3083
AX422230/c
LOCUS       AX422230                  17 bp    RNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 566 from Patent WO0188124.
```

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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 933 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        553 CGGGCTGGAGGCGGGCG 569
              |||| |||||| |||||
Db         17 CGGGGTGGAGGGGGGCG 1


RESULT 3075
AX215749/c
LOCUS       AX215749                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 1191 from Patent WO0159103.
ACCESSION   AX215749
VERSION     AX215749.1  GI:15525792
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 1191 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2479 CTTTTAATGGTGATGGG 2495
              ||| |||||||||||  |
Db         17 CTTCTAATGGTGATGAG 1


RESULT 3076
AX216347
LOCUS       AX216347                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 1789 from Patent WO0159103.
ACCESSION   AX216347
VERSION     AX216347.1  GI:15526408
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 1789 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         52 CGGCGGGGGCGGCGGCA 68
              |||||| |||||| |||
Db          1 CGGCGGCGGCGGCAGCA 17


RESULT 3077
AX216730/c
LOCUS       AX216730                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 2172 from Patent WO0159103.
ACCESSION   AX216730
VERSION     AX216730.1  GI:15526791
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 2172 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2160 TTCTCCTTTTTTTTTTT 2176
              |||| || |||||||||
Db         17 TTCTTCTATTTTTTTTT 1


RESULT 3078
AX217796/c
LOCUS       AX217796                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 3238 from Patent WO0159103.
ACCESSION   AX217796
VERSION     AX217796.1  GI:15527857
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3238 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        262 CTCCTCCGCCGGGCAGC 278
              ||||||| |||| ||||
Db          1 CTCCTCCCCCGGCCAGC 17


RESULT 3070
AX215486/c
LOCUS       AX215486                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 928 from Patent WO0159103.
ACCESSION   AX215486
VERSION     AX215486.1  GI:15525529
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 928 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        558 TGGAGGCGGGCGCGGTG 574
              |||||| |||||||| |
Db         17 TGGAGGGGGGCGCGGCG 1


RESULT 3071
AX215488/c
LOCUS       AX215488                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 930 from Patent WO0159103.
ACCESSION   AX215488
VERSION     AX215488.1  GI:15525531
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 930 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        556 GCTGGAGGCGGGCGCGG 572
              | ||||||| ||||||||
Db         17 GGTGGAGGGGGGCGCGG 1


RESULT 3072
AX215489/c
LOCUS       AX215489                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 931 from Patent WO0159103.
ACCESSION   AX215489
VERSION     AX215489.1  GI:15525532
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 931 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        555 GGCTGGAGGCGGGCGCG 571
              || |||||| |||||||
Db         17 GGGTGGAGGGGGGCGCG 1


RESULT 3073
AX215490/c
LOCUS       AX215490                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 932 from Patent WO0159103.
ACCESSION   AX215490
VERSION     AX215490.1  GI:15525533
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 932 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        554 GGGCTGGAGGCGGGCGC 570
              ||| |||||| ||||||
Db         17 GGGGTGGAGGGGGGCGC 1


RESULT 3074
AX215491/c
LOCUS       AX215491                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 933 from Patent WO0159103.
ACCESSION   AX215491
VERSION     AX215491.1  GI:15525534
KEYWORDS    .
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          Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1720 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2313 CAATTTGTTGCTGCTTG 2329
              | | ||||||||||||||
Db          1 CCAGTTGTTGCTGCTTG 17


RESULT 3066
AX037439
LOCUS       AX037439                 17 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 64 from Patent WO0056922.
ACCESSION   AX037439
VERSION     AX037439.1  GI:11226864
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Norberg,L.T., Olaisson,E., Jonsson,L., Lindstrom,P.H. and
            Sanders,R.
  TITLE     Genetic polymorphism and polymorphic pattern for assessing disease
            status, and compositions for use thereof
  JOURNAL   Patent: WO 0056922-A 64 28-SEP-2000;
            NORBERG LEIF TORBJORN (SE) ; OLAISSON ERIK (SE) ; JONSSON LENA (SE)
            ; GEMINI GENOMICS AB (SE) ; LINDSTROM PER HARRY RUTGER (SE) ;
            SANDERS RHIANNON (SE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        483 GCCAGAGCCAGGAGGGA 499
              |||||||||| || ||
Db          1 GCCAGAGCCAGCAGAGA 17


RESULT 3067
AX214607/c
LOCUS       AX214607                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 49 from Patent WO0159103.
ACCESSION   AX214607
VERSION     AX214607.1  GI:15524650
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 49 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        552 CCGGGCTGGAGGCGGGC 568
              ||||| |||||| ||||
Db         17 CCGGGGTGGAGGGGGGC 1


RESULT 3068
AX214795/c
LOCUS       AX214795                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 237 from Patent WO0159103.
ACCESSION   AX214795
VERSION     AX214795.1  GI:15524838
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 237 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTTTT 2174
              |||||| || |||||||
Db         17 TTTTCTTCTATTTTTTT 1


RESULT 3069
AX215462
LOCUS       AX215462                 17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 904 from Patent WO0159103.
ACCESSION   AX215462
VERSION     AX215462.1  GI:15525505
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 904 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
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DEFINITION  Sequence 484 from patent US 6656700.
ACCESSION   AR434061
VERSION     AR434061.1  GI:40196904
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 484 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              ||||||||| ||| |||
Db          1 AAAAAAAAAGAAAGAAA 17


RESULT 3061
AR434061/c
LOCUS       AR434061                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 484 from patent US 6656700.
ACCESSION   AR434061
VERSION     AR434061.1  GI:40196904
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 484 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||| ||| |||||||||
Db         17 TTTCTTTCTTTTTTTT 1


RESULT 3062
AR435294
LOCUS       AR435294                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1717 from patent US 6656700.
ACCESSION   AR435294
VERSION     AR435294.1  GI:40198137
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1717 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGC 2326
              |||| | ||||||||||
Db          1 AAGCCAGTTGTTGCTGC 17


RESULT 3063
AR435295
LOCUS       AR435295                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1718 from patent US 6656700.
ACCESSION   AR435295
VERSION     AR435295.1  GI:40198138
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1718 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2311 AGCAATTTGTTGCTGCT 2327
              ||| | ||||||||||
Db          1 AGCCAGTTGTTGCTGCT 17


RESULT 3064
AR435296
LOCUS       AR435296                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1719 from patent US 6656700.
ACCESSION   AR435296
VERSION     AR435296.1  GI:40198139
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1719 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2312 GCAATTTGTTGCTGCTT 2328
              || | ||||||||||||
Db          1 GCCAGTTGTTGCTGCTT 17


RESULT 3065
AR435297
LOCUS       AR435297                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1720 from patent US 6656700.
ACCESSION   AR435297
VERSION     AR435297.1  GI:40198140
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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RESULT 3055
AR398176
LOCUS       AR398176                  17 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 557 from patent US 6617438.
ACCESSION   AR398176
VERSION     AR398176.1  GI:40135774
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Oligoribonucleotides with enzymatic activity
  JOURNAL   Patent: US 6617438-A 557 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||| |||| |||
Db          1 CTTTTTTTGTTTTGTTT 17


RESULT 3056
AR398177
LOCUS       AR398177                  17 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 558 from patent US 6617438.
ACCESSION   AR398177
VERSION     AR398177.1  GI:40135776
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Oligoribonucleotides with enzymatic activity
  JOURNAL   Patent: US 6617438-A 558 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||| |||| ||||||||
Db          1 TTTGTTTTGTTTTTTA 17


RESULT 3057
AR402322
LOCUS       AR402322                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 662 from patent US 6623962.
ACCESSION   AR402322
VERSION     AR402322.1  GI:40149772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and McSwiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases of conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: US 6623962-A 662 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTT 2169
              |||  ||||||||||||
Db          1 GATAGTTTTCTCCTTTT 17


RESULT 3058
AR433789/c
LOCUS       AR433789                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 212 from patent US 6656700.
ACCESSION   AR433789
VERSION     AR433789.1  GI:40196632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 212 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2312 GCAATTTGTTGCTGCTT 2328
              |||||||| |||| |||
Db         17 GCAATTTGATGCTTCTT 1


RESULT 3059
AR434060
LOCUS       AR434060                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 483 from patent US 6656700.
ACCESSION   AR434060
VERSION     AR434060.1  GI:40196903
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 483 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              |||||||||| ||| ||
Db          1 GAAAAAAAAAGAAAGAA 17


RESULT 3060
AR434061
LOCUS       AR434061                  17 bp    DNA     linear   PAT 18-DEC-2003
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RESULT 3050
AR326200/c
LOCUS       AR326200                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3602 from patent US 6566127.
ACCESSION   AR326200
VERSION     AR326200.1  GI:33712008
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 3602 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              ||| |||||| ||||||
Db         17 AAACAAAAAACAAAAAA 1


RESULT 3051
AR326201
LOCUS       AR326201                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3603 from patent US 6566127.
ACCESSION   AR326201
VERSION     AR326201.1  GI:33712009
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 3603 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              ||||| |||||| ||||
Db          1 TTTTTGTTTTTTGTTTT 17


RESULT 3052
AR326201/c
LOCUS       AR326201                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3603 from patent US 6566127.
ACCESSION   AR326201
VERSION     AR326201.1  GI:33712009
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 3603 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              ||| |||||| ||||||
Db         17 AAACAAAAAACAAAAAA 1


RESULT 3053
AR328033
LOCUS       AR328033                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 5435 from patent US 6566127.
ACCESSION   AR328033
VERSION     AR328033.1  GI:33713841
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 5435 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTTTT 2174
              || ||| ||||||||||
Db          1 TTCTCTACTTTTTTTTT 17


RESULT 3054
AR328926
LOCUS       AR328926                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 6328 from patent US 6566127.
ACCESSION   AR328926
VERSION     AR328926.1  GI:33714734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 6328 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAA 1519
              ||| |||||||||| |
Db          1 AGAGACACAGGAAATTA 17
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RESULT 3045
AR323678/c
LOCUS       AR323678                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1080 from patent US 6566127.
ACCESSION   AR323678
VERSION     AR323678.1  GI:33709486
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1080 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAA 2797
              | ||| ||||||||||||
Db         17 ATTTGGAAAAAAAAAAA 1


RESULT 3046
AR323679/c
LOCUS       AR323679                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1081 from patent US 6566127.
ACCESSION   AR323679
VERSION     AR323679.1  GI:33709487
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1081 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAA 2796
              || ||| ||||||||||
Db         17 GATTTGGAAAAAAAAAA 1


RESULT 3047
AR324663
LOCUS       AR324663                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 2065 from patent US 6566127.
ACCESSION   AR324663
VERSION     AR324663.1  GI:33710471
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 2065 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2552 AAGAGGATGCTGGGCTC 2568
              |||||||| |||| |||
Db          1 AAGAGGATTCTGGACTC 17


RESULT 3048
AR324664
LOCUS       AR324664                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 2066 from patent US 6566127.
ACCESSION   AR324664
VERSION     AR324664.1  GI:33710472
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 2066 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2553 AGAGGATGCTGGGCTCT 2569
              ||||||| |||| ||||
Db          1 AGAGGATTCTGGACTCT 17


RESULT 3049
AR326200
LOCUS       AR326200                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3602 from patent US 6566127.
ACCESSION   AR326200
VERSION     AR326200.1  GI:33712008
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 3602 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||||| |||||| |||
Db          1 TTTTTTGTTTTTTGTTT 17
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Db         17 AAACAAAAAACAAAAAA 1


RESULT 3040
AR192331
LOCUS       AR192331                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 7819 from patent US 6346398.
ACCESSION   AR192331
VERSION     AR192331.1  GI:20238296
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 7819 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||| |||||| ||||
Db          1 TTTTTGTTTTTTGTTTT 17


RESULT 3041
AR192331/c
LOCUS       AR192331                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 7819 from patent US 6346398.
ACCESSION   AR192331
VERSION     AR192331.1  GI:20238296
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 7819 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||| |||||| |||||
Db         17 AAAACAAAAAACAAAAA 1


RESULT 3042
AR286186
LOCUS       AR286186                  17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 558 from patent US 6528640.
ACCESSION   AR286186
VERSION     AR286186.1  GI:29723782
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 558 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              |||||||| |||| |||
Db          1 CTTTTTTTGTTTTGTTT 17


RESULT 3043
AR286187
LOCUS       AR286187                  17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 559 from patent US 6528640.
ACCESSION   AR286187
VERSION     AR286187.1  GI:29723783
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 559 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||| |||| ||||||||
Db          1 TTTGTTTTGTTTTTTA 17


RESULT 3044
AR323666
LOCUS       AR323666                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1068 from patent US 6566127.
ACCESSION   AR323666
VERSION     AR323666.1  GI:33709474
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1068 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTT 2175
              | ||| ||||||||||
Db          1 TCTCTACTTTTTTTTT 17
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                  |||||||| |||| |||
Db          1 AAGAGGATTCTGGACTC 17


RESULT 3035
AR188811
LOCUS       AR188811                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 4299 from patent US 6346398.
ACCESSION   AR188811
VERSION     AR188811.1  GI:20234776
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 4299 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2553 AGAGGATGCTGGGCTCT 2569
                |||||||| |||| ||||
Db          1 AGAGGATTCTGGACTCT 17


RESULT 3036
AR190370
LOCUS       AR190370                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 5858 from patent US 6346398.
ACCESSION   AR190370
VERSION     AR190370.1  GI:20236335
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 5858 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2552 AAGAGGATGCTGGGCTC 2568
                |||||||| |||| |||
Db          1 AAGAGGATTCTGGACTC 17


RESULT 3037
AR190371
LOCUS       AR190371                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 5859 from patent US 6346398.
ACCESSION   AR190371
VERSION     AR190371.1  GI:20236336
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 5859 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2553 AGAGGATGCTGGGCTCT 2569
                |||||||| |||| ||||
Db          1 AGAGGATTCTGGACTCT 17


RESULT 3038
AR192330
LOCUS       AR192330                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 7818 from patent US 6346398.
ACCESSION   AR192330
VERSION     AR192330.1  GI:20238295
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 7818 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
                |||||| |||||| |||
Db          1 TTTTTTGTTTTTTGTTT 17


RESULT 3039
AR192330/c
LOCUS       AR192330                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 7818 from patent US 6346398.
ACCESSION   AR192330
VERSION     AR192330.1  GI:20238295
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 7818 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
                ||| ||||||| |||||||
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              |||||||||| |||| |
Db          1 TTTTTTTTAATTTTGTA 17


RESULT 3030
I51720/c
LOCUS       I51720                  17 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 41 from patent US 5645985.
ACCESSION   I51720
VERSION     I51720.1  GI:2472921
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Froehler,B., Wagner,R., Matteucci,M., Jones,R.J., Gutierrez,A.J.
            and Pudlo,J.
  TITLE     Enhanced triple-helix and double-helix formation with oligomers
            containing modified pyrimidines
  JOURNAL   Patent: US 5645985-A 41 08-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTT 2172
              ||||| ||||||| |||
Db         17 TTTTTCCTCCTTTCTTT 1


RESULT 3031
AR187056
LOCUS       AR187056                17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2544 from patent US 6346398.
ACCESSION   AR187056
VERSION     AR187056.1  GI:20233021
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2544 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTT 2175
              | ||| ||||||||||
Db          1 TCTCTACTTTTTTTTTT 17


RESULT 3032
AR187068/c
LOCUS       AR187068                17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2556 from patent US 6346398.
ACCESSION   AR187068
VERSION     AR187068.1  GI:20233033
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2556 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAA 2797
              | ||| ||||||||||||
Db         17 ATTTGGAAAAAAAAAAA 1


RESULT 3033
AR187069/c
LOCUS       AR187069                17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2557 from patent US 6346398.
ACCESSION   AR187069
VERSION     AR187069.1  GI:20233034
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2557 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAA 2796
              || ||| ||||||||||
Db         17 GATTTGGAAAAAAAAAA 1


RESULT 3034
AR188810
LOCUS       AR188810                17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 4298 from patent US 6346398.
ACCESSION   AR188810
VERSION     AR188810.1  GI:20234775
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 4298 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2552 AAGAGGATGCTGGGCTC 2568
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Qy       1763 CATTAAGCTTTTTTTTT 1779
              ||||||  |||||||||
Db          1 CATTAATTTTTTTTTT 17


RESULT 3027
BD258180/c
LOCUS       BD258180                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258180
VERSION     BD258180.1  GI:33067950
KEYWORDS    JP 2002541795-A/5973.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 5973 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/5973
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2680 GTGGGTGAAATGGAGAT 2696
              ||| |||||||||| ||
Db         17 GTGTGTGAAATGGAAAT 1


RESULT 3028
BD258524/c
LOCUS       BD258524                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258524
VERSION     BD258524.1  GI:33068294
KEYWORDS    JP 2002541795-A/6317.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6317 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6317
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1971 TTACCTTGAAAAAAAGA 1987
              |||||||||| |||| |
Db         17 TTACCTTGAATAAAATA 1


RESULT 3029
BD258580
LOCUS       BD258580                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258580
VERSION     BD258580.1  GI:33068350
KEYWORDS    JP 2002541795-A/6373.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6373 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6373
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGAA 2195
```

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  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        483 GCCAGAGCCAGGAGGGA 499
              ||||||||||| || ||
Db          1 GCCAGAGCCAGCAGAGA 17


RESULT 3024
BD231300
LOCUS       BD231300                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Genes for assessing cardiovascular status and compositions for use
            thereof.
ACCESSION   BD231300
VERSION     BD231300.1  GI:33041070
KEYWORDS    JP 2002527079-A/64.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Norberg,L.T., Andersson,M.K., Lindstrom,P.H.R. and Jonsson,L.
  TITLE     Genes for assessing cardiovascular status and compositions for use
            thereof
  JOURNAL   Patent: JP 2002527079-A 64 27-AUG-2002;
            PAIROSEAKENSINGU AB
COMMENT     OS   Artificial Sequence
            PN   JP 2002527079-A/64
            PD   27-AUG-2002
            PF   13-OCT-1999 JP 2000576056
            PR   14-OCT-1998 US    60/104286,14-OCT-1998 US    60/104302 PI
            LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY  PI
            RUTGER LINDSTROM,
            PI   LENA JONSSON
            PC   C12Q1/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC   Genes
            for assessing cardiovascular status
            and compositions for
            CC            use thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        483 GCCAGAGCCAGGAGGGA 499
              ||||||||||| || ||
Db          1 GCCAGAGCCAGCAGAGA 17


RESULT 3025
BD254586/c
LOCUS       BD254586                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD254586
VERSION     BD254586.1  GI:33064356
KEYWORDS    JP 2002541795-A/2379.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2379 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/2379
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||| |||| ||
Db         17 CTTTTTTTTATTTTCTT 1


RESULT 3026
BD255418
LOCUS       BD255418                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255418
VERSION     BD255418.1  GI:33065188
KEYWORDS    JP 2002541795-A/3211.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 3211 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/3211
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAA 2188
              ||||||||||||||  ||
Db          1 TTTTTTTTTTTTTCCAA 17


RESULT 3019
A97980/c
LOCUS       A97980                    17 bp    DNA     linear   PAT 26-JAN-2000
DEFINITION  Sequence 10 from Patent WO9914366.
ACCESSION   A97980
VERSION     A97980.1  GI:6781218
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pongers-Willemse,M.J. and Van,D.J.
  TITLE     DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
  JOURNAL   Patent: WO 9914366-A 10 25-MAR-1999;
            DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        328 TCAGCCGCCACCCTACT 344
              |||||| ||||||| ||
Db         17 TCAGCCTCCACCCTGCT 1


RESULT 3020
AR005303
LOCUS       AR005303                  17 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 33 from patent US 5747660.
ACCESSION   AR005303
VERSION     AR005303.1  GI:3966182
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Orlicky,D.J.
  TITLE     Nucleic acid encoding prostaglandin F.sub.2.alpha. receptor
            regulatory protein
  JOURNAL   Patent: US 5747660-A 33 05-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1041 GGAGGCGGAAAGCCGCT 1057
              ||||||||| || ||||
Db          1 GGAGGCGGAGAGTCGCT 17


RESULT 3021
AR051160/c
LOCUS       AR051160                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 41 from patent US 5830653.
ACCESSION   AR051160
VERSION     AR051160.1  GI:5974524
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Froehler,B., Wagner,R., Matteucci,M., Jones,R.J., Gutierrez,A.J.
            and Pudlo,J.
  TITLE     Methods of using oligomers containing modified pyrimidines
  JOURNAL   Patent: US 5830653-A 41 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTT 2172
              ||||| ||||||| |||
Db         17 TTTTTCCTCCTTTCTTT 1


RESULT 3022
AR106325
LOCUS       AR106325                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6107027.
ACCESSION   AR106325
VERSION     AR106325.1  GI:12820855
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kay,M.A. and Lieber,A.
  TITLE     Ribozymes for treating hepatitis C
  JOURNAL   Patent: US 6107027-A 4 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        439 CCAGCCGGCGCCCACAG 455
              ||| ||| |||||||||
Db          1 CCAACCGTCGCCCACAG 17


RESULT 3023
AR137317
LOCUS       AR137317                  17 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 64 from patent US 6197505.
ACCESSION   AR137317
VERSION     AR137317.1  GI:14478826
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Norberg,L.Torbjorn., Andersson,M.Kristina. and
            Lindstrom,P.Harry.Rutger.
  TITLE     Methods for assessing cardiovascular status and compositions for
            use thereof
  JOURNAL   Patent: US 6197505-A 64 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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RESULT 3014
AX351707
LOCUS       AX351707                  30 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 3 from Patent WO0193902.
ACCESSION   AX351707
VERSION     AX351707.1  GI:18616990
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 3 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule: Synthetic
                     DNA/RNA oligonucleotide-Synthetic DNA/RNA oligonucleotide"

  Query Match             0.5%;  Score 14;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 3015
AX351708
LOCUS       AX351708                  30 bp    RNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 4 from Patent WO0193902.
ACCESSION   AX351708
VERSION     AX351708.1  GI:18616991
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 4 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule: Synthetic
                     oligonucleotide"

  Query Match             0.5%;  Score 14;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 3016
AX351715
LOCUS       AX351715                  30 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 11 from Patent WO0193902.
ACCESSION   AX351715
VERSION     AX351715.1  GI:18616998
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 11 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"

  Query Match             0.5%;  Score 14;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 3017
AR187066
LOCUS       AR187066                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2554 from patent US 6346398.
ACCESSION   AR187066
VERSION     AR187066.1  GI:20233031
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2554 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAA 2188
              |||||||||||||  ||
Db          1 TTTTTTTTTTTTCCAA 17


RESULT 3018
AR323676
LOCUS       AR323676                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1078 from patent US 6566127.
ACCESSION   AR323676
VERSION     AR323676.1  GI:33709484
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1078 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"
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            PI   QUANG TRI NGUYEN,CHENON ANTOINE GARBARG,VERONIQUE AUGUSTE PC
            C12N15/09,A61K39/12,A61K48/00,C07K14/015,C07K16/08,C12Q1/68, PC
            G01N33/53,
            PC   C12N15/00
            CC   Erythrovirus and application thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Erythrovirus'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Erythrovirus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:40121"

  Query Match             0.5%;  Score 14;  DB 1;  Length 23;
  Best Local Similarity   77.3%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2804
              || ||||| | ||||||  |||
Db          1 TTAAAAAATATAAAAAATGAAA 22


RESULT 3010
AX042825
LOCUS       AX042825                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 391 from Patent WO0065088.
ACCESSION   AX042825
VERSION     AX042825.1  GI:11341433
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 391 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-B Homozygote Primer Sequence"

  Query Match             0.5%;  Score 14;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3011
AX042543/c
LOCUS       AX042543                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 109 from Patent WO0065088.
ACCESSION   AX042543
VERSION     AX042543.1  GI:11341151
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 109 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Homozygote primer sequence"

  Query Match             0.5%;  Score 14;  DB 1;  Length 25;
  Best Local Similarity   77.3%;  Pred. No. 4.2e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAA 2797
              | | | | | ||||||||||||
Db         22 GCTCGTAGTTAAAAAAAAAAAA 1


RESULT 3012
AX351705
LOCUS       AX351705                 30 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 1 from Patent WO0193902.
ACCESSION   AX351705
VERSION     AX351705.1  GI:18616988
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 1 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"

  Query Match             0.5%;  Score 14;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 3013
AX351706
LOCUS       AX351706                 30 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 2 from Patent WO0193902.
ACCESSION   AX351706
VERSION     AX351706.1  GI:18616989
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 2 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule: Synthetic
                     DNA/RNA oligonucleotide-Synthetic DNA/RNA oligonucleotide"

  Query Match             0.5%;  Score 14;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14
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ACCESSION   AX048417
VERSION     AX048417.1  GI:12225581
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 16 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 14;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 3006
AX095144
LOCUS       AX095144                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 322 from Patent WO0118250.
ACCESSION   AX095144
VERSION     AX095144.1  GI:13511347
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 322 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         27 TGACCCGGACAGCAAG 42
              || ||:||||||||||
Db          6 TGCCCYGGACAGCAAG 21


RESULT 3007
AX095158
LOCUS       AX095158                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 336 from Patent WO0118250.
ACCESSION   AX095158
VERSION     AX095158.1  GI:13511361
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 336 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1460 GACCAGAGTCCAGCTG 1475
              | ||||:|||||||||
Db          5 GCCCAGRGTCCAGCTG 20


RESULT 3008
AX003445
LOCUS       AX003445                 23 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 25 from Patent WO9928439.
ACCESSION   AX003445
VERSION     AX003445.1  GI:9927249
KEYWORDS    .
SOURCE      B19 virus
  ORGANISM  B19 virus
            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.
REFERENCE   1
  AUTHORS   Auguste,V., Garbarg-Chenon,A. and Nguyen,Q.T.
  TITLE     Erythrovirus and its applications
  JOURNAL   Patent: WO 9928439-A 25 10-JUN-1999;
            ASSIST PUBL HOPITAUX DE PARIS (FR); AUGUSTE VERONIQUE (FR); GARBARG
            CHENON ANTOINE (FR); NGUYEN QUANG TRI (FR)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="B19 virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10798"

  Query Match             0.5%;  Score 14;  DB 1;  Length 23;
  Best Local Similarity   77.3%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAAA 2804
              || ||||| | ||||||  |||
Db          1 TTAAAAAATATAAAAAATGAAA 22


RESULT 3009
BD087061
LOCUS       BD087061                 23 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Erythrovirus and application thereof.
ACCESSION   BD087061
VERSION     BD087061.1  GI:22632671
KEYWORDS    JP 2001525163-A/25.
SOURCE      Erythrovirus
  ORGANISM  Erythrovirus
            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Nguyen,Q.T., Garbarg,C.A. and Auguste,V.
  TITLE     Erythrovirus and application thereof
  JOURNAL   Patent: JP 2001525163-A 25 11-DEC-2001;
            ASSISTANCE PUBLIQUE HOPITAUX DE PARIS
COMMENT     OS   Erythrovirus
            PN   JP 2001525163-A/25
            PD   11-DEC-2001
            PF   03-DEC-1998 JP 2000523317
            PR   03-DEC-1997 FR     97/15197
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          Mollegaard,N.E.
  TITLE     Cleaving double-stranded DNA with peptide nucleic acids
  JOURNAL   Patent: US 5641625-A 33 24-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   70.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||| |||||||
Db          1 TTTTTTTNNNNNNTTTTTTT 20


RESULT 3001
AR373640
LOCUS       AR373640                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 32 from patent US 6602857.
ACCESSION   AR373640
VERSION     AR373640.1  GI:40076051
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M., Wyatt,J., Monia,B.P., Butler,M.M. and McKay,R.
  TITLE     Antisense modulation of PTP1B expression
  JOURNAL   Patent: US 6602857-A 32 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2005 TCTTCAGAGATCAA 2018
              ||||||||||||||
Db          6 TCTTCAGAGATCAA 19


RESULT 3002
AX296837
LOCUS       AX296837                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 8599 from Patent WO0179548.
ACCESSION   AX296837
VERSION     AX296837.1  GI:17058526
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 8599 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        205 GGACTGCGAGGATC 218
              ||||||||||||||
Db          5 GGACTGCGAGGATC 18


RESULT 3003
AX418637
LOCUS       AX418637                 20 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 32 from Patent WO0210378.
ACCESSION   AX418637
VERSION     AX418637.1  GI:21523500
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Cowsert,L.M., Wyatt,J., Freier,S.M., Monia,B.P., Butler,M.M. and
            Mckay,R.
  TITLE     Antisense modulation of ptp1b expression
  JOURNAL   Patent: WO 0210378-A 32 07-FEB-2002;
            ISIS PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense Oligonucleotide"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2005 TCTTCAGAGATCAA 2018
              ||||||||||||||
Db          6 TCTTCAGAGATCAA 19


RESULT 3004
AX048417
LOCUS       AX048417                 21 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 16 from Patent WO0071747.
ACCESSION   AX048417
VERSION     AX048417.1  GI:12225581
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 16 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 14;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 3005
AX048417/c
LOCUS       AX048417                 21 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 16 from Patent WO0071747.
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RESULT 2996
AR087163
LOCUS       AR087163                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 33 from patent US 5986053.
ACCESSION   AR087163
VERSION     AR087163.1  GI:10013926
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and
            Mollegaard,N.E.
  TITLE     Peptide nucleic acids complexes of two peptide nucleic acid strands
            and one nucleic acid strand
  JOURNAL   Patent: US 5986053-A 33 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   70.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||       |||||||
Db          1 TTTTTTTNNNNNNTTTTTTT 20


RESULT 2997
AR173005/c
LOCUS       AR173005                 20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 130 from patent US 6303374.
ACCESSION   AR173005
VERSION     AR173005.1  GI:17912496
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zhang,H. and Cowsert,L.M.
  TITLE     Antisense modulation of caspase 3 expression
  JOURNAL   Patent: US 6303374-A 130 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2000 TAGCTTCTTCAGAG 2013
              ||||||||||||||
Db         20 TAGCTTCTTCAGAG 7


RESULT 2998
E36062
LOCUS       E36062                   20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Higher-order structure and binding of peptide nucleic acid.
ACCESSION   E36062
VERSION     E36062.1  GI:13022464
KEYWORDS    JP 1999236396-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bushato,O., Eguhorumu,M., Nielsen,P.A., Berg,R.H., Ekka,D.J. and
            Morugado,N.A.
  TITLE     Higher-order structure and binding of peptide nucleic acid
  JOURNAL   Patent: JP 1999236396-A 7 31-AUG-1999;
            ISIS PHARMACEUTICALS INC,BUCHARDT DORUTE,EGUHORUMU MICHAEL, IELSEN
            PATER A, BERGH RORUFU HO
COMMENT     OS   Unidentified
            PN   JP 1999236396-A/7
            PD   31-AUG-1999
            PF   14-OCT-1998 JP 1998291590
            PR   02-JUL-1993 US       088658
            PI   BUSHATO ORE,EGUHORUMU MICHAEL,NIELSEN PATER A,BERG RORUFU HO,
            PI   EKKA DAVID JAY,MORUGADO NILUS A
            PC   C07H21/04,A61K31/00,A61K31/00,A61K31/00,A61K31/70,A61K48/00,
            PC   C07H21/02,
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   70.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||       |||||||
Db          1 TTTTTTTNNNNNNTTTTTTT 20


RESULT 2999
I13508
LOCUS       I13508                   20 bp    DNA     linear   PAT 26-JUL-1995
DEFINITION  Sequence 17 from patent US 5436392.
ACCESSION   I13508
VERSION     I13508.1  GI:910849
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Thomas,J.C., Bohnert,H.J. and Kanost,M.R.
  TITLE     Transgenic plants expressing M. sexta protease inhibitor
  JOURNAL   Patent: US 5436392-A 17 25-JUL-1995;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        861 CGCTCCTCAGCTCT 874
              ||||||||||||||
Db          1 CGCTCCTCAGCTCT 14


RESULT 3000
I49618
LOCUS       I49618                   20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 33 from patent US 5641625.
ACCESSION   I49618
VERSION     I49618.1  GI:2471838
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and
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  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2179
              |||||||||||||
Db          1 TTTTTTTTTTTTT 14


RESULT 2992
E13188
LOCUS       E13188                    20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide.
ACCESSION   E13188
VERSION     E13188.1  GI:3251993
KEYWORDS    JP 1997140400-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okano,K. and Kanbara,H.
  TITLE     DETERMINATION OF BASE SEQUENCE
  JOURNAL   Patent: JP 1997140400-A 2 03-JUN-1997;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997140400-A/2
            PD   03-JUN-1997
            PF   13-SEP-1996 JP 1996242929
            PR   18-SEP-1995 JP 95P   238141
            PI   OKANO KAZUNOBU, KANBARA HIDEKI
            PC   C12Q1/68,G01N27/447,G01N33/58//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2179
              |||||||||||||
Db          1 TTTTTTTTTTTTT 14


RESULT 2993
AX104239/c
LOCUS       AX104239                  20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 431 from Patent WO0122972.
ACCESSION   AX104239
VERSION     AX104239.1  GI:13920436
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 431 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2799
              |||||||||||||
Db         20 AAAAAAAAAAAAA 7


RESULT 2994
AX355709/c
LOCUS       AX355709                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 737 from Patent WO0197843.
ACCESSION   AX355709
VERSION     AX355709.1  GI:18620377
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 737 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide~phosphorothioate
                     backbone"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2799
              |||||||||||||
Db         20 AAAAAAAAAAAAA 7


RESULT 2995
AX547292/c
LOCUS       AX547292                  20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 431 from Patent WO02053141.
ACCESSION   AX547292
VERSION     AX547292.1  GI:25812436
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 431 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAA 2799
              |||||||||||||
Db         20 AAAAAAAAAAAAA 7
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  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3650 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdc25 hs ribozyme binding site"

  Query Match             0.5%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTT 2192
              ||||||||||||||
Db         18 TTTTTTTTAACTTT 5


RESULT 2988
AX132433/c
LOCUS       AX132433                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3651 from Patent WO0130362.
ACCESSION   AX132433
VERSION     AX132433.1  GI:14138738
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3651 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdc25 hs ribozyme binding site"

  Query Match             0.5%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTT 2192
              ||||||||||||||
Db         17 TTTTTTTTAACTTT 4


RESULT 2989
AR086109
LOCUS       AR086109                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 3 from patent US 5985556.
ACCESSION   AR086109
VERSION     AR086109.1  GI:10012875
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Okano,K.
  TITLE     DNA sequencing method and DNA sample preparation method
  JOURNAL   Patent: US 5985556-A 3 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2990
AR086110
LOCUS       AR086110                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from patent US 5985556.
ACCESSION   AR086110
VERSION     AR086110.1  GI:10012876
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Okano,K.
  TITLE     DNA sequencing method and DNA sample preparation method
  JOURNAL   Patent: US 5985556-A 4 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2991
E13187
LOCUS       E13187                   20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide.
ACCESSION   E13187
VERSION     E13187.1  GI:3251992
KEYWORDS    JP 1997140400-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okano,K. and Kanbara,H.
  TITLE     DETERMINATION OF BASE SEQUENCE
  JOURNAL   Patent: JP 1997140400-A 1 03-JUN-1997;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997140400-A/1
            PD   03-JUN-1997
            PF   13-SEP-1996 JP 1996242929
            PR   18-SEP-1995 JP 95P   238141
            PI   OKANO KAZUNOBU, KANBARA HIDEKI
            PC   C12Q1/68,G01N27/447,G01N33/58//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
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ACCESSION   BD065501
VERSION     BD065501.1  GI:22611104
KEYWORDS    JP 2001511000-A/136.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 136 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/136
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                 Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unknown'.
FEATURES            Location/Qualifiers
     source         1. .18
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        431 CCCCTGCACCAGCC 444
              ||||||||||||||
Db         16 CCCCTGCACCAGCC 3


RESULT 2984
BD065502/c
LOCUS       BD065502                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD065502
VERSION     BD065502.1  GI:22611105
KEYWORDS    JP 2001511000-A/137.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 137 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/137
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                 Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unknown'.
FEATURES            Location/Qualifiers
     source         1. .18
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        431 CCCCTGCACCAGCC 444
              ||||||||||||||
Db         18 CCCCTGCACCAGCC 5


RESULT 2985
A31922/c
LOCUS       A31922                   19 bp    DNA     linear   PAT 04-DEC-1995
DEFINITION  Synthetic calmodulin gene primer.
ACCESSION   A31922
VERSION     A31922.1  GI:1247280
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   .
  JOURNAL   Patent: FR 2641792-A 3 20-JUL-1990;
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTT 2177
              ||||||||||||||
Db         14 CCTTTTTTTTTTTT 1


RESULT 2986
AR228127/c
LOCUS       AR228127                 19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 28 from patent US 6448003.
ACCESSION   AR228127
VERSION     AR228127.1  GI:27266873
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Guida,M. and Kurth,J.
  TITLE     Genotyping the human phenol sulfotransferbase 2 gene STP2
  JOURNAL   Patent: US 6448003-A 28 10-SEP-2002;
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="unknown"
                    /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTT 2176
              ||||||||||||||
Db         17 TCCTTTTTTTTTTT 4


RESULT 2987
AX132432/c
LOCUS       AX132432                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3650 from Patent WO0130362.
ACCESSION   AX132432
VERSION     AX132432.1  GI:14138737
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
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  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 137 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        431 CCCCTGCACCAGCC 444
              ||||||||||||||
Db         18 CCCCTGCACCAGCC 5


RESULT 2979
A89955/c
LOCUS       A89955                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 136 from Patent EP0856579.
ACCESSION   A89955
VERSION     A89955.1  GI:6738469
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 136 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        431 CCCCTGCACCAGCC 444
              ||||||||||||||
Db         16 CCCCTGCACCAGCC 3


RESULT 2980
A89956/c
LOCUS       A89956                   18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 137 from Patent EP0856579.
ACCESSION   A89956
VERSION     A89956.1  GI:6738470
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 137 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        431 CCCCTGCACCAGCC 444
              ||||||||||||||
Db         18 CCCCTGCACCAGCC 5


RESULT 2981
AR264960
LOCUS       AR264960                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 44 from patent US 6492121.
ACCESSION   AR264960
VERSION     AR264960.1  GI:29693347
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 44 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              ||||||||||||||
Db          5 GAAAAAAAAAAAAA 18


RESULT 2982
AR293194
LOCUS       AR293194                 18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4929 from patent US 6537751.
ACCESSION   AR293194
VERSION     AR293194.1  GI:31680478
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4929 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        886 CAAAGTGACAGTGG 899
              ||||||||||||||
Db          4 CAAAGTGACAGTGG 17


RESULT 2983
BD065501/c
LOCUS       BD065501                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
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Qy        883 ATACAAAGTGACAG 896
              ||||||||||||||
Db         17 ATACAAAGTGACAG 4


RESULT 2975
BD200669
LOCUS       BD200669                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD200669
VERSION     BD200669.1  GI:33010439
KEYWORDS    JP 2002509721-A/3695.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 3695 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/3695
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2629 GTCTCGTTCCTGTT 2642
              ||||||||||||||
Db          2 GTCTCGTTCCTGTT 15


RESULT 2976
BD200670
LOCUS       BD200670                  17 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION   BD200670
VERSION     BD200670.1  GI:33010440
KEYWORDS    JP 2002509721-A/3696.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
  TITLE     Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
  JOURNAL   Patent: JP 2002509721-A 3696 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509721-A/3696
            PD   02-APR-2002
            PF   24-MAR-1999 JP 2000541291
            PR   27-MAR-1998 US    60/079678
            PI   PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI   JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
             A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
              C12N5/00
            CC   Method and reagent for treating diseases or conditions  CC
                   concerning molecule
            CC   participating in vasculogenic response
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2629 GTCTCGTTCCTGTT 2642
              ||||||||||||||
Db          1 GTCTCGTTCCTGTT 14


RESULT 2977
A87988/c
LOCUS       A87988                    18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 136 from Patent WO9833904.
ACCESSION   A87988
VERSION     A87988.1  GI:6736558
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 136 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        431 CCCCTGCACCAGCC 444
              ||||||||||||||
Db         16 CCCCTGCACCAGCC 3


RESULT 2978
A87989/c
LOCUS       A87989                    18 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 137 from Patent WO9833904.
ACCESSION   A87989
VERSION     A87989.1  GI:6736559
KEYWORDS    .
SOURCE      unidentified
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  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 1065 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2074 ATCTGACACACTCT 2087
              ||||||||||||||
Db          2 ATCTGACACACTCT 15


RESULT 2971
AX738493
LOCUS       AX738493                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4083 from Patent WO03025177.
ACCESSION   AX738493
VERSION     AX738493.1  GI:30517781
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 4083 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTT 2178
              ||||||||||||||
Db          4 CTTTTTTTTTTTTT 17


RESULT 2972
AX757648
LOCUS       AX757648                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 969 from Patent WO03040369.
ACCESSION   AX757648
VERSION     AX757648.1  GI:32252264
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 969 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1865 CACTTAGCCATTGA 1878
              ||||||||||||||
Db          4 CACTTAGCCATTGA 17


RESULT 2973
AX757892
LOCUS       AX757892                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 1213 from Patent WO03040369.
ACCESSION   AX757892
VERSION     AX757892.1  GI:32252508
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 1213 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTT 2178
              ||||||||||||||
Db          4 CTTTTTTTTTTTTT 17


RESULT 2974
AX762764/c
LOCUS       AX762764                 17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 6085 from Patent WO03040369.
ACCESSION   AX762764
VERSION     AX762764.1  GI:32257380
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 6085 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2465 AATTTTAATATTAA 2478
              ||||||||||||||
Db         15 AATTTTAATATTAA 2


RESULT 2966
AX217350/c
LOCUS       AX217350                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 2792 from Patent WO0159103.
ACCESSION   AX217350
VERSION     AX217350.1  GI:15527411
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 2792 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2465 AATTTTAATATTAA 2478
              ||||||||||||||
Db         14 AATTTTAATATTAA 1


RESULT 2967
AX475807/c
LOCUS       AX475807                  17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1028 from Patent WO0224750.
ACCESSION   AX475807
VERSION     AX475807.1  GI:22215092
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 1028 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1740 GTGACAAGTACTGG 1753
              ||||||||||||||
Db         17 GTGACAAGTACTGG 4


RESULT 2968
AX475811/c
LOCUS       AX475811                  17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1032 from Patent WO0224750.
ACCESSION   AX475811
VERSION     AX475811.1  GI:22215096
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 1032 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1739 GGTGACAAGTACTG 1752
              ||||||||||||||
Db         14 GGTGACAAGTACTG 1


RESULT 2969
AX676082/c
LOCUS       AX676082                  17 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 35 from Patent WO02059381.
ACCESSION   AX676082
VERSION     AX676082.1  GI:29333766
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Slaugenhaupt,S. and Gusella,J.F.
  TITLE     Gene for identifying individuals with familial dysautonomia
  JOURNAL   Patent: WO 02059381-A 35 01-AUG-2002;
            The General Hospital Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10095"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 2970
AX723378
LOCUS       AX723378                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1065 from Patent WO03025176.
ACCESSION   AX723378
VERSION     AX723378.1  GI:30423879
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
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Qy       1770 CTTTTTTTTTTTGA 1783
              ||||||||||||||
Db          1 CTTTTTTTTTTTGA 14


RESULT 2961
AR323988
LOCUS       AR323988                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1390 from patent US 6566127.
ACCESSION   AR323988
VERSION     AR323988.1  GI:33709796
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1390 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1339 TCATTTCAGCCTGA 1352
              ||||||||||||||
Db          4 TCATTTCAGCCTGA 17


RESULT 2962
AR323989
LOCUS       AR323989                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1391 from patent US 6566127.
ACCESSION   AR323989
VERSION     AR323989.1  GI:33709797
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1391 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1339 TCATTTCAGCCTGA 1352
              ||||||||||||||
Db          3 TCATTTCAGCCTGA 16


RESULT 2963
AR435300
LOCUS       AR435300                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1723 from patent US 6656700.
ACCESSION   AR435300
VERSION     AR435300.1  GI:40198143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1723 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2317 TTGTTGCTGCTTGT 2330
              ||||||||||||||
Db          2 TTGTTGCTGCTTGT 15


RESULT 2964
AR435301
LOCUS       AR435301                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1724 from patent US 6656700.
ACCESSION   AR435301
VERSION     AR435301.1  GI:40198144
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1724 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2317 TTGTTGCTGCTTGT 2330
              ||||||||||||||
Db          1 TTGTTGCTGCTTGT 14


RESULT 2965
AX217349/c
LOCUS       AX217349                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 2791 from Patent WO0159103.
ACCESSION   AX217349
VERSION     AX217349.1  GI:15527410
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 2791 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTG 1782
              ||||||||||||||
Db          4 GCTTTTTTTTTTTG 17


RESULT 2956
AR186700
LOCUS       AR186700                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2188 from patent US 6346398.
ACCESSION   AR186700
VERSION     AR186700.1  GI:20232665
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2188 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1770 CTTTTTTTTTTGA 1783
              |||||||||||||
Db          1 CTTTTTTTTTTGA 14


RESULT 2957
AR187378
LOCUS       AR187378                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2866 from patent US 6346398.
ACCESSION   AR187378
VERSION     AR187378.1  GI:20233343
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2866 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1339 TCATTTCAGCCTGA 1352
              ||||||||||||||
Db          4 TCATTTCAGCCTGA 17


RESULT 2958
AR187379
LOCUS       AR187379                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2867 from patent US 6346398.
ACCESSION   AR187379
VERSION     AR187379.1  GI:20233344
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2867 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1339 TCATTTCAGCCTGA 1352
              ||||||||||||||
Db          3 TCATTTCAGCCTGA 16


RESULT 2959
AR323327
LOCUS       AR323327                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 729 from patent US 6566127.
ACCESSION   AR323327
VERSION     AR323327.1  GI:33709135
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 729 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTG 1782
              ||||||||||||||
Db          4 GCTTTTTTTTTTTG 17


RESULT 2960
AR323331
LOCUS       AR323331                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 733 from patent US 6566127.
ACCESSION   AR323331
VERSION     AR323331.1  GI:33709139
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 733 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAA 1784
              ||||||||||||||
Db          2 TTTTTTTTTTTGAA 15


RESULT 2953
BD255424
LOCUS       BD255424                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255424
VERSION     BD255424.1  GI:33065194
KEYWORDS    JP 2002541795-A/3217.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 3217 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/3217
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAA 1784
              ||||||||||||||
Db          1 TTTTTTTTTTTGAA 14


RESULT 2954
BD259216/c
LOCUS       BD259216                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD259216
VERSION     BD259216.1  GI:33068986
KEYWORDS    JP 2002541795-A/7009.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 7009 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/7009
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2233 TGTTCCCTTAAGGT 2246
              ||||||||||||||
Db         17 TGTTCCCTTAAGGT 4


RESULT 2955
AR186696
LOCUS       AR186696                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2184 from patent US 6346398.
ACCESSION   AR186696
VERSION     AR186696.1  GI:20232661
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2184 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
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RESULT 2949
AR323675
LOCUS       AR323675                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1077 from patent US 6566127.
ACCESSION   AR323675
VERSION     AR323675.1  GI:33709483
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1077 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2950
BD255421
LOCUS       BD255421                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255421
VERSION     BD255421.1  GI:33065191
KEYWORDS    JP 2002541795-A/3214.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 3214 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/3214
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAA 1784
              ||||||||||||||
Db          4 TTTTTTTTTTTGAA 17


RESULT 2951
BD255422
LOCUS       BD255422                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255422
VERSION     BD255422.1  GI:33065192
KEYWORDS    JP 2002541795-A/3215.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 3215 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/3215
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAA 1784
              ||||||||||||||
Db          3 TTTTTTTTTTTGAA 16


RESULT 2952
BD255423
LOCUS       BD255423                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD255423
VERSION     BD255423.1  GI:33065193
KEYWORDS    JP 2002541795-A/3216.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 3216 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/3216
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
```

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REFERENCE   1  (bases 1 to 16)
  AUTHORS   Murray,J.A.H.
  TITLE     Plants with modified growth
  JOURNAL   Patent: US 6559358-A 17 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2690 TGGAGATTTGGAATTG 2705
              |||:|||||||| |||
Db          1 TGGWGATTTGGATTTG 16


RESULT 2945
BD058105
LOCUS       BD058105                 16 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Plants with modified growth.
ACCESSION   BD058105
VERSION     BD058105.1  GI:22603711
KEYWORDS    JP 2001519659-A/12.
SOURCE      Helianthus tuberosus
  ORGANISM  Helianthus tuberosus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Asteroideae;
            Heliantheae; Helianthus.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Murray,J.A.H.
  TITLE     Plants with modified growth
  JOURNAL   Patent: JP 2001519659-A 12 23-OCT-2001;
            CAMBRIDGE UNIV TECHNICAL SERVICES LTD
COMMENT     PN   JP 2001519659-A/12
            PD   23-OCT-2001
            PF   24-MAR-1998 JP 1998542072
            PI   JAMES AUGUSTUS HENRY MURRAY
            PC   C12N15/82,C12N15/29,A01H5/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   /desc = 'oligonucleotide primer 6 for PCR'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Helianthus tuberosus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4233"

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2690 TGGAGATTTGGAATTG 2705
              |||:|||||||| |||
Db          1 TGGWGATTTGGATTTG 16


RESULT 2946
AR187060/c
LOCUS       AR187060                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2548 from patent US 6346398.
ACCESSION   AR187060
VERSION     AR187060.1  GI:20233025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2548 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         17 AAAAAAAAAAAAAA 4


RESULT 2947
AR187065
LOCUS       AR187065                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2553 from patent US 6346398.
ACCESSION   AR187065
VERSION     AR187065.1  GI:20233030
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2553 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2948
AR323670/c
LOCUS       AR323670                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1072 from patent US 6566127.
ACCESSION   AR323670
VERSION     AR323670.1  GI:33709478
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1072 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         17 AAAAAAAAAAAAAA 4
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  JOURNAL   Patent: US 5473060-A 6 05-DEC-1995;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         16 AAAAAAAAAAAAAA 3


RESULT 2940
I28367/c
LOCUS       I28367                   16 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 6 from patent US 5571677.
ACCESSION   I28367
VERSION     I28367.1  GI:1819143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromomolecular structures
  JOURNAL   Patent: US 5571677-A 6 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         16 AAAAAAAAAAAAAA 3


RESULT 2941
AX359760
LOCUS       AX359760                 16 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 64 from Patent WO0200691.
ACCESSION   AX359760
VERSION     AX359760.1  GI:18675467
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Tchernev,V., Putturajan,M., Malyankar,U.M., Gusev,V.,
            Herrmann,J.L., Macdougall,J.R., Rastelli,L., Zhong,H., Spytek,K.A.,
            Shenoy,S., Gerlach,V.L., Gangolli,E.A., Stone,D.J. and Smithson,G.
  TITLE     Novel polynucleotides and polypeptides encoded thereby
  JOURNAL   Patent: WO 0200691-A 64 03-JAN-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         1 AAAAAAAAAAAAAA 14


RESULT 2942
A85068
LOCUS       A85068                   16 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 12 from Patent WO9842851.
ACCESSION   A85068
VERSION     A85068.1  GI:6733809
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Murray,J.A.
  TITLE     PLANTS WITH MODIFIED GROWTH
  JOURNAL   Patent: WO 9842851-A 12 01-OCT-1998;
            MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2690 TGGAGATTTGGAATTG 2705
              |||:|||||||| |||
Db         1 TGGWGATTTGGATTTG 16


RESULT 2943
I07164/c
LOCUS       I07164                   16 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 10 from Patent EP 0331356.
ACCESSION   I07164
VERSION     I07164.1  GI:590048
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Arthos,J., Clark,P.E., Fornwald,J.A., Brawner,M.E., Deen,K.C.,
            Gorman,J.A., Sathe,G.M., Sweet,R.W. and Taylor,D.P.
  TITLE     Expression of HIV binding proteins
  JOURNAL   Patent: EP 0331356-A2 10 06-SEP-1989;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 GCGGGGGCGGCGGC 67
              ||||||||||||||
Db         15 GCGGGGGCGGCGGC 2


RESULT 2944
AR316384
LOCUS       AR316384                 16 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 17 from patent US 6559358.
ACCESSION   AR316384
VERSION     AR316384.1  GI:31711177
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
             ||||||||||||||
Db         15 AAAAAAAAAAAAAA 2


RESULT 2935
AX633205/c
LOCUS       AX633205                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 344 from Patent EP1260586.
ACCESSION   AX633205
VERSION     AX633205.1  GI:28468819
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 344 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
             ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 2936
AR002257/c
LOCUS       AR002257                 16 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5741643.
ACCESSION   AR002257
VERSION     AR002257.1  GI:3963811
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps
  JOURNAL   Patent: US 5741643-A 6 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
             ||||||||||||||
Db         16 AAAAAAAAAAAAAA 3


RESULT 2937
AR045207/c
LOCUS       AR045207                 16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5817795.
ACCESSION   AR045207
VERSION     AR045207.1  GI:5966672
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic and therapeutic
            applications
  JOURNAL   Patent: US 5817795-A 6 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
             ||||||||||||||
Db         16 AAAAAAAAAAAAAA 3


RESULT 2938
AR051238/c
LOCUS       AR051238                 16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5830658.
ACCESSION   AR051238
VERSION     AR051238.1  GI:5974602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5830658-A 6 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
             ||||||||||||||
Db         16 AAAAAAAAAAAAAA 3


RESULT 2939
I16032/c
LOCUS       I16032                   16 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 6 from patent US 5473060.
ACCESSION   I16032
VERSION     I16032.1  GI:1250940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic applications
```

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RESULT 2930
AR241870
LOCUS       AR241870                  15 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 158 from patent US 6472154.
ACCESSION   AR241870
VERSION     AR241870.1  GI:27287682
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 158 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2180
              ||||||||||| |||
Db          1 TTTTTTTTTTNTTT 15


RESULT 2931
AR241870/c
LOCUS       AR241870                  15 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 158 from patent US 6472154.
ACCESSION   AR241870
VERSION     AR241870.1  GI:27287682
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 158 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||| ||||||||||||
Db         15 AAANAAAAAAAAAAA 1


RESULT 2932
AX460877
LOCUS       AX460877                  15 bp    DNA     linear   PAT 08-JUL-2002
DEFINITION  Sequence 8 from Patent WO0212470.
ACCESSION   AX460877
VERSION     AX460877.1  GI:21726123
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Evans,M.J., Scicchitano,M.S., Bapat,A.R., Beer,E., Bhat,R.A.,
            Ferris,E., Mastroeni,R., Zhang,J. and Karathanasis,S.K.
  TITLE     A member of the lysyl oxidase gene family
  JOURNAL   Patent: WO 0212470-A 8 14-FEB-2002;
            Wyeth (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1768 AGCTTTTTTTTTTT 1781
              ||||||||||||||
Db          1 AGCTTTTTTTTTTT 14


RESULT 2933
AX633195
LOCUS       AX633195                  15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 334 from Patent EP1260586.
ACCESSION   AX633195
VERSION     AX633195.1  GI:28468809
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 334 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          2 TTTTTTTTTTTTTT 15


RESULT 2934
AX633195/c
LOCUS       AX633195                  15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 334 from Patent EP1260586.
ACCESSION   AX633195
VERSION     AX633195.1  GI:28468809
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 334 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
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RESULT 2925
I28366/c
LOCUS       I28366                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 5 from patent US 5571677.
ACCESSION   I28366
VERSION     I28366.1  GI:1819142
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromomolecular structures
  JOURNAL   Patent: US 5571677-A 5 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
             ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 2926
I29065
LOCUS       I29065                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5576427.
ACCESSION   I29065
VERSION     I29065.1  GI:1819856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 3 19-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2800
             ||||||||||||| |
Db          1 AAAAAAAAAAAAANA 15


RESULT 2927
I29065/c
LOCUS       I29065                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5576427.
ACCESSION   I29065
VERSION     I29065.1  GI:1819856
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 3 19-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             | ||||||||||||||
Db         15 TNTTTTTTTTTTTTT 1


RESULT 2928
I29066
LOCUS       I29066                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 4 from patent US 5576427.
ACCESSION   I29066
VERSION     I29066.1  GI:1819857
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 4 19-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2800
             ||||||||||||| ||
Db          1 AAAAAAAAAAAAANAA 15


RESULT 2929
I29066/c
LOCUS       I29066                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 4 from patent US 5576427.
ACCESSION   I29066
VERSION     I29066.1  GI:1819857
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 4 19-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             || ||||||||||||
Db         15 TTNTTTTTTTTTTTT 1
```

```
RESULT 2920
AR113914
LOCUS       AR113914                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 360 from patent US 6132967.
ACCESSION   AR113914
VERSION     AR113914.1  GI:14094236
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 360 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          2 TTTTTTTTTTTTTT 15


RESULT 2921
AR113914/c
LOCUS       AR113914                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 360 from patent US 6132967.
ACCESSION   AR113914
VERSION     AR113914.1  GI:14094236
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 360 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         15 AAAAAAAAAAAAAA 2


RESULT 2922
AR113919/c
LOCUS       AR113919                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 365 from patent US 6132967.
ACCESSION   AR113919
VERSION     AR113919.1  GI:14094241
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 365 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 2923
AR127784/c
LOCUS       AR127784                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 5 from patent US 6180777.
ACCESSION   AR127784
VERSION     AR127784.1  GI:14114379
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Horn,T.
  TITLE     Synthesis of branched nucleic acids
  JOURNAL   Patent: US 6180777-A 5 30-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 2924
I16031/c
LOCUS       I16031                    15 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 5 from patent US 5473060.
ACCESSION   I16031
VERSION     I16031.1  GI:1250939
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic applications
  JOURNAL   Patent: US 5473060-A 5 05-DEC-1995;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1
```

```
Db         14 TGAAAAAAAAAAAA 1


RESULT 2915
AR051237/c
LOCUS       AR051237                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5830658.
ACCESSION   AR051237
VERSION     AR051237.1  GI:5974601
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5830658-A 5 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
             ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 2916
AR056156
LOCUS       AR056156                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 360 from patent US 5837542.
ACCESSION   AR056156
VERSION     AR056156.1  GI:5981733
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 360 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
             ||||||||||||||
Db          2 TTTTTTTTTTTTTT 15


RESULT 2917
AR056156/c
LOCUS       AR056156                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 360 from patent US 5837542.
ACCESSION   AR056156
VERSION     AR056156.1  GI:5981733
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 360 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
             ||||||||||||||
Db         15 AAAAAAAAAAAAAA 2


RESULT 2918
AR056161/c
LOCUS       AR056161                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 365 from patent US 5837542.
ACCESSION   AR056161
VERSION     AR056161.1  GI:5981738
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 365 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
             ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 2919
AR084519/c
LOCUS       AR084519                 15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 8 from patent US 5981185.
ACCESSION   AR084519
VERSION     AR084519.1  GI:10011290
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 8 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAA 2188
             ||||||||||||||
Db         15 TTTTTTTTTTTTAA 2
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LOCUS       AR056159                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 363 from patent US 5837542.
ACCESSION   AR056159
VERSION     AR056159.1  GI:5981736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 363 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2911
AR113917
LOCUS       AR113917                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 363 from patent US 6132967.
ACCESSION   AR113917
VERSION     AR113917.1  GI:14094239
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 363 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2912
AX633201
LOCUS       AX633201                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 340 from Patent EP1260586.
ACCESSION   AX633201
VERSION     AX633201.1  GI:28468815
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 340 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2913
AR002256/c
LOCUS       AR002256                 15 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5741643.
ACCESSION   AR002256
VERSION     AR002256.1  GI:3963810
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps
  JOURNAL   Patent: US 5741643-A 5 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 2914
AR045206/c
LOCUS       AR045206                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5817795.
ACCESSION   AR045206
VERSION     AR045206.1  GI:5966671
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic and therapeutic
            applications
  JOURNAL   Patent: US 5817795-A 5 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTA 2187
||||||||||||||
Db 1 TTTTTTTTTTTTTA 14

RESULT 2907
BD176802/c
LOCUS BD176802 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression.
ACCESSION BD176802
VERSION BD176802.1 GI:29122514
KEYWORDS WO 02074951-A/49.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 49 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT OS Artificial Sequence
PN WO 02074951-A/49
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1. .14
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .14
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAA 2798
||||||||||||||
Db 14 GAAAAAAAAAAAAA 1

RESULT 2908
BD176804
LOCUS BD176804 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression.
ACCESSION BD176804
VERSION BD176804.1 GI:29122516
KEYWORDS WO 02074951-A/51.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 51 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT OS Artificial Sequence
PN WO 02074951-A/51
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1. .14
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .14
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTT 2179
||||||||||||||
Db 1 TTTTTTTTTTTTTT 14

RESULT 2909
BD176804/c
LOCUS BD176804 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression.
ACCESSION BD176804
VERSION BD176804.1 GI:29122516
KEYWORDS WO 02074951-A/51.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 51 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT OS Artificial Sequence
PN WO 02074951-A/51
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1. .14
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .14
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2799
||||||||||||||
Db 14 AAAAAAAAAAAAAA 1

RESULT 2910
AR056159

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COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/42
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 2904
BD176795/c
LOCUS       BD176795                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176795
VERSION     BD176795.1  GI:29122507
KEYWORDS    WO 02074951-A/42.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 42 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/42
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          14 TTTTTTTTTTTTTT 1


RESULT 2905
BD176797/c
LOCUS       BD176797                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176797
VERSION     BD176797.1  GI:29122509
KEYWORDS    WO 02074951-A/44.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 44 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/44
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTT 2178
              ||||||||||||||
Db          14 CTTTTTTTTTTTTT 1


RESULT 2906
BD176801
LOCUS       BD176801                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176801
VERSION     BD176801.1  GI:29122513
KEYWORDS    WO 02074951-A/48.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 48 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
COMMENT     OS   Artificial Sequence
            PN   WO 02074951-A/48
            PD   26-SEP-2002
            PF   13-MAR-2002 WO 2002JP002338
            PR   15-MAR-2001 JP 01P   073959
            PI   MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
            C12N15/09,C12Q1/68
            CC   Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
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  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2900
BD096965/c
LOCUS       BD096965                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Oligonucleotide for SNP detection.
ACCESSION   BD096965
VERSION     BD096965.1  GI:22642553
KEYWORDS    JP 2001346579-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Komiyama,M. and Asanuma,H.
  TITLE     Oligonucleotide for SNP detection
  JOURNAL   Patent: JP 2001346579-A 4 18-DEC-2001;
            MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT     OS   Artificial Sequence
            PN   JP 2001346579-A/4
            PD   18-DEC-2001
            PF   02-JUN-2000 JP 2000165441
            PI   MAKOTO KOMIYAMA,HIROYUKI ASANUMA
            PC   C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/566,
            PC   C12N15/00,
            PC   C12N15/00
            CC   Oligonucleotide for SNP detection
            FH   Key             Location/Qualifiers
            FT   modified_base   1.
FEATURES            Location/Qualifiers
     source         1. .14
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 2901
BD132850
LOCUS       BD132850                  14 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Methods of nucleic acid detection.
ACCESSION   BD132850
VERSION     BD132850.1  GI:23227795
KEYWORDS    JP 2002509443-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
  TITLE     Methods of nucleic acid detection
  JOURNAL   Patent: JP 2002509443-A 1 26-MAR-2002;
            GEN PROBE INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002509443-A/1
            PD   26-MAR-2002
            PF   30-OCT-1998 JP 1999526687
            PR   31-OCT-1997 US    60/063969
            PI   WILLIAM G WEISBURG,PAUL D STULL,MICHAEL R RESHATOFF PC
            C12Q1/68
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .14
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2902
BD132850/c
LOCUS       BD132850                  14 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Methods of nucleic acid detection.
ACCESSION   BD132850
VERSION     BD132850.1  GI:23227795
KEYWORDS    JP 2002509443-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
  TITLE     Methods of nucleic acid detection
  JOURNAL   Patent: JP 2002509443-A 1 26-MAR-2002;
            GEN PROBE INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002509443-A/1
            PD   26-MAR-2002
            PF   30-OCT-1998 JP 1999526687
            PR   31-OCT-1997 US    60/063969
            PI   WILLIAM G WEISBURG,PAUL D STULL,MICHAEL R RESHATOFF PC
            C12Q1/68
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .14
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 2903
BD176795
LOCUS       BD176795                  14 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression.
ACCESSION   BD176795
VERSION     BD176795.1  GI:29122507
KEYWORDS    WO 02074951-A/42.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
  TITLE     Method of constructing cDNA tag for identifying expressed gene and
            method of analyzing gene expression
  JOURNAL   Patent: WO 02074951-A 42 26-SEP-2002;
            KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
            KUNITAKA HIROSE,JUN SAKAI
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            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Polymorphisms and new genes in the region of the human
            hemochromatosis gene
  JOURNAL   Patent: JP 2001525663-A 15 11-DEC-2001;
            PROGENTIOR INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001525663-A/15
            PD   11-DEC-2001
            PF   30-SEP-1997 JP 1998516815
            PR   01-OCT-1996 US     08/724394,07-MAY-1997 US     08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC   Polymorphisms
            and new genes in the region of the human CC   hemochromatosis gene
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 2897
BD096963
LOCUS       BD096963                 14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Oligonucleotide for SNP detection.
ACCESSION   BD096963
VERSION     BD096963.1  GI:22642551
KEYWORDS    JP 2001346579-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Komiyama,M. and Asanuma,H.
  TITLE     Oligonucleotide for SNP detection
  JOURNAL   Patent: JP 2001346579-A 2 18-DEC-2001;
            MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT     OS   Artificial Sequence
            PN   JP 2001346579-A/2
            PD   18-DEC-2001
            PF   02-JUN-2000 JP 2000165441
            PI   MAKOTO KOMIYAMA,HIROYUKI ASANUMA
            PC   C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/566,
            PC   C12N15/00,
            PC   C12N15/00
            CC   Oligonucleotide for SNP detection
            FH   Key             Location/Qualifiers
            FT   modified_base   1.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2898
BD096963/c
LOCUS       BD096963                 14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Oligonucleotide for SNP detection.
ACCESSION   BD096963
VERSION     BD096963.1  GI:22642551
KEYWORDS    JP 2001346579-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Komiyama,M. and Asanuma,H.
  TITLE     Oligonucleotide for SNP detection
  JOURNAL   Patent: JP 2001346579-A 2 18-DEC-2001;
            MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT     OS   Artificial Sequence
            PN   JP 2001346579-A/2
            PD   18-DEC-2001
            PF   02-JUN-2000 JP 2000165441
            PI   MAKOTO KOMIYAMA,HIROYUKI ASANUMA
            PC   C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/566,
            PC   C12N15/00,
            PC   C12N15/00
            CC   Oligonucleotide for SNP detection
            FH   Key             Location/Qualifiers
            FT   modified_base   1.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 2899
BD096965
LOCUS       BD096965                 14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Oligonucleotide for SNP detection.
ACCESSION   BD096965
VERSION     BD096965.1  GI:22642553
KEYWORDS    JP 2001346579-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Komiyama,M. and Asanuma,H.
  TITLE     Oligonucleotide for SNP detection
  JOURNAL   Patent: JP 2001346579-A 4 18-DEC-2001;
            MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT     OS   Artificial Sequence
            PN   JP 2001346579-A/4
            PD   18-DEC-2001
            PF   02-JUN-2000 JP 2000165441
            PI   MAKOTO KOMIYAMA,HIROYUKI ASANUMA
            PC   C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/566,
            PC   C12N15/00,
            PC   C12N15/00
            CC   Oligonucleotide for SNP detection
            FH   Key             Location/Qualifiers
            FT   modified_base   1.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
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VERSION     BD073882.1  GI:22619485
KEYWORDS    JP 2001512698-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Suishelm,K., Hosier,S. and Kubbies,M.
  TITLE     Isolation of novel aging factor gene P23
  JOURNAL   Patent: JP 2001512698-A 7 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS   Unidentified
            PN   JP 2001512698-A/7
            PD   28-AUG-2001
            PF   05-AUG-1998 JP 2000506375
            PR   08-AUG-1997 US    08/908873
            PI   KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02,
            PC   C12P21/08,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Isolation of novel aging factor gene P23
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 2894
BD084126
LOCUS       BD084126                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION   BD084126
VERSION     BD084126.1  GI:22629736
KEYWORDS    JP 2001525663-A/14.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Polymorphisms and new genes in the region of the human
            hemochromatosis gene
  JOURNAL   Patent: JP 2001525663-A 14 11-DEC-2001;
            PROGENTIOR INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001525663-A/14
            PD   11-DEC-2001
            PF   30-SEP-1997 JP 1998516815
            PR   01-OCT-1996 US    08/724394,07-MAY-1997 US    08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC   Polymorphisms
            and new genes in the region of the human CC   hemochromatosis gene
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .14
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match              0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTT 2178
              ||||||||||||||
Db          1 CTTTTTTTTTTTTT 14


RESULT 2895
BD084127
LOCUS       BD084127                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION   BD084127
VERSION     BD084127.1  GI:22629737
KEYWORDS    JP 2001525663-A/15.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Polymorphisms and new genes in the region of the human
            hemochromatosis gene
  JOURNAL   Patent: JP 2001525663-A 15 11-DEC-2001;
            PROGENTIOR INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001525663-A/15
            PD   11-DEC-2001
            PF   30-SEP-1997 JP 1998516815
            PR   01-OCT-1996 US    08/724394,07-MAY-1997 US    08/852495 PI
            JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
            WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
            C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC   Polymorphisms
            and new genes in the region of the human CC   hemochromatosis gene
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .14
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match              0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 2896
BD084127/c
LOCUS       BD084127                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION   BD084127
VERSION     BD084127.1  GI:22629737
KEYWORDS    JP 2001525663-A/15.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
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LOCUS       AX827014                  14 bp    RNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 11 from Patent EP1344835.
ACCESSION   AX827014
VERSION     AX827014.1  GI:39837221
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
            Liu,D.
  TITLE     Real-time nucleic acid detection processes and compositions
  JOURNAL   Patent: EP 1344835-A 11 17-SEP-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
             ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 2890
AX839906
LOCUS       AX839906                  14 bp    RNA     linear   PAT 16-DEC-2003
DEFINITION  Sequence 11 from Patent EP1348713.
ACCESSION   AX839906
VERSION     AX839906.1  GI:39978437
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stavrianopoulos,J.G. and Rabbani,E.
  TITLE     Labeling reagents and labeled tabeled targets, target labeling
            processes and other processes for using same in nucleic acid
            determinations and analyses
  JOURNAL   Patent: EP 1348713-A 11 01-OCT-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
             ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 2891
AX839906/c
LOCUS       AX839906                  14 bp    RNA     linear   PAT 16-DEC-2003
DEFINITION  Sequence 11 from Patent EP1348713.
ACCESSION   AX839906
VERSION     AX839906.1  GI:39978437
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stavrianopoulos,J.G. and Rabbani,E.
  TITLE     Labeling reagents and labeled tabeled targets, target labeling
            processes and other processes for using same in nucleic acid
            determinations and analyses
  JOURNAL   Patent: EP 1348713-A 11 01-OCT-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
             ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 2892
BD073880
LOCUS       BD073880                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Isolation of novel aging factor gene P23.
ACCESSION   BD073880
VERSION     BD073880.1  GI:22619483
KEYWORDS    JP 2001512698-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Suishelm,K., Hosier,S. and Kubbies,M.
  TITLE     Isolation of novel aging factor gene P23
  JOURNAL   Patent: JP 2001512698-A 5 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS   Unidentified
            PN   JP 2001512698-A/5
            PD   28-AUG-2001
            PF   05-AUG-1998 JP 2000506375
            PR   08-AUG-1997 US    08/908873
            PI   KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02,
            PC   C12P21/08,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Isolation of novel aging factor gene P23
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAA 2188
             ||||||||||||||
Db          1 TTTTTTTTTTTTAA 14


RESULT 2893
BD073882/c
LOCUS       BD073882                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Isolation of novel aging factor gene P23.
ACCESSION   BD073882
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
  TITLE     Polynucleotide phosphorodithioate
  JOURNAL   Patent: US 5453496-A 5 26-SEP-1995;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 2885
AR364949/c
LOCUS       AR364949                  14 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 5 from patent US 5453496.
ACCESSION   AR364949
VERSION     AR364949.1  GI:34428169
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
  TITLE     Polynucleotide phosphorodithioate
  JOURNAL   Patent: US 5453496-A 5 26-SEP-1995;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 2886
AX048406
LOCUS       AX048406                  14 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 5 from Patent WO0071747.
ACCESSION   AX048406
VERSION     AX048406.1  GI:12225570
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 5 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Region A"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2887
AX048406/c
LOCUS       AX048406                  14 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 5 from Patent WO0071747.
ACCESSION   AX048406
VERSION     AX048406.1  GI:12225570
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 5 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Region A"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 2888
AX827014
LOCUS       AX827014                  14 bp    RNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 11 from Patent EP1344835.
ACCESSION   AX827014
VERSION     AX827014.1  GI:39837221
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
            Liu,D.
  TITLE     Real-time nucleic acid detection processes and compositions
  JOURNAL   Patent: EP 1344835-A 11 17-SEP-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 2889
AX827014/c
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LOCUS       AR222460                 14 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 20 from patent US 6429300.
ACCESSION   AR222460
VERSION     AR222460.1  GI:23329991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 20 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 2880
AR222460/c
LOCUS       AR222460                 14 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 20 from patent US 6429300.
ACCESSION   AR222460
VERSION     AR222460.1  GI:23329991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 20 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 2881
AR241806/c
LOCUS       AR241806                 14 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 94 from patent US 6472154.
ACCESSION   AR241806
VERSION     AR241806.1  GI:27287618
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 94 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              ||||||||||||||
Db         14 GAAAAAAAAAAAAA 1


RESULT 2882
AR364948
LOCUS       AR364948                 14 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 4 from patent US 5453496.
ACCESSION   AR364948
VERSION     AR364948.1  GI:34428168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
  TITLE     Polynucleotide phosphorodithioate
  JOURNAL   Patent: US 5453496-A 4 26-SEP-1995;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2883
AR364948/c
LOCUS       AR364948                 14 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 4 from patent US 5453496.
ACCESSION   AR364948
VERSION     AR364948.1  GI:34428168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
  TITLE     Polynucleotide phosphorodithioate
  JOURNAL   Patent: US 5453496-A 4 26-SEP-1995;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 2884
AR364949
LOCUS       AR364949                 14 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 5 from patent US 5453496.
ACCESSION   AR364949
VERSION     AR364949.1  GI:34428169
KEYWORDS    .
SOURCE      Unknown.
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REFERENCE   1  (bases 1 to 14)
  AUTHORS   Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
  TITLE     Retinoid metabolizing protein
  JOURNAL   Patent: US 6306624-A 17 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAA 2188
              ||||||||||||||
Db          1 TTTTTTTTTTTTAA 14


RESULT 2876
AR174031/c
LOCUS       AR174031                  14 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 21 from patent US 6306624.
ACCESSION   AR174031
VERSION     AR174031.1  GI:17914351
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
  TITLE     Retinoid metabolizing protein
  JOURNAL   Patent: US 6306624-A 21 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 2877
BD237464
LOCUS       BD237464                  14 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Nucleic acid having blocked terminals modified with an acid-stable
            skeleton and therapeutic method thereof.
ACCESSION   BD237464
VERSION     BD237464.1  GI:33047234
KEYWORDS    JP 2002534434-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Dale,R.M.K., Gatton,S.L. and Arrow,A.
  TITLE     Nucleic acid having blocked terminals modified with an acid-stable
            skeleton and therapeutic method thereof
  JOURNAL   Patent: JP 2002534434-A 2 15-OCT-2002;
            OLIGOS ETC INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002534434-A/2
            PD   15-OCT-2002
            PF   16-DEC-1999 JP 2000592300
            PR   30-DEC-1998 US    09/223498,19-JUL-1999 US    09/356069 PI
            RODERIC M K DALE,STEVEN L GATTON,AMY ARROW
            PC   C07H21/00,A61K9/127,A61K9/50,A61K31/7088,A61K47/44,A61K48/00,
            PC   A61P3/00,
            PC   A61P17/02,A61P29/00,A61P31/04,A61P31/10,A61P31/12,A61P35/00,
            PC   C12N5/10,
            PC   C12N15/09,C12N15/00,C12N5/00
            CC   Nucleic acid having blocked terminals modified with an acid-
            CC          stable
            CC   skeleton and therapeutic method thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 2878
BD237464/c
LOCUS       BD237464                  14 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Nucleic acid having blocked terminals modified with an acid-stable
            skeleton and therapeutic method thereof.
ACCESSION   BD237464
VERSION     BD237464.1  GI:33047234
KEYWORDS    JP 2002534434-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Dale,R.M.K., Gatton,S.L. and Arrow,A.
  TITLE     Nucleic acid having blocked terminals modified with an acid-stable
            skeleton and therapeutic method thereof
  JOURNAL   Patent: JP 2002534434-A 2 15-OCT-2002;
            OLIGOS ETC INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002534434-A/2
            PD   15-OCT-2002
            PF   16-DEC-1999 JP 2000592300
            PR   30-DEC-1998 US    09/223498,19-JUL-1999 US    09/356069 PI
            RODERIC M K DALE,STEVEN L GATTON,AMY ARROW
            PC   C07H21/00,A61K9/127,A61K9/50,A61K31/7088,A61K47/44,A61K48/00,
            PC   A61P3/00,
            PC   A61P17/02,A61P29/00,A61P31/04,A61P31/10,A61P31/12,A61P35/00,
            PC   C12N5/10,
            PC   C12N15/09,C12N15/00,C12N5/00
            CC   Nucleic acid having blocked terminals modified with an acid-
            CC          stable
            CC   skeleton and therapeutic method thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 2879
AR222460
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          been generated in the framework of the French plant genomics
          program 'Genoplante' (http://www.genoplante.com and
          http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="498E01"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .28
                     /note="T-DNA flanking sequence
                     right border"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 28;
  Best Local Similarity   84.2%;  Pred. No. 4.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||  ||| | ||||
Db          1 AAAAAAAACAAACACAAAA 19


RESULT 2871
AR029886
LOCUS       AR029886                 14 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 75 from patent US 5861244.
ACCESSION   AR029886
VERSION     AR029886.1  GI:5943100
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 75 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 2872
AR029886/c
LOCUS       AR029886                 14 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 75 from patent US 5861244.
ACCESSION   AR029886
VERSION     AR029886.1  GI:5943100
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 75 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 2873
AR029887
LOCUS       AR029887                 14 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 76 from patent US 5861244.
ACCESSION   AR029887
VERSION     AR029887.1  GI:5943101
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 76 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 2874
AR029887/c
LOCUS       AR029887                 14 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 76 from patent US 5861244.
ACCESSION   AR029887
VERSION     AR029887.1  GI:5943101
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 76 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 2875
AR174027
LOCUS       AR174027                 14 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 17 from patent US 6306624.
ACCESSION   AR174027
VERSION     AR174027.1  GI:17914347
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 17 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAAAA 1521
              | ||| |||| ||||||||
Db         21 AAAAATACAGAAAATAAAA 3


RESULT 2867
AR409906/c
LOCUS       AR409906                 22 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 19 from patent US 6635422.
ACCESSION   AR409906
VERSION     AR409906.1  GI:40161041
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 19 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAAAA 1521
              | ||| |||| ||||||||
Db         21 AAAAATACAGAAAATAAAA 3


RESULT 2868
AX771993/c
LOCUS       AX771993                 23 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 8 from Patent WO03006065.
ACCESSION   AX771993
VERSION     AX771993.1  GI:32438641
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Braun,K., Waldeck,W., Pipkorn,R., Braun,I. and Debus,J.
  TITLE     PNA conjugate for the treatment of diseases associated with HIV
  JOURNAL   Patent: WO 03006065-A 8 23-JAN-2003;
            Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
            (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PNA I"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 23;
  Best Local Similarity   84.2%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTGTA 1997
              |||||||||||||| | | |
Db         19 AAAAAAAGAAAAGGGGGGA 1


RESULT 2869
AX042823
LOCUS       AX042823                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 389 from Patent WO0065088.
ACCESSION   AX042823
VERSION     AX042823.1  GI:11341431
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 389 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-B Homozygote Primer Sequence"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 25;
  Best Local Similarity   84.2%;  Pred. No. 4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTCCCAA 19


RESULT 2870
AJ600024
LOCUS       AJ600024                 28 bp    DNA     linear   PLN 23-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, right border, clone
            498E01.
ACCESSION   AJ600024
VERSION     AJ600024.1  GI:37949652
KEYWORDS    right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 28)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
```

```
RESULT 2862
AX352320/c
LOCUS       AX352320                  22 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 616 from Patent WO0193902.
ACCESSION   AX352320
VERSION     AX352320.1  GI:18617603
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 616 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||| | || |||
Db         22 AAAAAAAAAAGAGAACAAA 4


RESULT 2863
AR003289/c
LOCUS       AR003289                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 11 from patent US 5744300.
ACCESSION   AR003289
VERSION     AR003289.1  GI:3964548
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 11 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              ||||||||| |||||  ||
Db         22 TGAAAAAAAAAAAAGCTTG 4


RESULT 2864
I30200/c
LOCUS       I30200                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 29 from patent US 5580726.
ACCESSION   I30200
VERSION     I30200.1  GI:1820991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 29 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              ||||||||| |||||  ||
Db         22 TGAAAAAAAAAAAAGCTTG 4


RESULT 2865
BD206202/c
LOCUS       BD206202                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206202
VERSION     BD206202.1  GI:33015972
KEYWORDS    JP 2002515252-A/15.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 15 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/15
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              ||||||||| |||||  ||
Db         22 TGAAAAAAAAAAAAGCTTG 4


RESULT 2866
AR409904/c
LOCUS       AR409904                  22 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 17 from patent US 6635422.
ACCESSION   AR409904
VERSION     AR409904.1  GI:40161039
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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```
Db         21 CTGGGGGGTTYCTGGTGTCAA 1


RESULT 2859
BD196794/c
LOCUS       BD196794                  21 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Prostatic cancer gene.
ACCESSION   BD196794
VERSION     BD196794.1  GI:33006564
KEYWORDS    JP 2002516657-A/383.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
  TITLE     Prostatic cancer gene
  JOURNAL   Patent: JP 2002516657-A 383 11-JUN-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002516657-A/383
            PD   11-JUN-2002
            PF   22-DEC-1998 JP 2000525562
            PR   22-DEC-1997 US    08/996306,09-SEP-1998 US    60/099658 PI
            DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
            C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
            C12N1/19,
            PC   C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
            ,C12N15/00,C12N5/00,
            PC   C12N5/00,C12N15/00
            CC   downstream amplification primer for SEQ 237, SEQ 314 FH   Key
                       Location/Qualifiers
            FT   primer_bind     1. .21.
FEATURES                Location/Qualifiers
     source             1. .21
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2685 TGAAATGGAGATTTGGAAT 2703
              |||||||||  | ||||||
Db         20 TGAAATGGACTTCTGGAAT 2


RESULT 2860
BD225398
LOCUS       BD225398                  21 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Targeting antisense library.
ACCESSION   BD225398
VERSION     BD225398.1  GI:33035168
KEYWORDS    JP 2002509733-A/32.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Ruffner,D.E., Pierce,M.L. and Chen,Z.
  TITLE     Targeting antisense library
  JOURNAL   Patent: JP 2002509733-A 32 02-APR-2002;
            UNIVERSITY OF UTAH RESEARCH FOUNDATION
COMMENT     OS   Herpes simplex virus
            PN   JP 2002509733-A/32
            PD   02-APR-2002
            PF   28-MAR-1999 JP 2000541344
            PR   28-MAR-1998 US    60/079792,06-NOV-1998 US    60/107504 PI
            DUANE E RUFFNER,MICHAEL L PIERCE,ZHIDONG CHEN PC
            C12N15/09,C12Q1/68//A61K48/00,C12N15/00
            CC   Targeting antisense library
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Herpes simplex virus'.
FEATURES                Location/Qualifiers
     source             1. .21
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       151 GGGGACGCCGGACGCCATG 169
             ||||||  | |||||||||
Db         1 GGGGACCACCGACGCCATG 19


RESULT 2861
AJ589672/c
LOCUS       AJ589672                  21 bp    DNA     linear   PLN 23-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            555B04.
ACCESSION   AJ589672
VERSION     AJ589672.1  GI:37939296
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES                Location/Qualifiers
     source             1. .21
                        /organism="Arabidopsis thaliana"
                        /mol_type="genomic DNA"
                        /cultivar="Wassillewskija"
                        /db_xref="taxon:3702"
                        /clone="555B04"
                        /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature       1. .21
                        /note="T-DNA flanking sequence
                        left border"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2421 AAATACTGGTGCACTTCTT 2439
              |||||||| |||| || ||
Db         21 AAATACTGATGCATTTTTT 3
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FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1169 ACCAGACCTCATCTTGGAG 1187
              |||||||||||  ||  |||
Db         19 ACCAGACCTCAGCTATGAG 1


RESULT 2856
BD091837/c
LOCUS       BD091837                  21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel cytokines.
ACCESSION   BD091837
VERSION     BD091837.1  GI:22637448
KEYWORDS    WO 0073442-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Tulin,E.E. and Onoda,N.
  TITLE     Novel cytokines
  JOURNAL   Patent: WO 0073442-A 9 07-DEC-2000;
            CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, EDGARDO E
            TULIN, NOBUHISA ONODA
COMMENT     OS   Artificial Sequence
            PN   WO 0073442-A/9
            PD   07-DEC-2000
            PF   31-MAY-2000 WO 2000JP003505
            PR   01-JUN-1999 JP 99P   154365
            PI   EDGARDO E TULIN,NOBUHISA ONODA
            PC   C12N15/12,C12N15/63,C12N5/10,C12P21/02,C07K14/52,C07K14/715,
            PC   C12Q1/02
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           primer
            CC   sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1169 ACCAGACCTCATCTTGGAG 1187
              |||||||||||  ||  |||
Db         19 ACCAGACCTCAGCTATGAG 1


RESULT 2857
BD129746/c
LOCUS       BD129746                  21 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Asthma-associated gene.
ACCESSION   BD129746
VERSION     BD129746.1  GI:23224691
KEYWORDS    JP 2002500895-A/36.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Wilson,A.R.B., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
            Miller,A. and North,M.
  TITLE     Asthma-associated gene
  JOURNAL   Patent: JP 2002500895-A 36 15-JAN-2002;
            AXYS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002500895-A/36
            PD   15-JAN-2002
            PF   21-JAN-1998 JP 2000528715
            PI   ANGELA R BROOKS WILSON,ALAN BUCKLER,LON
            CARDON,ALISOUN H CAREY,
            PI   MARGARET GALVIN,ANDREW MILLER,MICHAEL NORTH
            PC   C12Q1/68,A01K67/027,C07K14/47,C12N15/09,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Asthma-associated gene
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        115 CTGGGGGGATCCTGGATTTAA 135
              ||||||| |:||||  | ||
Db         21 CTGGGGGGTTYCTGGTGTCAA 1


RESULT 2858
BD129825/c
LOCUS       BD129825                  21 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Asthma-associated gene.
ACCESSION   BD129825
VERSION     BD129825.1  GI:23224770
KEYWORDS    JP 2002500895-A/115.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Wilson,A.R.B., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
            Miller,A. and North,M.
  TITLE     Asthma-associated gene
  JOURNAL   Patent: JP 2002500895-A 115 15-JAN-2002;
            AXYS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002500895-A/115
            PD   15-JAN-2002
            PF   21-JAN-1998 JP 2000528715
            PI   ANGELA R BROOKS WILSON,ALAN BUCKLER,LON
            CARDON,ALISOUN H CAREY,
            PI   MARGARET GALVIN,ANDREW MILLER,MICHAEL NORTH
            PC   C12Q1/68,A01K67/027,C07K14/47,C12N15/09,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Asthma-associated gene
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        115 CTGGGGGGATCCTGGATTTAA 135
              ||||||| |:||||  | ||
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  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1992 TGTGTATCTAGCTTCTTCA 2010
              ||||| |||  ||||||||
Db         20 TGTGTTTCTGCCTTCTTCA 2

RESULT 2852
AX486786
LOCUS       AX486786                 21 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 4086 from Patent WO02053728.
ACCESSION   AX486786
VERSION     AX486786.1  GI:22320934
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 4086 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Candida albicans"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:5476"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1888 TTGATGTGCCCTAGATCAA 1906
              |||||| | || |||||||
Db          1 TTGATGGGTCCGAGATCAA 19

RESULT 2853
AX587363/c
LOCUS       AX587363                 21 bp    DNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 139 from Patent WO0236761.
ACCESSION   AX587363
VERSION     AX587363.1  GI:27656228
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   D'Andrea,A.D., Taniguchi,T., Timmers,C. and Grompe,M.
  TITLE     Methods and compositions for the diagnosis of cancer
            susceptibilities and defective dna repair mechanisms and treatment
            thereof
  JOURNAL   Patent: WO 0236761-A 139 10-MAY-2002;
            DANA FARBER CANCER INSTITUTE (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="MG755"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        231 GCAGCAATGGGAATCCGCG 249
              ||| |||||||| ||| ||
Db         21 GCATCAATGGGATTCCACG 3

RESULT 2854
BD056583/c
LOCUS       BD056583                 21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method to diagnose and treat pathological conditions resulting from
            deficient ion transport.
ACCESSION   BD056583
VERSION     BD056583.1  GI:22602189
KEYWORDS    JP 2001508291-A/40.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Lifton,R.P. and Simon,D.B.
  TITLE     Method to diagnose and treat pathological conditions resulting from
            deficient ion transport
  JOURNAL   Patent: JP 2001508291-A 40 26-JUN-2001;
            YALE UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2001508291-A/40
            PD   26-JUN-2001
            PF   19-DEC-1997 JP 1998530123
            PR   31-DEC-1996 US    08/778052
            PI   RICHARD P LIFTON,DAVID B SIMON
            PC   C12N15/09,C07K14/435,C07K16/00,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12Q1/68,G01N33/53,C12N15/00,C12N5/00 CC   Primer
            for analysis of human TSC gene
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          97 GGATTTACCGCTTGGGGGC 115
               ||| |||| |||||| |||
Db          19 GGACTTACGGCTTGGTGGC 1

RESULT 2855
BD091833/c
LOCUS       BD091833                 21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel cytokines.
ACCESSION   BD091833
VERSION     BD091833.1  GI:22637444
KEYWORDS    WO 0073442-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Tulin,E.E. and Onoda,N.
  TITLE     Novel cytokines
  JOURNAL   Patent: WO 0073442-A 5 07-DEC-2000;
            CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, EDGARDO E
            TULIN, NOBUHISA ONODA
COMMENT     OS   Artificial Sequence
            PN   WO 0073442-A/5
            PD   07-DEC-2000
            PF   31-MAY-2000 WO 2000JP003505
            PR   01-JUN-1999 JP 99P   154365
            PI   EDGARDO E TULIN,NOBUHISA ONODA
            PC   C12N15/12,C12N15/63,C12N5/10,C12P21/02,C07K14/52,C07K14/715,
            PC   C12Q1/02
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers.
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KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Roy,F., Goossens,S., Janssens,B. and Vanpoucke,G.
  TITLE     Novel _g(a) expressed in heart and testis
  JOURNAL   Patent: WO 0204636-A 50 17-JAN-2002;
            Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="lower primer FVR2520"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1793 TTTCCTTCTCTGAAAGTGG 1811
              |||| |||||||||  |||
Db         20 TTTCATTCTCTGAACCTGG 2


RESULT 2848
AX404559
LOCUS       AX404559                21 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 385 from Patent WO0224747.
ACCESSION   AX404559
VERSION     AX404559.1  GI:21437840
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U. and Hoffmeyer,S.
  TITLE     Polymorphisms in human genes of cardiovascular regulators and their
            use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 0224747-A 385 28-MAR-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        818 ATGAACCCCACTGAGGTCT 836
              | ||||||||  |||||||
Db          2 AAGAACCCCAGAGAGGTCT 20


RESULT 2849
AX404560/c
LOCUS       AX404560                21 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 386 from Patent WO0224747.
ACCESSION   AX404560
VERSION     AX404560.1  GI:21437841
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U. and Hoffmeyer,S.
  TITLE     Polymorphisms in human genes of cardiovascular regulators and their
            use in diagnostic and therapeutic applications
  JOURNAL   Patent: WO 0224747-A 386 28-MAR-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        818 ATGAACCCCACTGAGGTCT 836
              | ||||||||  |||||||
Db         20 AAGAACCCCAGAGAGGTCT 2


RESULT 2850
AX430795/c
LOCUS       AX430795                21 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 11 from Patent WO0240709.
ACCESSION   AX430795
VERSION     AX430795.1  GI:21655877
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Nielsen,V.H., Hoej,A., Jonker,M., Aasberg,A., Holm,L.E., Horn,P.,
            Jensen,H., Jeppesen,M., Panitz,F., Svendsen,S., Thomsen,B. and
            Bendixen,C.
  TITLE     Genetic test for the identification of carriers of complex
            vertebral malformations in cattle
  JOURNAL   Patent: WO 0240709-A 11 23-MAY-2002;
            MINISTERIET FOR FOEDERVARER LA (DK); DANSK KVAEGAVL (DK)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA Primer"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1508 CACAGGAAATAAAATTGGA 1526
              | ||||||| |||| ||||
Db         21 CCCAGGAAAGAAAACTGGA 3


RESULT 2851
AX449621/c
LOCUS       AX449621                21 bp    DNA     linear   PAT 03-JUL-2002
DEFINITION  Sequence 50 from Patent WO0210216.
ACCESSION   AX449621
VERSION     AX449621.1  GI:21698230
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Casman,S.,
            Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Gerlach,V.L.,
            Macdougall,J.R. and Smithson,G.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0210216-A 50 07-FEB-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primers"
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  Best Local Similarity   80.0%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        550 CTCCGGGCTGGAGGCGGGCG 569
              | || ||||  |||||||||
Db          2 CACCTGGCTNCAGGCGGGCG 21


RESULT 2843
AX146232
LOCUS       AX146232                 21 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 423 from Patent WO0134840.
ACCESSION   AX146232
VERSION     AX146232.1  GI:14284750
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Au,K.G., Chen,J.G., Patil,N. and Thomas,D.
  TITLE     Genetic compositions and methods
  JOURNAL   Patent: WO 0134840-A 423 17-MAY-2001;
            GLAXO GROUP LIMITED (GB) ; Affymetrix, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     variation       1. .21
                     /note="'n' represents a polymorphic base"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   80.0%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        129 GATTTAACTGGCGACTGTTT 148
              ||||||||| | |||  |||
Db          2 GATTTAACTNGAGACCTTTT 21


RESULT 2844
AX148061
LOCUS       AX148061                 21 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 61 from Patent WO0134848.
ACCESSION   AX148061
VERSION     AX148061.1  GI:14347031
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brown,B.A., Kilpatrick,D.R., Pallansch,M.A. and Oberste,M.S.
  TITLE     Serotype-specific identification of enterovirus 71 by rt-pcr
  JOURNAL   Patent: WO 0134848-A 61 17-MAY-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     modified_base   3
                     /mod_base=i
     modified_base   9
                     /mod_base=i
     modified_base   15
                     /mod_base=i

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1824 TAGAATCTTTTAAATACAT 1842
              |||||| |||| ||||||
Db          2 TAGAATTATTTACATACAT 20


RESULT 2845
AX179540
LOCUS       AX179540                 21 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 1 from Patent WO0132841.
ACCESSION   AX179540
VERSION     AX179540.1  GI:14599152
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ruiz,M., Kinter,A., Dybul,M., Catanzaro,A. and Fauci,A.S.
  TITLE     Method of in vitro t cell differentiation of cd34?+ progenitor
            cells
  JOURNAL   Patent: WO 0132841-A 1 10-MAY-2001;
            The Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR Primer"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1786 CCCATTCTTTCCTTCTCTG 1804
              | ||  ||||||||||||||
Db          3 CACACCCTTTCCTTCTCTG 21


RESULT 2846
AX241164
LOCUS       AX241164                 21 bp    DNA     linear   PAT 26-SEP-2001
DEFINITION  Sequence 402 from Patent WO0160975.
ACCESSION   AX241164
VERSION     AX241164.1  GI:15798039
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C. and Bussey,H.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 0160975-A 402 23-AUG-2001;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA primer"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1888 TTGATGTGCCCTAGATCAA 1906
              |||||| | || |||||||
Db          1 TTGATGGGTCCGAGATCAA 19


RESULT 2847
AX353518/c
LOCUS       AX353518                 21 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 50 from Patent WO0204636.
ACCESSION   AX353518
VERSION     AX353518.1  GI:18618593
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REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 481 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        432 CCCTGCACCAGCCGGCGCCCA 452
              ||| | | ||:|||| |||||
Db         21 CCCCGAAGCARCCGGTGCCCA 1


RESULT 2839
AX095750
LOCUS       AX095750                21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 928 from Patent WO0118250.
ACCESSION   AX095750
VERSION     AX095750.1  GI:13511977
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 928 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        189 ATGTCAAGTACGAAGAGGACT 209
              ||| || | |:|| |||||||
Db          1 ATGACATGGAYGAGGAGGACT 21


RESULT 2840
AX096493
LOCUS       AX096493                21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 1671 from Patent WO0118250.
ACCESSION   AX096493
VERSION     AX096493.1  GI:13512747
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1671 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2271 TTTCAGATGTTTCGAGTAAAC 2291
              || ||||||| : | ||| |||
Db          1 TTCCAGATGTKACCAGTCAAC 21


RESULT 2841
AX097185
LOCUS       AX097185                21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 2363 from Patent WO0118250.
ACCESSION   AX097185
VERSION     AX097185.1  GI:13513522
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 2363 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        758 ATTTCCATGACCAAGAACCCT 778
              |||   ||||:||||| ||||
Db          1 ATTGGAATGASCAAGATCCCT 21


RESULT 2842
AX145917
LOCUS       AX145917                21 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 108 from Patent WO0134840.
ACCESSION   AX145917
VERSION     AX145917.1  GI:14284435
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Au,K.G., Chen,J.G., Patil,N. and Thomas,D.
  TITLE     Genetic compositions and methods
  JOURNAL   Patent: WO 0134840-A 108 17-MAY-2001;
            GLAXO GROUP LIMITED (GB) ; Affymetrix, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     variation       1. .21
                     /note="'n' represents a polymorphic base"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 10341 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        340 CTACTTTCCCCCTCCCTAC 358
              ||||||||||| || | ||
Db          3 CTACTTTCCCCATCTCCAC 21


RESULT 2834
AR349596
LOCUS       AR349596                 21 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 32 from patent US 6586180.
ACCESSION   AR349596
VERSION     AR349596.1  GI:33750394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Ruffner,D.E., Pierce,M.L. and Chen,Z.
  TITLE     Directed antisense libraries
  JOURNAL   Patent: US 6586180-A 32 01-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        151 GGGGACGCCGGACGCCATG 169
              ||||||  | |||||||||
Db          1 GGGGACCACCGACGCCATG 19


RESULT 2835
AR400768/c
LOCUS       AR400768                 21 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 20 from patent US 6620985.
ACCESSION   AR400768
VERSION     AR400768.1  GI:40145614
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Glazebrook,J., Jirage,D., Tootle,T.L., Zhou,N. and Feys,B.J.F.
  TITLE     PAD4 nucleic acid compositions from Arabidopsis and methods
            therefor
  JOURNAL   Patent: US 6620985-A 20 16-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1096 TGTTCATTTGGCTAGGGAC 1114
              || |||||||||| || | |
Db         20 TGATCATTTGGCTATGGGC 2


RESULT 2836
AR409398/c
LOCUS       AR409398                 21 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 10 from patent US 6632934.
ACCESSION   AR409398
VERSION     AR409398.1  GI:40160323
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Moreadith,R.W., Zinn,A.R., Watson,M.L., Inoue,N., Hess,K.D. and
            Albright,G.M.
  TITLE     MORC gene compositions and methods of use
  JOURNAL   Patent: US 6632934-A 10 14-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        611 CTGCTGCCCCACGCACACG 629
              ||| || ||||||| ||||
Db         19 CTGTTGGCCCACGCCCACG 1


RESULT 2837
AR435626
LOCUS       AR435626                 21 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 56 from patent US 6656716.
ACCESSION   AR435626
VERSION     AR435626.1  GI:40198607
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Plowman,G., Martinez,R. and Whyte,D.
  TITLE     Polypeptide fragments of human PAK5 protein kinase
  JOURNAL   Patent: US 6656716-A 56 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        919 GTCCCCACCTGAATGCTTA 937
              ||||||||| ||| | |||
Db          2 GTCCCCACCAGAAGGTTTA 20


RESULT 2838
AX095303/c
LOCUS       AX095303                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 481 from Patent WO0118250.
ACCESSION   AX095303
VERSION     AX095303.1  GI:13511506
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Xu,S.-y.
  TITLE     Method for cloning and expression of Rhodothermus Obamensis DNA
            polymerase I large fragment in E. coli
  JOURNAL   Patent: US 6440715-A 7 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1373 CAGGCCATCTGTGCCGCGG 1391
              |||| | | ||||||||||
Db          3 CAGGGCGTTTGTGCCGCGG 21


RESULT 2829
AR228193
LOCUS       AR228193                 21 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 94 from patent US 6448003.
ACCESSION   AR228193
VERSION     AR228193.1  GI:27266939
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Guida,M. and Kurth,J.
  TITLE     Genotyping the human phenol sulfotransferbase 2 gene STP2
  JOURNAL   Patent: US 6448003-A 94 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        373 CTCCCAGTCGGCCGACCCC 391
              ||||||| |||| | ||||
Db          3 CTCCCAGGCGGCAGTCCCC 21


RESULT 2830
AR236360
LOCUS       AR236360                 21 bp    RNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6465176.
ACCESSION   AR236360
VERSION     AR236360.1  GI:27280288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Giordano,T., Beach,D.L. and Temeles,G.L.
  TITLE     Method for identifying compounds RNA/RNA binding protein
            interactions
  JOURNAL   Patent: US 6465176-A 8 15-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2255 TTTATTTGCATATTTATTT 2273
              |||||||   |||||||||
Db          2 TTTATTTATTTATTTATTT 20


RESULT 2831
AR292244/c
LOCUS       AR292244                 21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3979 from patent US 6537751.
ACCESSION   AR292244
VERSION     AR292244.1  GI:31679528
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 3979 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2280 TTTCGAGTAAACTTGAAAA 2298
              | |||| ||||| ||||||
Db         20 TGTCGAATAAACCTGAAAA 2


RESULT 2832
AR296511/c
LOCUS       AR296511                 21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 8246 from patent US 6537751.
ACCESSION   AR296511
VERSION     AR296511.1  GI:31683795
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 8246 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2685 TGAAATGGAGATTTGGAAT 2703
              |||||||||  | ||||||
Db         20 TGAAATGGACTTCTGGAAT 2


RESULT 2833
AR298606
LOCUS       AR298606                 21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 10341 from patent US 6537751.
ACCESSION   AR298606
VERSION     AR298606.1  GI:31685890
KEYWORDS    .
SOURCE      Unknown.
```

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            PI   GREGORY PLOWMAN,RICARDO MARTINEZ,DAVID WHYTE
            PC   C12N15/09,A61K38/55,A61P9/00,A61P9/10,A61P13/12,A61P25/00, PC
             A61P35/00,
            PC   A61P37/00,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   12,C12Q1/68,
            PC   C12N15/00,A61K37/64,C12N5/00
            CC   Synthesized nucleic acid molecule
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        919 GTCCCCACCTGAATGCTTA 937
              ||||||||| ||| | |||
Db          2 GTCCCCACCAGAAGGTTTA 20


RESULT 2824
I24714/c
LOCUS       I24714                    21 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 18 from patent US 5545545.
ACCESSION   I24714
VERSION     I24714.1  GI:1604584
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Gengenbach,B.G., Somers,D.A., Bittel,D.C., Shaver,J.M. and
            Sellner,J.M. deceased.
  TITLE     Lysine-insensitive maize dihydrodipicolinic acid synthase
  JOURNAL   Patent: US 5545545-A 18 13-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2027 GTAGGAGGCAAAGGTTCTA 2045
              | ||||||| ||||||||
Db         19 GAAGGAGGCCCAGGTTCTA 1


RESULT 2825
I43369
LOCUS       I43369                    21 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 3 from patent US 5631162.
ACCESSION   I43369
VERSION     I43369.1  GI:2468613
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   LeBoulch,P., London,I.M. and Tuan,D.
  TITLE     Retroviral vectors for transducing .beta.-globin gene and
            .beta.-locus control region derivatives
  JOURNAL   Patent: US 5631162-A 3 20-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              || || ||||||||| |||
Db          2 GAGAAGAAAAAAAAAGAAA 20


RESULT 2826
I43369/c
LOCUS       I43369                    21 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 3 from patent US 5631162.
ACCESSION   I43369
VERSION     I43369.1  GI:2468613
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   LeBoulch,P., London,I.M. and Tuan,D.
  TITLE     Retroviral vectors for transducing .beta.-globin gene and
            .beta.-locus control region derivatives
  JOURNAL   Patent: US 5631162-A 3 20-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              |||| ||||||||| || |
Db         21 CTTTCTTTTTTTTCTTCT 3


RESULT 2827
AR212771/c
LOCUS       AR212771                  21 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 18 from patent US 6403303.
ACCESSION   AR212771
VERSION     AR212771.1  GI:23309637
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Shipman,R., Leushner,J. and Dunn,J.M.
  TITLE     Method and reagents for testing for mutations in the BRCA1 gene
  JOURNAL   Patent: US 6403303-A 18 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2149 GATTGATTTTTTCTCCTT 2167
              ||||||| ||| |||| ||
Db         19 GATTGATGTTTCTCTCTTT 1


RESULT 2828
AR224252
LOCUS       AR224252                  21 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 7 from patent US 6440715.
ACCESSION   AR224252
VERSION     AR224252.1  GI:23333016
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LOCUS       AR029928                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 117 from patent US 5861244.
ACCESSION   AR029928
VERSION     AR029928.1  GI:5943142
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 117 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              || || ||||||||| |||
Db         20 GAGAAGAAAAAAAAAAGAAA 2

RESULT 2820
AR103516/c
LOCUS       AR103516                 21 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 40 from patent US 6087485.
ACCESSION   AR103516
VERSION     AR103516.1  GI:12815104
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Brooks-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
            Miller,A. and North,M.
  TITLE     Asthma related genes
  JOURNAL   Patent: US 6087485-A 40 11-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        115 CTGGGGGGATCCTGGATTTAA 135
              |||||||| |:|||| | ||
Db         21 CTGGGGGGTTYCTGGTGTCAA 1

RESULT 2821
AR103595/c
LOCUS       AR103595                 21 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 119 from patent US 6087485.
ACCESSION   AR103595
VERSION     AR103595.1  GI:12815183
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Brooks-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
            Miller,A. and North,M.
  TITLE     Asthma related genes
  JOURNAL   Patent: US 6087485-A 119 11-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        115 CTGGGGGGATCCTGGATTTAA 135
              |||||||| |:|||| | ||
Db         21 CTGGGGGGTTYCTGGTGTCAA 1

RESULT 2822
BD242493
LOCUS       BD242493                 21 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Methylated CpG island amplification (MCA).
ACCESSION   BD242493
VERSION     BD242493.1  GI:33052263
KEYWORDS    JP 2002533061-A/58.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Issa,J.P., Baylin,S. and Toyota,M.
  TITLE     Methylated CpG island amplification (MCA)
  JOURNAL   Patent: JP 2002533061-A 58 08-OCT-2002;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Artificial Sequence
            PN   JP 2002533061-A/58
            PD   08-OCT-2002
            PF   02-NOV-1999 JP 2000579773
            PR   03-NOV-1998 US    60/106925,10-MAY-1999 US    09/309175 PI
            JEAN PIERRE ISSA,STEPHEN BAYLIN,MINORU TOYOTA PC
            C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68,C12N15/ PC
            00,C12N5/00
            CC   primer for PCR
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1536 GGTTAGGAGAGTAGGGAAG 1554
              || | |||||||||||| ||
Db          1 GGGTTGGAGAGTAGGGGAG 19

RESULT 2823
BD243873
LOCUS       BD243873                 21 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  STE20-related protein kinases.
ACCESSION   BD243873
VERSION     BD243873.1  GI:33053643
KEYWORDS    JP 2002522009-A/35.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Plowman,G., Martinez,R. and Whyte,D.
  TITLE     STE20-related protein kinases
  JOURNAL   Patent: JP 2002522009-A 35 23-JUL-2002;
            SUGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002522009-A/35
            PD   23-JUL-2002
            PF   13-APR-1999 JP 2000543584
            PR   14-APR-1998 US    60/081784
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REFERENCE   2  (bases 1 to 20)
  AUTHORS   Zardi,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-SEP-1996) L. Zardi, Istituto Nazionale per la Ricerca
            sul Cancro, Laboratory of Cell Biology, Largo R.Benzi, 10, 16132
            Genova, ITALY
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /dev_stage="adult"
     intron          <1. .9
                     /number=8
     gene            10. .20
                     /gene="tenascin-R"
     exon            10. .>20
                     /gene="tenascin-R"
                     /number=9

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1248 AATTCACAGAACTTCTCAG 1266
              ||| |||||||||| |||
Db          1 AATCCACAGAACTTGACAG 19


RESULT 2815
AR029929/c
LOCUS       AR029929                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 118 from patent US 5861244.
ACCESSION   AR029929
VERSION     AR029929.1  GI:5943143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 118 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||| |||||||||| || |
Db         21 GAAAGAAAAAAAAAGAAGA 3


RESULT 2816
A98982/c
LOCUS       A98982                   21 bp    DNA     linear   PAT 26-JAN-2000
DEFINITION  Sequence 5 from Patent WO9909172.
ACCESSION   A98982
VERSION     A98982.1  GI:6781943
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Mock,P. and Bellet,D.
  TITLE     METHOD FOR IDENTIFYING AND LOCATING EXPRESSED EPIL PEPTIDES, CODED
            BY THE INSL4 GENE AND THEIR USES
  JOURNAL   Patent: WO 9909172-A 5 25-FEB-1999;
            MOCK PASCAL (CH); ROUSSY INST GUSTAVE (FR)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTT 2179
              ||||||| ||||| ||| |
Db         21 TCTCCTTATTTTTGTTTCT 3


RESULT 2817
AR029927
LOCUS       AR029927                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 116 from patent US 5861244.
ACCESSION   AR029927
VERSION     AR029927.1  GI:5943141
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 116 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTT 2173
              |||| ||| ||||| ||||
Db          3 TTTTCTTCCCCTTTCTTTT 21


RESULT 2818
AR029928
LOCUS       AR029928                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 117 from patent US 5861244.
ACCESSION   AR029928
VERSION     AR029928.1  GI:5943142
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 117 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2183
              |||| ||||||||| || |
Db          1 CTTTCTTTTTTTTTCTTCT 19


RESULT 2819
AR029928/c
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            PN   WO 02077280-A/7
            PD   03-OCT-2002
            PF   26-SEP-2001 WO 2001JP008370
            PR   26-MAR-2001 JP 01P    88062
            PI   TAKASHI SAITO,HISASHI ARASE
            PC   C12Q1/02,C12Q1/68,C12N5/10,C12N15/09,C07K14/47,G01N33/50, PC
            G01N33/566
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTT 2172
              | ||||| ||||||| |||
Db         20 AGTTTTTCCTCCTTTCTTT 2

RESULT 2812
BD182217/c
LOCUS       BD182217                 20 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Polynucleotide probe and primer for detecting beer-clouding lactic
            acid bacterium and method of detecting beer-clouding lactic acid
            bacterium.
ACCESSION   BD182217
VERSION     BD182217.1  GI:30793135
KEYWORDS    WO 02095028-A/30.
SOURCE      Lactobacillus brevis
  ORGANISM  Lactobacillus brevis
            Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
            Lactobacillus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fujii,T.
  TITLE     Polynucleotide probe and primer for detecting beer-clouding lactic
            acid bacterium and method of detecting beer-clouding lactic acid
  JOURNAL   Patent: WO 02095028-A 30 28-NOV-2002;
            KIRIN BREWERY CO LTD,TOSHIO FUJII
COMMENT     OS   Lactobacillus brevis
            PN   WO 02095028-A/30
            PD   28-NOV-2002
            PF   23-MAY-2002 WO 2002JP005022
            PR   23-MAY-2001 JP 01P   154085
            PI   TOSHIO FUJII
            PC   C12N15/11,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C07K14/335, PC
            C07K16/12,
            PC   C12P21/02,C12Q1/04,C12Q1/68
            CC   Polynucleotide probe and primer for detecting beer-clouding
            CC            lactic acid
            CC   bacterium and method of detecting beer-clouding lactic acid
            CC            bacterium
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Lactobacillus brevis'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Lactobacillus brevis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1580"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1177 TCATCTTGGAGGACGAAAT 1195
              |||||||||||| ||  ||
Db         20 TCATCTTGGAGGTCGGCAT 2

RESULT 2813
BD188620/c
LOCUS       BD188620                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Polynucleotide probe and primer for detecting beer-clouding lactic
            acid bacterium and method of detecting beer-clouding lactic acid
            bacterium.
ACCESSION   BD188620
VERSION     BD188620.1  GI:32998359
KEYWORDS    JP 2003000251-A/30.
SOURCE      Lactobacillus brevis
  ORGANISM  Lactobacillus brevis
            Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
            Lactobacillus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fujii,T.
  TITLE     Polynucleotide probe and primer for detecting beer-clouding lactic
            acid bacterium and method of detecting beer-clouding lactic acid
  JOURNAL   Patent: JP 2003000251-A 30 07-JAN-2003;
            KIRIN BREWERY CO LTD
COMMENT     OS   Lactobacillus brevis
            PN   JP 2003000251-A/30
            PD   07-JAN-2003
            PF   23-MAY-2001 JP 2001154085
            PI   TOSHIO FUJII
            PC   C12N15/09,C07K14/335,C07K16/12,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12P21/02,C12Q1/68,G01N33/14,G01N33/53,G01N33/566,G01N33/569//
            PC   C12P21/08,
            PC   (C12Q1/68,C12R1:24),C12N15/00,C12N5/00
            CC   Polynucleotide probe and primer for detecting beer-clouding
            CC            lactic acid
            CC   bacterium and method of detecting beer-clouding lactic acid
            CC            bacterium
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Lactobacillus brevis'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Lactobacillus brevis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1580"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1177 TCATCTTGGAGGACGAAAT 1195
              |||||||||||| ||  ||
Db         20 TCATCTTGGAGGTCGGCAT 2

RESULT 2814
HSTNRAS8
LOCUS       HSTNRAS8                 20 bp    DNA     linear   PRI 05-JUN-1997
DEFINITION  Homo sapiens TN-R gene acceptor splice site intron 8.
ACCESSION   Y13510 Y07980
VERSION     Y13510.1  GI:2181899
KEYWORDS    tenascin-R.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Leprini,A., Gherzi,R., Siri,A., Querze,G., Viti,F. and Zardi,L.
  TITLE     The human tenascin-R gene
  JOURNAL   J. Biol. Chem. 271 (49), 31251-31254 (1996)
  MEDLINE   97094894
   PUBMED   8940128
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KEYWORDS    WO 0168817-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Takeuchi,K., Kato,Y., Sekine,S., Kikuchi,Y. and Sakurad,K.
  TITLE     Kidney repairing factor
  JOURNAL   Patent: WO 0168817-A 16 20-SEP-2001;
            KYOWA HAKKO KOGYO CO LTD,KYOKO TAKEUCHI,YOKO KATO,SUSUMU SEKINE,
            YASUHIRO KIKUCHI,KAZUHIRO SAKURADA
COMMENT     OS   Artificial Sequence
            PN   WO 0168817-A/16
            PD   20-SEP-2001
            PF   16-MAR-2001 WO 2001JP002087
            PR   16-MAR-2000 JP 00P    73632
            PI   KYOKO TAKEUCHI,YOKO KATO,SUSUMU SEKINE,YASUHIRO KIKUCHI, PI
            KAZUHIRO SAKURADA
            PC   C12N15/12,C12N15/63,C12N5/10,C12N5/12,C07K14/47,C07K16/18, PC
             C12Q1/68,
            PC   G01N33/53,A61K38/17,A61K39/395,A61K48/00,A61P13/12,C12P21/02,
            PC   C12P21/08,
            PC   A01K67/027
            CC   forward primer for amplification of human KRGF-1 DNA FH   Key
                      Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1576 TCTCCACCGCACAGACTGG 1594
              |||| ||| ||||| ||||
Db         19 TCTCAACCTCACAGCCTGG 1


RESULT 2809
BD104302
LOCUS       BD104302                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kit and method for determining HLA type.
ACCESSION   BD104302
VERSION     BD104302.1  GI:22649876
KEYWORDS    WO 0192572-A/406.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
            Nishida,M.
  TITLE     Kit and method for determining HLA type
  JOURNAL   Patent: WO 0192572-A 406 06-DEC-2001;
            NISSHINBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
            KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
            NISHIDA
COMMENT     OS   Artificial Sequence
            PN   WO 0192572-A/406
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004662
            PR   01-JUN-2000 JP 00P   164798
            PI   HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI  PI
            MATSUMURA,
            PI   SHOGO MORIYA,MICHIO NISHIDA
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N33/53
            CC   Description of Artificial Sequence:primer
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        255 CCCACCTCTCCTCCGCCGG 273
              | |||||||||||| || ||
Db          1 CTCACCTCTCCTCTGCAGG 19


RESULT 2810
BD176501
LOCUS       BD176501                 20 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  A method of arraying genome clone.
ACCESSION   BD176501
VERSION     BD176501.1  GI:29122209
KEYWORDS    WO 02072815-A/301.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: WO 02072815-A 301 19-SEP-2002;
            EIICHI SOEDA,TAKESHI KUKITA
COMMENT     OS   Artificial Sequence
            PN   WO 02072815-A/301
            PD   19-SEP-2002
            PF   17-MAY-2001 WO 2001JP004139
            PR   12-MAR-2001 JP 01P    68285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12Q1/68
            CC   Description of Artificial Sequence: Synthetic DNA FH   Key
                    Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1170 CCAGACCTCATCTTGGAGG 1188
              |||||||||| | || |||
Db          2 CCAGACCTCAACCTGAAGG 20


RESULT 2811
BD178308/c
LOCUS       BD178308                 20 bp    DNA     linear   PAT 16-APR-2003
DEFINITION  Method of screening nucleic acid encoding signal transducer and kit
            and cells to be used in the method.
ACCESSION   BD178308
VERSION     BD178308.1  GI:30015573
KEYWORDS    WO 02077280-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Saito,T. and Arase,H.
  TITLE     Method of screening nucleic acid encoding signal transducer and kit
            and cells to be used in the method
  JOURNAL   Patent: WO 02077280-A 7 03-OCT-2002;
            TAKASHI SAITO,HISASHI ARASE
COMMENT     OS   Artificial Sequence
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  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          51 GCGGCGGGGGCGGCGGCAG 69
               || |||| ||||| |||||
Db          19 GCCGCGGCGGCGGAGGCAG 1


RESULT 2805
BD074596
LOCUS       BD074596                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisence oligonucleotide composition and modulation method of JNK
            protein.
ACCESSION   BD074596
VERSION     BD074596.1  GI:22620199
KEYWORDS    JP 2001514905-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mckay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
  TITLE     Antisence oligonucleotide composition and modulation method of JNK
            protein
  JOURNAL   Patent: JP 2001514905-A 20 18-SEP-2001;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001514905-A/20
            PD   18-SEP-2001
            PF   07-AUG-1998 JP 2000509875
            PR   13-AUG-1997 US    08/910629
            PI   ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
            NERO,WILLIAM A GAARDE
            PC   C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
            PC   C12N15/00
            CC   antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         813 CCGTAATGAACCCCACTGA 831
               || ||||| ||||||| ||
Db           2 CCATAATGCACCCCACAGA 20


RESULT 2806
BD090423
LOCUS       BD090423                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD090423
VERSION     BD090423.1  GI:22636033
KEYWORDS    JP 2001321190-A/2667.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 2667 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/2667
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
              Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        1170 CCAGACCTCATCTTGGAGG 1188
               |||||||||| | || |||
Db           2 CCAGACCTCAACCTGAAGG 20


RESULT 2807
BD094674
LOCUS       BD094674                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Methods for mapping genes.
ACCESSION   BD094674
VERSION     BD094674.1  GI:22640262
KEYWORDS    WO 0179482-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Inoko,H.
  TITLE     Methods for mapping genes
  JOURNAL   Patent: WO 0179482-A 8 25-OCT-2001;
            HIDETOSHI INOKO
COMMENT     OS   Artificial Sequence
            PN   WO 0179482-A/8
            PD   25-OCT-2001
            PF   30-OCT-2000 WO 2000JP007621
            PR   13-APR-2000 JP 00P   112699
            PI   HIDETOSHI INOKO
            PC   C12N15/09,C07K14/47,C07K16/18,C12Q1/68
            CC   Description of Artificial Sequence: artificially synthesized
            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         126 CTGGATTTAACTGGCGACT 144
               ||||||| | |||| ||||
Db           1 CTGGATTAACCTGGAGACT 19


RESULT 2808
BD101848/c
LOCUS       BD101848                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Kidney repairing factor.
ACCESSION   BD101848
VERSION     BD101848.1  GI:22647422
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LOCUS       AX716655                 20 bp    DNA     linear   PAT 15-APR-2003
DEFINITION  Sequence 3339 from Patent EP1293569.
ACCESSION   AX716655
VERSION     AX716655.1  GI:29889971
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE     Full-length cDNAs
  JOURNAL   Patent: EP 1293569-A 3339 19-MAR-2003;
            Helix Research Institute (JP) ; Research Association for
            Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="an artificially synthesized primer sequence"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1917 ATACCTTTTTTTTCAGTGT 1935
              ||| || || |||||||||
Db          1 ATAGCTCTTGTTTCAGTGT 19


RESULT 2802
AX787157/c
LOCUS       AX787157                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sequence 18 from Patent WO03013598.
ACCESSION   AX787157
VERSION     AX787157.1  GI:32954357
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Lam,D.M., Zeng,F. and Leung,F.C.
  TITLE     Novel vaccine compositions and methods of vaccine preparation for
            veterinary and human diseases
  JOURNAL   Patent: WO 03013598-A 18 20-FEB-2003;
            Lam, Dominic M. K., VaxGene Corporation (CN) ; Zeng, Fanya, VaxGene
            Corporation (CN) ; Leung, Frederick C. VaxGene Corporation (CN)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="genus Anterivirus of Arteriviridae"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1212 AGAACATGCTATTGGCGGC 1230
              || ||||| ||||| ||||
Db         19 AGCACATGGTATTGTCGGC 1


RESULT 2803
BD006253/c
LOCUS       BD006253                 20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Antisense inhibition of ras gene with chimeric and alternating
            oligonucleotides.
ACCESSION   BD006253
VERSION     BD006253.1  GI:18634624
KEYWORDS    JP 2001500530-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ecker,D.J., Cook,P.D., Monia,B.P., Freier,S.M. and Sang,Y.S.
  TITLE     Antisense inhibition of ras gene with chimeric and alternating
            oligonucleotides
  JOURNAL   Patent: JP 2001500530-A 20 16-JAN-2001;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001500530-A/20
            PD   16-JAN-2001
            PF   30-APR-1998 JP 1998547418
            PR   30-APR-1997 US    08/848840
            PI   DAVID J ECKER,PHILIP DAN COOK,BRETT P MONIA,SUSAN M FREIER, PI
              YOGESH S SANGHVI
            PC   C12Q1/68,C12P19/34,C07H19/16,C07H19/167,C07H19/173,C07H19/067,
            PC   C07H19/06,
            PC   C07H19/09,C07H21/04,A61K48/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              || |||| ||||| |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 2804
BD073147/c
LOCUS       BD073147                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antisense oligonucleotide inhibition of RAS.
ACCESSION   BD073147
VERSION     BD073147.1  GI:22618750
KEYWORDS    JP 2001509394-A/20.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Cowcert,L.M. and Manoharan,M.
  TITLE     Antisense oligonucleotide inhibition of RAS
  JOURNAL   Patent: JP 2001509394-A 20 24-JUL-2001;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2001509394-A/20
            PD   24-JUL-2001
            PF   06-JUL-1998 JP 2000502223
            PR   08-JUL-1997 US    08/889296
            PI   BRETT P MONIA,LEX M COWCERT,MUSIA MANOHARAN
            PC   C12N15/09,A61K31/7088,A61K48/00,A61P35/00,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense oligonucleotide inhibition of RAS
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
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  JOURNAL   Patent: WO 0214366-A 59 21-FEB-2002;
            Universiteit Utrecht (NL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sense primer OtS2-B9"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        644 GGCCTGGCCGAGAACCTGG 662
              | ||||| ||||| |||||
Db          1 GACCTGGACGAGACCCTGG 19


RESULT 2797
AX487419
LOCUS       AX487419                 20 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 4719 from Patent WO02053728.
ACCESSION   AX487419
VERSION     AX487419.1  GI:22321567
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 4719 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Candida albicans"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:5476"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        690 ACGAGGTGCAGAATGTCGA 708
              ||| |||||  ||||||||
Db          1 ACGTGGTGCGAAATGTCGA 19


RESULT 2798
AX487788
LOCUS       AX487788                 20 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 5088 from Patent WO02053728.
ACCESSION   AX487788
VERSION     AX487788.1  GI:22321868
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 5088 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Candida albicans"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:5476"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         87 CCCCGATTTTGGATTTACC 105
              ||||||| || ||||| ||
Db          1 CCCCGATCTTCGATTTTCC 19


RESULT 2799
AX662813
LOCUS       AX662813                 20 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 24 from Patent WO02061134.
ACCESSION   AX662813
VERSION     AX662813.1  GI:29163394
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Roninson,I.B. and Chang,B.D.
  TITLE     Reagents and methods for identifying and modulating expression of
            tumor senescence genes
  JOURNAL   Patent: WO 02061134-A 24 08-AUG-2002;
            THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1397 GCCCTGCAGAACTACATCA 1415
              ||||| ||||||| || ||
Db          1 GCCCTTCAGAACTTCAGCA 19


RESULT 2800
AX708914
LOCUS       AX708914                 20 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 96 from Patent WO02101045.
ACCESSION   AX708914
VERSION     AX708914.1  GI:29564642
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Patapoutian,A., Song,C., Ganju,P., Peier,A., Mcintyre,P. and
            Bevan,S.
  TITLE     Vanilloid receptor-related nucleic acids and polypeptides
  JOURNAL   Patent: WO 02101045-A 96 19-DEC-2002;
            Novartis AG (CH) ; IRM LLC (BM)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        193 CAAGTACGAAGAGGACTGC 211
              |||| || || ||||||||
Db          2 CAAGGACAAAAAGGACTGC 20


RESULT 2801
AX716655
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Db          1 GTTGGGATGAACCAGAAGG 19


RESULT 2792
AX109872
LOCUS       AX109872                 20 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 605 from Patent WO0123604.
ACCESSION   AX109872
VERSION     AX109872.1  GI:13925551
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 605 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"


  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2720 AAATGTTCCCCAAATAATT 2738
              |||||||||  |||| |||
Db          2 AAATGTTCCGTAAATTATT 20


RESULT 2793
AX241251
LOCUS       AX241251                 20 bp    DNA     linear   PAT 26-SEP-2001
DEFINITION  Sequence 489 from Patent WO0160975.
ACCESSION   AX241251
VERSION     AX241251.1  GI:15798126
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C. and Bussey,H.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 0160975-A 489 23-AUG-2001;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA primer"


  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         87 CCCCGATTTTGGATTTACC 105
              |||||||  ||  |||||  ||
Db          1 CCCCGATCTTCGATTTTCC 19


RESULT 2794
AX294679/c
LOCUS       AX294679                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 6441 from Patent WO0179548.
ACCESSION   AX294679
VERSION     AX294679.1  GI:17056362
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 6441 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"


  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        498 GAGCGGGGCTGCCCTCGCA 516
              ||| || ||||||  |||||
Db         19 GAGAGGTGCTGCCGTCGCA 1


RESULT 2795
AX316300/c
LOCUS       AX316300                 20 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 94 from Patent WO0190371.
ACCESSION   AX316300
VERSION     AX316300.1  GI:17899474
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Julier,C., Delepine,M. and Nicolino,M.
  TITLE     Mutated eukariotic translation initiation factor 2 alpha kinase 3,
            eif2ak3, in patients with neonatal insulin-dependent diabetes and
            multiple epip hyseal dysplasia (wolcott-rallison syndrome)
  JOURNAL   Patent: WO 0190371-A 94 29-NOV-2001;
            INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
            (FR) ; Centre National de Genotypage (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Forward primer."


  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2668 AGTACAGTGTGTGTGGGTG 2686
              |||||||||  |||||  ||
Db         19 AGTACAGTGGGTGTGCATG 1


RESULT 2796
AX394084
LOCUS       AX394084                 20 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 59 from Patent WO0214366.
ACCESSION   AX394084
VERSION     AX394084.1  GI:19702034
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Groot,P.C., van Bergenhenegouwen,B.J. and van Oosterhout,A.J.
  TITLE     Genes involved in immune related responses observed with asthma
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AR311200
LOCUS       AR311200                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1737 from patent US 6559294.
ACCESSION   AR311200
VERSION     AR311200.1  GI:31704626
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 1737 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        769 CAAGAACCCTCTGAACCTC 787
              ||| ||||||  |||||||
Db          1 CAACAACCCTTGGAACCTC 19


RESULT 2788
AR314483/c
LOCUS       AR314483                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5020 from patent US 6559294.
ACCESSION   AR314483
VERSION     AR314483.1  GI:31707909
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 5020 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1585 CACAGACTGGGAACCCCTC 1603
              |||||| |||||| ||| |
Db         19 CACAGATTGGGAAGCCCCC 1


RESULT 2789
AR342466/c
LOCUS       AR342466                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 16 from patent US 6576423.
ACCESSION   AR342466
VERSION     AR342466.1  GI:33737476
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Batra,S.K., Brand,R.E., Ringel,J., Faulmann,G., Lohr,M. and
            Varshney,G.C.
  TITLE     Specific mucin expression as a marker for pancreatic cancer
  JOURNAL   Patent: US 6576423-A 16 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        601 CTCCGACCTGCTGCTGCCC 619
              |||||  || |||||||||
Db         20 CTCCGTGCTCCTGCTGCCC 2


RESULT 2790
AX020020
LOCUS       AX020020                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 34 from Patent WO9937764.
ACCESSION   AX020020
VERSION     AX020020.1  GI:10043849
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Veugelers,M.P. and David,G.J.
  TITLE     New members of the glypican gene family
  JOURNAL   Patent: WO 9937764-A 34 29-JUL-1999;
            VEUGELERS MARK PAUL DITTMAR (BE); VLAAMS INTERUNIV INST BIOTECH
            (BE); DAVID GUIDO JOSEPH FRANS (BE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2315 ATTTGTTGCTGCTTGTCAC 2333
              ||||  ||||||| |||||
Db          1 ATTTCCTGCTGCTGGTCAC 19


RESULT 2791
AX094814
LOCUS       AX094814                  20 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 36 from Patent WO0118191.
ACCESSION   AX094814
VERSION     AX094814.1  GI:13511023
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Nimmo,H.G., Jenkins,G.I. and Hartwell,J.
  TITLE     Plant gene
  JOURNAL   Patent: WO 0118191-A 36 15-MAR-2001;
            THE UNIVERSITY COURT OF THE UNIVERSITY OF GLASGOW (GB)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="RT-PCR actin forward"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2640 GTTGGGCTGAACCCTAAGG 2658
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ACCESSION   AR264950
VERSION     AR264950.1  GI:29693337
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 34 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2517 GGTTTTATTCATATATATA 2535
              || ||| || |||||||||
Db         20 GGGTTTTTTTATATATATA 2


RESULT 2783
AR264952/c
LOCUS       AR264952                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 36 from patent US 6492121.
ACCESSION   AR264952
VERSION     AR264952.1  GI:29693339
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 36 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2517 GGTTTTATTCATATATATA 2535
              | ||||  || |||||||||
Db         20 GTTTTTTTTTATATATATA 2


RESULT 2784
AR293466/c
LOCUS       AR293466                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5201 from patent US 6537751.
ACCESSION   AR293466
VERSION     AR293466.1  GI:31680750
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 5201 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1518 AAAATTGGAACGAAGAAAG 1536
              ||||| |||| |||| |||
Db         19 AAAATAGGAAGGAAGGAAG 1


RESULT 2785
AR294519
LOCUS       AR294519                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6254 from patent US 6537751.
ACCESSION   AR294519
VERSION     AR294519.1  GI:31681803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 6254 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        794 CAGAAGGAGCTGGTGGGGG 812
              ||||| ||| |||||| ||
Db          2 CAGAATGAGGTGGTGGTGG 20


RESULT 2786
AR298863
LOCUS       AR298863                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 10598 from patent US 6537751.
ACCESSION   AR298863
VERSION     AR298863.1  GI:31686147
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 10598 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2558 ATGCTGGGCTCTGTTCTTG 2576
              ||||||| ||||||| | |
Db          2 ATGCTGGTCTCTGTTTTGG 20


RESULT 2787
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RESULT 2777
AR224560
LOCUS       AR224560                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 19 from patent US 6440738.
ACCESSION   AR224560
VERSION     AR224560.1  GI:23333400
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of casein kinase 2-beta expression
  JOURNAL   Patent: US 6440738-A 19 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1270 AGACCGGACACCCCATGGG 1288
              || ||||| |||||||| |
Db          1 AGTCCGGAGACCCCATGTG 19


RESULT 2778
AR229041/c
LOCUS       AR229041                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 51 from patent US 6448081.
ACCESSION   AR229041
VERSION     AR229041.1  GI:27268183
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F. and Freier,S.M.
  TITLE     Antisense modulation of interleukin 12 p40 subunit expression
  JOURNAL   Patent: US 6448081-A 51 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1169 ACCAGACCTCATCTTGGAG 1187
              || | | ||||||||||||
Db         20 ACTATAGCTCATCTTGGAG 2


RESULT 2779
AR229057/c
LOCUS       AR229057                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 67 from patent US 6448081.
ACCESSION   AR229057
VERSION     AR229057.1  GI:27268199
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F. and Freier,S.M.
  TITLE     Antisense modulation of interleukin 12 p40 subunit expression
  JOURNAL   Patent: US 6448081-A 67 10-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1117 TGCCTATGTCTGTGAAGCC 1135
              | || |||||||||||| |
Db         20 TTCCCATGTCTGTGAAGAC 2


RESULT 2780
AR230940
LOCUS       AR230940                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 200 from patent US 6451602.
ACCESSION   AR230940
VERSION     AR230940.1  GI:27271727
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Popoff,I. and Cowsert,L.M.
  TITLE     Antisense modulation of PARP expression
  JOURNAL   Patent: US 6451602-A 200 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2679 TGTGGGTGAAATGGAGATT 2697
              ||| | |||| ||||||||
Db          1 TGTTGTTGAACTGGAGATT 19


RESULT 2781
AR241068/c
LOCUS       AR241068                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 39 from patent US 6468796.
ACCESSION   AR241068
VERSION     AR241068.1  GI:27286285
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Watt,A.T.
  TITLE     Antisense modulation of bifunctional apoptosis regulator expression
  JOURNAL   Patent: US 6468796-A 39 22-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGAAAG 2197
              ||  |||||||||||| ||
Db         19 TTGCTTTTAACTTTGACAG 1


RESULT 2782
AR264950/c
LOCUS       AR264950                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 34 from patent US 6492121.
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            PC   C12Q1/68,C12N15/09,C12Q1/10//(C12N15/09,C12R1:19),(C12Q1/10,
            PC   C12R1:19),
            PC   C12N15/00,(C12N15/00,C12R1:19)
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Escherichia coli'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Escherichia coli"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:562"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2445 TTTTTTGAGACATGGGATC 2463
                | ||| ||||||||||| |
Db          2 TATTTGGAGACATGGGAGC 20


RESULT 2773
E41503
LOCUS       E41503                    20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for detecting intestinal hemorrhagic Escherichia coli.
ACCESSION   E41503
VERSION     E41503.1  GI:22553163
KEYWORDS    JP 2001095576-A/1.
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ohashi,T.
  TITLE     Method for detecting intestinal hemorrhagic Escherichia coli
  JOURNAL   Patent: JP 2001095576-A 1 10-APR-2001;
            SHIMADZU CORP
COMMENT     OS   Escherichia coli
            PN   JP 2001095576-A/1
            PD   10-APR-2001
            PF   28-SEP-1999 JP 1999273560
            PI   TETSUO OHASHI
            PC   C12N15/09,C12Q1/04,C12Q1/68//(C12N15/09,C12R1:19),C12N15/00,
            PC   (C12N15/00,C12R1:19)
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Escherichia coli"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:562"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2445 TTTTTTGAGACATGGGATC 2463
                | ||| ||||||||||| |
Db          2 TATTTGGAGACATGGGAGC 20


RESULT 2774
AR201438/c
LOCUS       AR201438                  20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 20 from patent US 6359124.
ACCESSION   AR201438
VERSION     AR201438.1  GI:20252326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ecker,D.J., Cook,P.Dan., Monia,B.P., Freier,S.M. and Sanghvi,Y.S.
  TITLE     Antisense inhibition of ras gene with chimeric and alternating
            oligonucleotides
  JOURNAL   Patent: US 6359124-A 20 19-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              || |||| ||||| |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 2775
AR212010
LOCUS       AR212010                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 66 from patent US 6399378.
ACCESSION   AR212010
VERSION     AR212010.1  GI:21515483
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ward,D.T. and Watt,A.T.
  TITLE     Antisense modulation of RECQL2 expression
  JOURNAL   Patent: US 6399378-A 66 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        344 TTTCCCCCCTCCCTACCAGC 362
              ||||||| || || |||||
Db          1 TTTCCCCATCTCTTCCAGC 19


RESULT 2776
AR216074/c
LOCUS       AR216074                  20 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 121 from patent US 6410518.
ACCESSION   AR216074
VERSION     AR216074.1  GI:23314362
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P.
  TITLE     Antisense oligonucleotide inhibition of raf gene expression
  JOURNAL   Patent: US 6410518-A 121 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1531 AGAAAGGTTAGGAGAGTAG 1549
              ||| || | ||||||||||
Db         20 AGAGAGTTCAGGAGAGTAG 2
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Qy       2175 TTTTTTTTTTTTAACTTTG 2193
              ||||| |||||||||  ||
Db          1 TTTTTCTTTTTTAACCCTG 19


RESULT 2769
AR176783
LOCUS       AR176783                  20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 38 from patent US 6312900.
ACCESSION   AR176783
VERSION     AR176783.1  GI:17919138
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of activating protein 1
  JOURNAL   Patent: US 6312900-A 38 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        318 TCGCCGAATATCAGCCGCC 336
              ||||| ||  |||||||||
Db          2 TCGCCCAACTTCAGCCGCC 20


RESULT 2770
E05742/c
LOCUS       E05742                    20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer to detect ADV.
ACCESSION   E05742
VERSION     E05742.1  GI:2173929
KEYWORDS    JP 1993276998-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uruno,K., Nunofuji,S., Tsuna,M., Mise,S. and Shibata,I.
  TITLE     METHOD FOR DETECTING VIRUS OF AUJESZKI DISEASE VIRUS
  JOURNAL   Patent: JP 1993276998-A 3 26-OCT-1993;
            NIPPON FLOUR MILLS CO LTD, NATL FEDELATION OF AGRICULT COOP ASSOC
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1993276998-A/3
            PD   26-OCT-1993
            PF   01-APR-1992 JP 1992079881
            PI   URUNO KATSUYOSHI, NUNOFUJI SATOSHI, TSUNA MIKA, MISE SHIZUO,
            PI   SHIBATA ISAO
            PC   C12Q1/68,C07H21/04,C12N15/11,C12Q1/70,(C12Q1/70,C12R1:92); CC
             strandedness: Single;
            CC   topology: Linear.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        549 TCTCCGGGCTGGAGGCGGG 567
              |||||||| || || ||||
Db         19 TCTCCGGGATGAAGACGGG 1


RESULT 2771
E30155
LOCUS       E30155                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Oligonucleotide for detecting enterohemorrhagic Escherichia coli
            and detection method by using the same.
ACCESSION   E30155
VERSION     E30155.1  GI:13016999
KEYWORDS    JP 1999332599-A/6.
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shigeru,F. and Naoko,T.
  TITLE     Oligonucleotide for detecting enterohemorrhagic Escherichia coli
            and detection method by using the same
  JOURNAL   Patent: JP 1999332599-A 6 07-DEC-1999;
            SHIMADZU CORP
COMMENT     OS   Escherichia coli
            PN   JP 1999332599-A/6
            PD   07-DEC-1999
            PF   29-MAY-1998 JP 1998149749
            PR
            PI   SHIGERU FUKUSHIMA,NAOKO TAKAOKA
            PC   C12Q1/68,C12N15/09,C12Q1/10//(C12N15/09,C12R1:19),(C12Q1/10,
            PC   C12R1:19),
            PC   C12N15/00,(C12N15/00,C12R1:19)
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Escherichia coli'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Escherichia coli"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:562"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2445 TTTTTTGAGACATGGGATC 2463
              | ||| ||||||||||| |
Db          2 TATTTGGAGACATGGGAGC 20


RESULT 2772
E30160
LOCUS       E30160                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Oligonucleotide for detecting pathogenic Escherichia coli O-157 and
            detection method by using the same.
ACCESSION   E30160
VERSION     E30160.1  GI:13017004
KEYWORDS    JP 1999332600-A/2.
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shigeru,F. and Naoko,T.
  TITLE     Oligonucleotide for detecting pathogenic Escherichia coli O-157 and
            detection method by using the same
  JOURNAL   Patent: JP 1999332600-A 2 07-DEC-1999;
            SHIMADZU CORP
COMMENT     OS   Escherichia coli
            PN   JP 1999332600-A/2
            PD   07-DEC-1999
            PF   29-MAY-1998 JP 1998149750
            PR
            PI   SHIGERU FUKUSHIMA,NAOKO TAKAOKA
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                    /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2284 GAGTAAACTTGAAAAGGGT 2302
              ||| ||||| ||||||| |
Db         20 GAGAAAACTGGAAAAGGAT 2


RESULT 2764
AR123336
LOCUS       AR123336                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2 from patent US 6169176.
ACCESSION   AR123336
VERSION     AR123336.1  GI:14108302
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bruice,T.C. and Dev,A.P.
  TITLE     Deoxynucleic alkyl thiourea compounds and uses thereof
  JOURNAL   Patent: US 6169176-A 2 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| |||| |||| ||||
Db          2 AAAACAAAACAAAACAAAA 20


RESULT 2765
AR123336/c
LOCUS       AR123336                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2 from patent US 6169176.
ACCESSION   AR123336
VERSION     AR123336.1  GI:14108302
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bruice,T.C. and Dev,A.P.
  TITLE     Deoxynucleic alkyl thiourea compounds and uses thereof
  JOURNAL   Patent: US 6169176-A 2 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||| |||| |||| ||||
Db         20 TTTTGTTTTGTTTTGTTTT 2


RESULT 2766
AR129678/c
LOCUS       AR129678                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 82 from patent US 6187545.
ACCESSION   AR129678
VERSION     AR129678.1  GI:14117575
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Butler,M.M., Wyatt,J. and Cowsert,L.M.
  TITLE     Antisense modulation of pepck-cytosolic expression
  JOURNAL   Patent: US 6187545-A 82 13-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        216 ATCGCCACGACGGGAGCAG 234
              ||| ||||  |||||||||
Db         19 ATCACCACACCGGGAGCAG 1


RESULT 2767
AR130151
LOCUS       AR130151                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 54 from patent US 6187587.
ACCESSION   AR130151
VERSION     AR130151.1  GI:14118048
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Popoff,I., Brown-Driver,V.L. and Cowsert,L.M.
  TITLE     Antisense inhibition of e2f transcription factor 1 expression
  JOURNAL   Patent: US 6187587-A 54 13-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2017 AAGTCCTCTGGTAGGAGGC 2035
              || ||||| || |||||||
Db          2 AACTCCTCAGGGAGGAGGC 20


RESULT 2768
AR158937
LOCUS       AR158937                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 559 from patent US 6251588.
ACCESSION   AR158937
VERSION     AR158937.1  GI:16221353
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 559 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1531 AGAAAGGTTAGGAGAGTAG 1549
              ||| || | ||||||||||
Db         20 AGAGAGTTCAGGAGAGTAG 2


RESULT 2759
AR086217
LOCUS       AR086217                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 38 from patent US 5985558.
ACCESSION   AR086217
VERSION     AR086217.1  GI:10012983
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
  TITLE     Antisense oligonucleotide compositions and methods for the
            inibition of c-Jun and c-Fos
  JOURNAL   Patent: US 5985558-A 38 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        318 TCGCCGAATATCAGCCGCC 336
              ||||| ||  |||||||||
Db          2 TCGCCCAACTTCAGCCGCC 20


RESULT 2760
AR102403/c
LOCUS       AR102403                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 28 from patent US 6083923.
ACCESSION   AR102403
VERSION     AR102403.1  GI:12813201
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hardee,G.E., Geary,R.S., Levin,A., Templin,M.V., Howard,R. and
            Mehta,R.C.
  TITLE     Liposomal oligonucleotide compositions for modulating RAS gene
            expression
  JOURNAL   Patent: US 6083923-A 28 04-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              || |||| ||||| |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 2761
AR116439
```

```
LOCUS       AR116439                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 20 from patent US 6133246.
ACCESSION   AR116439
VERSION     AR116439.1  GI:14096761
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
  TITLE     Antisense oligonucleotide compositions and methods for the
            modulation of JNK proteins
  JOURNAL   Patent: US 6133246-A 20 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         813 CCGTAATGAACCCCACTGA 831
               || ||||| ||||||| ||
Db           2 CCATAATGCACCCCACAGA 20


RESULT 2762
AR122372
LOCUS       AR122372                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 6 from patent US 6165724.
ACCESSION   AR122372
VERSION     AR122372.1  GI:14106689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fukushima,S. and Takaoka,N.
  TITLE     Oligonucleotides for detecting enteric hemorrhagic E.coli and
            detection method using the same
  JOURNAL   Patent: US 6165724-A 6 26-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        2445 TTTTTTGAGACATGGGATC 2463
               | ||| |||||||||||| |
Db          2 TATTTGGAGACATGGGAGC 20


RESULT 2763
AR123087/c
LOCUS       AR123087                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 31 from patent US 6168950.
ACCESSION   AR123087
VERSION     AR123087.1  GI:14108053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Gaarde,W., Ward,D.T. and Cowsert,L.M.
  TITLE     Antisense modulation of MEKK1 expression
  JOURNAL   Patent: US 6168950-A 31 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
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                     /db_xref="taxon:1270"
     gene            1. .20
                     /gene="tRNA(GGCAla)"
     tRNA            1. .20
                     /gene="tRNA(GGCAla)"
                     /product="tRNA-Ala"
                     /note="codon recognized: GGC"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        299 CCCCTCTCCCACACTGGAG 317
              ||  ||||||| |||||||
Db          2 CCAGTCTCCCAAACTGGAG 20


RESULT 2754
A10280
LOCUS       A10280                   20 bp    DNA     linear   PAT 25-AUG-1993
DEFINITION  oligonucleotide.
ACCESSION   A10280
VERSION     A10280.1  GI:413528
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  JOURNAL   Patent: DE 3802040-A 1 03-AUG-1989;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1011 TGGACAAGATCGGGTTGAA 1029
              | || |||||| |||||||
Db          1 TAGAGAAGATCTGGTTGAA 19


RESULT 2755
AR026579
LOCUS       AR026579                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5856104.
ACCESSION   AR026579
VERSION     AR026579.1  GI:5937419
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Chee,M. and Fan,J.-B.
  TITLE     Polymorphisms in the glucose-6 phosphate dehydrogenase locus
  JOURNAL   Patent: US 5856104-A 5 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2718 GTAAATGTTCCCCAAATAA 2736
              ||||||| ||  |||||||
Db          1 GTAAATGCTCTGCAAATAA 19


RESULT 2756
AR036620/c
LOCUS       AR036620                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 20 from patent US 5872242.
ACCESSION   AR036620
VERSION     AR036620.1  GI:5953288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Cowsert,L.M. and Manoharan,M.
  TITLE     Antisense oligonucleotide inhibition of ras
  JOURNAL   Patent: US 5872242-A 20 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              || |||| ||||| |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 2757
AR079640/c
LOCUS       AR079640                 20 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 20 from patent US 5965722.
ACCESSION   AR079640
VERSION     AR079640.1  GI:10006381
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ecker,D.J., Cook,P.Dan., Monia,B.P., Freier,S.M. and Sanghvi,Y.S.
  TITLE     Antisense inhibition of ras gene with chimeric and alternating
            oligonucleotides
  JOURNAL   Patent: US 5965722-A 20 12-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              || |||| ||||| |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 2758
AR085554/c
LOCUS       AR085554                 20 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 32 from patent US 5981731.
ACCESSION   AR085554
VERSION     AR085554.1  GI:10012321
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P.
  TITLE     Antisense oligonucleotide modulation of B-raf gene expression
  JOURNAL   Patent: US 5981731-A 32 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
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RESULT 2749
AR360403
LOCUS       AR360403                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 18 from patent US 6596489.
ACCESSION   AR360403
VERSION     AR360403.1  GI:33767433
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 18 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||  | |||||||
Db          2 AAAAAAAATTATAAAAAAA 20


RESULT 2750
AR360430
LOCUS       AR360430                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 18 from patent US 6596490.
ACCESSION   AR360430
VERSION     AR360430.1  GI:33767460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 18 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||  | |||||||
Db          2 AAAAAAAATTATAAAAAAA 20


RESULT 2751
AX441514
LOCUS       AX441514                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 18 from Patent WO0206531.
ACCESSION   AX441514
VERSION     AX441514.1  GI:21690475
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 18 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02025"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||  | |||||||
Db          2 AAAAAAAATTATAAAAAAA 20


RESULT 2752
AX594032/c
LOCUS       AX594032                 20 bp    DNA     linear   PAT 13-FEB-2003
DEFINITION  Sequence 110 from Patent WO0246477.
ACCESSION   AX594032
VERSION     AX594032.1  GI:28375269
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Garcia,P., Hardy,S.F., Williams,L.T. and Escobedo,J.
  TITLE     Endogenous retroviruses up-regulated in prostate cancer
  JOURNAL   Patent: WO 0246477-A 110 13-JUN-2002;
            CHIRON CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              | ||||||||  |||||||
Db         20 TTCTTTTTTTGATTTTTTT 2


RESULT 2753
S58563
LOCUS       S58563                   20 bp    tRNA    linear   BCT 07-MAY-1993
DEFINITION  tRNA(GGCAla) [Micrococcus luteus, tRNA Partial ggc Ala, 20 nt].
ACCESSION   S58563
VERSION     S58563.1  GI:236658
KEYWORDS    .
SOURCE      Micrococcus luteus
  ORGANISM  Micrococcus luteus
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Micrococcineae; Micrococcaceae; Micrococcus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kano,A., Andachi,Y., Ohama,T. and Osawa,S.
  TITLE     Novel anticodon composition of transfer RNAs in Micrococcus luteus,
            a bacterium with a high genomic G + C content. Correlation with
            codon usage
  JOURNAL   J. Mol. Biol. 221 (2), 387-401 (1991)
  MEDLINE   92015235
   PUBMED   1717697
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 58563] from the original journal article.
            This sequence comes from Fig. 2.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Micrococcus luteus"
                     /mol_type="tRNA"
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RESULT 2745
AX132839/c
LOCUS       AX132839                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 4057 from Patent WO0130362.
ACCESSION   AX132839
VERSION     AX132839.1  GI:14139149
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 4057 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="PCNA HH ribozyme binding site"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1491 TGGAGAAAATGGAGAAACA 1509
              |||||| ||| |||||| |
Db         19 TGGAGAGAATAGAGAAAAA 1


RESULT 2746
BD221962/c
LOCUS       BD221962                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Nucleic acid encoding retinoblastoma-binding protein (RBP-7) and
            polymorphic marker relating to the nucleic acid.
ACCESSION   BD221962
VERSION     BD221962.1  GI:33031732
KEYWORDS    JP 2002519027-A/101.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bougueleret,L.
  TITLE     Nucleic acid encoding retinoblastoma-binding protein (RBP-7) and
            polymorphic marker relating to the nucleic acid
  JOURNAL   Patent: JP 2002519027-A 101 02-JUL-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002519027-A/101
            PD   02-JUL-2002
            PF   30-JUN-1999 JP 2000557360
            PR   30-JUN-1998 US    60/091315,10-DEC-1998 US    60/111909 PI
            LYDIE BOUGUELERET
            PC   C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N5/10,
            PC   C12Q1/68,
            PC   G01N33/53,G01N33/566,C12N15/00,C12N5/00,C12N15/00 CC
            microsequencing oligo for 5-124-273.mis1
            FH   Key             Location/Qualifiers
            FT   primer_bind     1. .19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2533 ATACAGGGTATTAAGAATT 2551
              ||  |||||||||||||| |
Db         19 ATCTAGGGTATTAAGAAGT 1


RESULT 2747
AR118884
LOCUS       AR118884                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 10 from patent US 6150092.
ACCESSION   AR118884
VERSION     AR118884.1  GI:14100794
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
  TITLE     Antisense nucleic acid compound targeted to VEGF
  JOURNAL   Patent: US 6150092-A 10 21-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||| ||||| || ||
Db          1 AAAAAAACAAAAACAACAA 19


RESULT 2748
E59334/c
LOCUS       E59334                   20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for purifying oligonucleotide.
ACCESSION   E59334
VERSION     E59334.1  GI:18622511
KEYWORDS    JP 2000342265-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hirose,K. and Yoshida,T.
  TITLE     Method for purifying oligonucleotide
  JOURNAL   Patent: JP 2000342265-A 15 12-DEC-2000;
            TOAGOSEI CHEM IND CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000342265-A/15
            PD   12-DEC-2000
            PF   02-JUN-1999 JP 1999154974
            PR
            PI   KUNIHIKO HIROSE,TADAO YOSHIDA
            PC   C12N15/09,B01D15/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| |||| |||| ||||
Db         20 AAAATAAAACAAAAGAAAA 2
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     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PRIMER"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        226 CGGGAGCAGCAATGGGAAT 244
              ||||||||||  || |||
Db          1 CGGGAGCAGCACAGGAAAT 19


RESULT 2741
AX039843
LOCUS       AX039843                 19 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 232 from Patent WO0063441.
ACCESSION   AX039843
VERSION     AX039843.1  GI:11229872
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Herrnstadt,C. and Davis,R.E.
  TITLE     Single nucleotide polymorphisms in mitochondrial genes that segreg
            ate with alzheimer's disease
  JOURNAL   Patent: WO 0063441-A 232 26-OCT-2000;
            MITOKOR (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        384 CCGACCCCTACTCGCATCT 402
              || || ||| |||||||||
Db          1 CCTACTCCTGCTCGCATCT 19


RESULT 2742
AX131090/c
LOCUS       AX131090                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 2308 from Patent WO0130362.
ACCESSION   AX131090
VERSION     AX131090.1  GI:14137395
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 2308 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin E ribozyme binding site"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        208 CTGCGAGGATCGCCACGAC 226
              |||||||||  |||||| |
Db         19 CTGCGAGGAGAGCCACGCC 1


RESULT 2743
AX132096/c
LOCUS       AX132096                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3314 from Patent WO0130362.
ACCESSION   AX132096
VERSION     AX132096.1  GI:14138401
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3314 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cyclin B1 ribozyme binding site"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTGA 1427
              ||||||| ||||  |||||
Db         19 TACATCAGAGAAAGCCTGA 1


RESULT 2744
AX132836/c
LOCUS       AX132836                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 4054 from Patent WO0130362.
ACCESSION   AX132836
VERSION     AX132836.1  GI:14139146
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 4054 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="PCNA HH ribozyme binding site"

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              ||||| || |||||||| |
Db         19 AGAATAGAGAAAAAAAATA 1
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Nishikawa,S., Fukuda,K., Funaji,K., Uragami,S. and Seki,S.
  TITLE     New functional nucleic acids targeting NS3 protease and helicase of
            hepatitis C virus
  JOURNAL   Patent: JP 2002345475-A 26 03-DEC-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            MITSUBISHI GAS CHEMICAL CO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002345475-A/26
            PD   03-DEC-2002
            PF   25-MAY-2001 JP 2001156957
            PI   SATOSHI NISHIKAWA,KOTARO FUKUDA,KOHEI FUNAJI,SADAJI URAGAMI,
            PI   SATOSHI SEKIYA
            PC   C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K48/00,A61P1/16,
            PC   A61P31/14,
            PC   A61P43/00,C12N9/99,C12Q1/06,C12N15/00
            CC   Description of Artificial Sequence: Synthetic DNA FH   Key
                 Location/Qualifiers
            FT   source          1. .28
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .28
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 28;
  Best Local Similarity   75.0%;  Pred. No. 4.1e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1514 AAATAAAATTGGAACGAAGAAAGG 1537
             ||| ||||  |||  || ||||||
Db          5 AAAAAAAAAAGGAGAGAGGAAAGG 28


RESULT 2737
I31281/c
LOCUS       I31281                  19 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 193 from patent US 5582979.
ACCESSION   I31281
VERSION     I31281.1  GI:1822072
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weber,J.L.
  TITLE     Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
            method of using the same
  JOURNAL   Patent: US 5582979-A 193 10-DEC-1996;
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1727 CTATTATCAGAAGGTGACA 1745
             ||||| |||| ||| ||||
Db         19 CTATTCTCAGCAGGAGACA 1


RESULT 2738
AR211892/c
LOCUS       AR211892                19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 102 from patent US 6399373.
ACCESSION   AR211892
VERSION     AR211892.1  GI:21515334
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Bougueleret,L.
  TITLE     Nucleic acid encoding a retinoblastoma binding protein (RBP-7) and
            polymorphic markers associated with said nucleic acid
  JOURNAL   Patent: US 6399373-A 102 04-JUN-2002;
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2533 ATACAGGGTATTAAGAATT 2551
             ||  |||||||||||||| |
Db         19 ATCTAGGGTATTAAGAAGT 1


RESULT 2739
AR294493/c
LOCUS       AR294493                19 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6228 from patent US 6537751.
ACCESSION   AR294493
VERSION     AR294493.1  GI:31681777
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 6228 25-MAR-2003;
FEATURES            Location/Qualifiers
     source         1. .19
                    /organism="unknown"
                    /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1231 CCAGCAACTGTGTAAAGAA 1249
             |||| || |||| ||||||
Db         19 CCAGTAATTGTGCAAAGAA 1


RESULT 2740
AX019945
LOCUS       AX019945                19 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 26 from Patent WO9937794.
ACCESSION   AX019945
VERSION     AX019945.1  GI:10043785
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hughes,S.G., Verhoeyen,M.E., Muir,S.R., Bovy,A.G., Van Tunen,A.J.,
            De Vos,C.H. and Van Der Hijden,H.T.
  TITLE     Methods and composition for modulating flavonoid content
  JOURNAL   Patent: WO 9937794-A 26 29-JUL-1999;
            HUGHES STEPHEN GLYN (GB); VERHOEYEN MARTINE ELISA (GB); UNILEVER
            PLC (GB); MUIR SHELAGH RACHAEL (GB); LEVER HINDUSTAN LTD (IN); BOVY
            ARNAUD GUILLAUME (NL); TUNEN ADRIANUS JOHANNES VAN (NL); UNILEVER
            NV (NL); DE VOS CORNELIS HENRICUS (NL); HIJDEN HENDRIKUS THEODORUS
            WIL (NL)
FEATURES            Location/Qualifiers
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     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2411 TGGGGTCTGTAAATAC 2426
              ||| ||||||||||||
Db         17 TGGAGTCTGTAAATAC 2

RESULT 2732
AX042547/c
LOCUS       AX042547                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 113 from Patent WO0065088.
ACCESSION   AX042547
VERSION     AX042547.1  GI:11341155
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 113 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Homozygote primer sequence"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 25;
  Best Local Similarity   75.0%;  Pred. No. 3.9e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAAA 2798
              |||   | ||  ||||||||||||
Db         24 TGTACCAGTTACAAAAAAAAAAAA 1

RESULT 2733
AX042616/c
LOCUS       AX042616                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 182 from Patent WO0065088.
ACCESSION   AX042616
VERSION     AX042616.1  GI:11341224
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 182 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Homozygote Primer Sequence"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 25;
  Best Local Similarity   75.0%;  Pred. No. 3.9e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAAA 2798
              |||  |  |  ||||||||||||
Db         24 TGTCTGGTTACAAAAAAAAAAAAA 1

RESULT 2734
AX043184/c
LOCUS       AX043184                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 750 from Patent WO0065088.
ACCESSION   AX043184
VERSION     AX043184.1  GI:11341792
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 750 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 25;
  Best Local Similarity   75.0%;  Pred. No. 3.9e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAAA 2798
              |||   | ||  ||||||||||||
Db         24 TGTACCAGTTACAAAAAAAAAAAA 1

RESULT 2735
AX043367/c
LOCUS       AX043367                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 933 from Patent WO0065088.
ACCESSION   AX043367
VERSION     AX043367.1  GI:11341975
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 933 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Heterozygote Primer Sequence"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 25;
  Best Local Similarity   75.0%;  Pred. No. 3.9e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAAA 2798
              |||  |  |  ||||||||||||
Db         24 TGTCTGGTTACAAAAAAAAAAAAA 1

RESULT 2736
BD183015
LOCUS       BD183015                 28 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  New functional nucleic acids targeting NS3 protease and helicase of
            hepatitis C virus.
ACCESSION   BD183015
VERSION     BD183015.1  GI:31875215
KEYWORDS    JP 2002345475-A/26.
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     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a Primer"

   Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
   Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
   Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2728
AX794404
LOCUS       AX794404                 22 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 5 from Patent WO03052123.
ACCESSION   AX794404
VERSION     AX794404.1  GI:37515482
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with antihistamines
  JOURNAL   Patent: WO 03052123-A 5 26-JUN-2003;
            Xanthus Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a Primer"

   Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
   Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
   Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2729
AX815443
LOCUS       AX815443                 22 bp    DNA     linear   PAT 09-DEC-2003
DEFINITION  Sequence 5 from Patent WO03067257.
ACCESSION   AX815443
VERSION     AX815443.1  GI:39646144
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with anxiolitics
  JOURNAL   Patent: WO 03067257-A 5 14-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a Primer"

   Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
   Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
   Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2730
BD061530/c
LOCUS       BD061530                 22 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Proliferation-inhibitory gene.
ACCESSION   BD061530
VERSION     BD061530.1  GI:22607135
KEYWORDS    JP 2001292773-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Watanabe,M., Nojima,H. and Tamai,K.
  TITLE     Proliferation-inhibitory gene
  JOURNAL   Patent: JP 2001292773-A 4 23-OCT-2001;
            MEDICAL & BIOLOGICAL LABORATORIES CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001292773-A/4
            PD   23-OCT-2001
            PF   10-APR-2000 JP 2000108525
            PI   MASAFUMI WATANABE,HIROSHI NOJIMA,KATSUYUKI TAMAI PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12Q1/68//C12P21/02,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence:AntisenceR1 FH   Key
                 Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

   Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
   Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
   Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2411 TGGGGTCTGTAAATAC 2426
              ||| ||||||||||||
Db         17 TGGAGTCTGTAAATAC 2


RESULT 2731
BD161593/c
LOCUS       BD161593                 22 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Proliferation-inhibitory gene.
ACCESSION   BD161593
VERSION     BD161593.1  GI:27867351
KEYWORDS    JP 2002186484-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Watanabe,M., Nojima,H. and Tamai,K.
  TITLE     Proliferation-inhibitory gene
  JOURNAL   Patent: JP 2002186484-A 4 02-JUL-2002;
            PRESIDENT OF OSAKA UNIVERSITY, MEDICAL & BIOLOGICAL LABORATORIES CO
            LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002186484-A/4
            PD   02-JUL-2002
            PF   20-DEC-2000 JP 2000387898
            PI   MASAFUMI WATANABE,HIROSHI NOJIMA,KATSUYUKI TAMAI PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/08,C12Q1/68,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence:AntisenceR1 FH   Key
                 Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20
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RESULT 2723
AX616971
LOCUS       AX616971                  22 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 3 from Patent WO02095402.
ACCESSION   AX616971
VERSION     AX616971.1  GI:28447776
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with hyperlipidemia agents
  JOURNAL   Patent: WO 02095402-A 3 28-NOV-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20
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RESULT 2724
AX643845
LOCUS       AX643845                  22 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 5 from Patent WO02099422.
ACCESSION   AX643845
VERSION     AX643845.1  GI:28551633
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with alzheimer's disease agents
  JOURNAL   Patent: WO 02099422-A 5 12-DEC-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20
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RESULT 2725
AX696030
LOCUS       AX696030                  22 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 7 from Patent WO03008637.
ACCESSION   AX696030
VERSION     AX696030.1  GI:29419192
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Use of genotyping in the individualization of therapy
  JOURNAL   Patent: WO 03008637-A 7 30-JAN-2003;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sequence to be used as a primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20
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RESULT 2726
AX773003
LOCUS       AX773003                  22 bp    DNA     linear   PAT 09-JUL-2003
DEFINITION  Sequence 5 from Patent WO03046583.
ACCESSION   AX773003
VERSION     AX773003.1  GI:32485172
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with anesthetics
  JOURNAL   Patent: WO 03046583-A 5 05-JUN-2003;
            Xanthus Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20
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RESULT 2727
AX781387
LOCUS       AX781387                  22 bp    DNA     linear   PAT 14-JUL-2003
DEFINITION  Sequence 5 from Patent WO03046559.
ACCESSION   AX781387
VERSION     AX781387.1  GI:32698388
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with antiviral agents
  JOURNAL   Patent: WO 03046559-A 5 05-JUN-2003;
            Xanthus Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
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DEFINITION  Sequence 3 from Patent WO02084288.
ACCESSION   AX592990
VERSION     AX592990.1  GI:27950833
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with antiarrhythmics
  JOURNAL   Patent: WO 02084288-A 3 24-OCT-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2719
AX593130
LOCUS       AX593130                 22 bp    DNA     linear   PAT 13-FEB-2003
DEFINITION  Sequence 5 from Patent WO02088753.
ACCESSION   AX593130
VERSION     AX593130.1  GI:28374591
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with erectile dysfunction agents
  JOURNAL   Patent: WO 02088753-A 5 07-NOV-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2720
AX593465
LOCUS       AX593465                 22 bp    DNA     linear   PAT 13-FEB-2003
DEFINITION  Sequence 5 from Patent WO02088714.
ACCESSION   AX593465
VERSION     AX593465.1  GI:28374828
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with antineoplastic agents
  JOURNAL   Patent: WO 02088714-A 5 07-NOV-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2721
AX597460
LOCUS       AX597460                 22 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 5 from Patent WO02090994.
ACCESSION   AX597460
VERSION     AX597460.1  GI:28397730
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with analgesics
  JOURNAL   Patent: WO 02090994-A 5 14-NOV-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2722
AX601670
LOCUS       AX601670                 22 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 5 from Patent WO02093162.
ACCESSION   AX601670
VERSION     AX601670.1  GI:28401715
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with antibiotic agents
  JOURNAL   Patent: WO 02093162-A 5 21-NOV-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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  JOURNAL   Patent: WO 02073197-A 5 19-SEP-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2714
AX557361
LOCUS       AX557361                  22 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 5 from Patent WO02073206.
ACCESSION   AX557361
VERSION     AX557361.1  GI:25900270
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Metabolic phenotyping in therapy with anxiolytics
  JOURNAL   Patent: WO 02073206-A 5 19-SEP-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2715
AX557386
LOCUS       AX557386                  22 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 5 from Patent WO02073205.
ACCESSION   AX557386
VERSION     AX557386.1  GI:25900295
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Metabolic phenotyping in therapy with immunosuppressants
  JOURNAL   Patent: WO 02073205-A 5 19-SEP-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2716
AX591097
LOCUS       AX591097                  22 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 5 from Patent WO02086504.
ACCESSION   AX591097
VERSION     AX591097.1  GI:27949612
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with gastroesophageal reflux disease
            agents
  JOURNAL   Patent: WO 02086504-A 5 31-OCT-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2717
AX592487
LOCUS       AX592487                  22 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 3 from Patent WO02064816.
ACCESSION   AX592487
VERSION     AX592487.1  GI:27950565
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Multiple determinants for metabolic phenotypes
  JOURNAL   Patent: WO 02064816-A 3 22-AUG-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2718
AX592990
LOCUS       AX592990                  22 bp    DNA     linear   PAT 27-JAN-2003
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FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2444 CTTTTTTGAGACATGG 2459
              ||||||||||||| ||
Db         21 CTTTTTTGAGACAGGG 6


RESULT 2710
E38362
LOCUS       E38362                    22 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel human cathepsin Y protein, gene encoding the same and
            utilization thereof Novel human cathepsin Y protein, gene encoding
            the same and utilization thereof.
ACCESSION   E38362
VERSION     E38362.1  GI:18624969
KEYWORDS    JP 2000157263-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   RopesuMotin,C., Santamaria,I., Verasuko,G., Pendasu,A.M., Aoki,T.
            and Iwata,K.
  TITLE     Novel human cathepsin Y protein, gene encoding the same and
            utilization thereof
  JOURNAL   Patent: JP 2000157263-A 4 13-JUN-2000;
            FUJI CHEMICAL INDUSTRIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000157263-A/4
            PD   13-JUN-2000
            PF   26-NOV-1998 JP 1998352110
            PR
            PI   CARLOS ROPESU-OTIN,INIGO SANTAMARIA,GLORIA VERASUKO, PI
            ALBERT M PENDASU,
            PI   TAKANORI AOKI,KAZUSHI IWATA
            PC   C12N9/50,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00, PC
              A61K31/00,
            PC   A61K31/00,A61K31/00,A61K31/00,A61K38/55,A61K39/395,A61K39/395,
            PC   A61K45/00,
            PC   A61K48/00,C07K16/40,C12N1/19,C12N1/21,C12N5/10,C12N15/09, PC
            C12P21/08,
            PC   C12Q1/68,G01N33/53,G01N33/573//(C12N1/21,C12R1:19),(C12N5/10,
            PC   C12R1:91),
            PC   A61K37/64,C12N5/00,C12N15/00,(C12N5/00,C12R1:91) CC
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        918 TGTCCCCACCTGAATG 933
              || |||||||||||||
Db          2 TGGCCCCACCTGAATG 17


RESULT 2711
AX546436
LOCUS       AX546436                  22 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 5 from Patent WO02073196.
ACCESSION   AX546436
VERSION     AX546436.1  GI:25811627
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with antipsychotics
  JOURNAL   Patent: WO 02073196-A 5 19-SEP-2002;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence to be used as a Primer"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 2712
AX556633/c
LOCUS       AX556633                  22 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 146 from Patent WO02057453.
ACCESSION   AX556633
VERSION     AX556633.1  GI:25899809
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gangolli,E.A., Patturajan,M., Vernet,C.A., Malyankar,U.M.,
            Kekuda,R., Stone,D.J., Anderson,D., Shimkets,R.A., Burgess,C.E.,
            Zerhusen,B.D., Liu,X., Spytek,K.A., Casman,S.J., Boldog,F.L.,
            Smithson,G., Li,L. and Ji,W.
  TITLE     Polypetides and nucleic acids encoding same
  JOURNAL   Patent: WO 02057453-A 146 25-JUL-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        360 AGCAGCTGGCCTACTC 375
              |||||||| |||||||
Db         18 AGCAGCTGACCTACTC 3


RESULT 2713
AX557277
LOCUS       AX557277                  22 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 5 from Patent WO02073197.
ACCESSION   AX557277
VERSION     AX557277.1  GI:25900231
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leyland-Jones,B.
  TITLE     Individualization of therapy with antidepressants
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  TITLE     Inhibitors of alternative alleles of genes encoding products that
            mediate cell response to environmental changes
  JOURNAL   Patent: US 6200754-A 34 13-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 3e+03;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||:|| | |||
Db         21 TTTTTTTTTYTTATGTTA 4


RESULT 2705
I82109/c
LOCUS       I82109                    21 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 46 from patent US 5712097.
ACCESSION   I82109
VERSION     I82109.1  GI:3210406
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kern,S.E. and Hahn,S.A.
  TITLE     Tumor suppressor gene, DPC4
  JOURNAL   Patent: US 5712097-A 46 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1483 CAAAACCCTGGAGAAA 1498
              |||||| |||||||||
Db         21 CAAAACTCTGGAGAAA 6


RESULT 2706
AR285509/c
LOCUS       AR285509                  21 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6528632.
ACCESSION   AR285509
VERSION     AR285509.1  GI:29723071
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Catanzariti,L., Kluttz,B.W., Vera-Garcia,M., Burg,J.L., Moe,J.G.
            and McKinley,G.A.
  TITLE     Nucleic acid assays
  JOURNAL   Patent: US 6528632-A 6 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2394 ATTTATGCGTAATTTA 2409
              |||||||||| |||||
Db         18 ATTTATGCGTCATTTA 3


RESULT 2707
AR337899
LOCUS       AR337899                  21 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6569423.
ACCESSION   AR337899
VERSION     AR337899.1  GI:33724541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Weinstein,D.E.
  TITLE     Methods of inducing nervous tissue regeneration
  JOURNAL   Patent: US 6569423-A 1 27-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1576 TCTCCACCGCACAGAC 1591
              |||||||| |||||||
Db          6 TCTCCACCCCACAGAC 21


RESULT 2708
AX498248
LOCUS       AX498248                  21 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 4 from Patent WO0218951.
ACCESSION   AX498248
VERSION     AX498248.1  GI:23343167
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 4 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              |||||||| |||||||
Db          1 GAAAAAAACAAAAAAA 16


RESULT 2709
AR066939/c
LOCUS       AR066939                  22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 287 from patent US 5851760.
ACCESSION   AR066939
VERSION     AR066939.1  GI:5998161
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Evans,G.A. and Smith,M.W.
  TITLE     Method for generation of sequence sampled maps of complex genomes
  JOURNAL   Patent: US 5851760-A 287 22-DEC-1998;
```

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          FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAAC 658
              ||||||||||||||| |
Db         17 GGGCCTGGCCGAGATC 2


RESULT 2700
A18724
LOCUS       A18724                   21 bp    DNA     linear   PAT 20-APR-1994
DEFINITION  oligonucleotide.
ACCESSION   A18724
VERSION     A18724.1  GI:513375
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Anson,D.S., Brownlee,G.G. and Jones,I.M.
  TITLE     Factor IX protein
  JOURNAL   Patent: EP 0430930-A 1 05-JUN-1991;
            NATIONAL RESEARCH DEVELOPMENT CORPORATION; BRITISH TECHNOLOGY GROUP
            LTD
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2141 AGCCTGCTGATTGATT 2156
              ||| ||||||||||||
Db          1 AGCTTGCTGATTGATT 16


RESULT 2701
A34958
LOCUS       A34958                   21 bp    DNA     linear   PAT 20-MAY-1996
DEFINITION  Synthetic pMLVIX/NEO oligo.
ACCESSION   A34958
VERSION     A34958.1  GI:1568320
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Anson,D.S., Brownlee,G.G. and Jones,I.M.
  TITLE     Factor IX protein
  JOURNAL   Patent: EP 0195592-A 3 24-SEP-1986;
            NATIONAL RESEARCH DEVELOPMENT CORPORATION; BRITISH TECHNOLOGY GROUP
            LTD
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2141 AGCCTGCTGATTGATT 2156
              ||| ||||||||||||
Db          1 AGCTTGCTGATTGATT 16


RESULT 2702
AR043258/c
LOCUS       AR043258                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 46 from patent US 5814457.
ACCESSION   AR043258
VERSION     AR043258.1  GI:5964266
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kern,S.E. and Hahn,S.A.
  TITLE     DPC4 polypeptide
  JOURNAL   Patent: US 5814457-A 46 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1483 CAAAACCCTGGAGAAA 1498
              |||||| |||||||||
Db         21 CAAAACTCTGGAGAAA 6


RESULT 2703
AR074913/c
LOCUS       AR074913                 21 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 46 from patent US 5955292.
ACCESSION   AR074913
VERSION     AR074913.1  GI:10001665
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kern,S.E. and Hahn,S.A.
  TITLE     Tumor suppressor gene, DPC4
  JOURNAL   Patent: US 5955292-A 46 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1483 CAAAACCCTGGAGAAA 1498
              |||||| |||||||||
Db         21 CAAAACTCTGGAGAAA 6


RESULT 2704
AR138736/c
LOCUS       AR138736                 21 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 34 from patent US 6200754.
ACCESSION   AR138736
VERSION     AR138736.1  GI:14481081
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Housman,D.E., Ledley,F.D. and Stanton,V.P. Jr.
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 6111 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1556 AACAGGACTGCAAAAA 1571
              || |||||||||||||
Db          4 AAGAGGACTGCAAAAA 19


RESULT 2696
AR429446
LOCUS       AR429446                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 35 from patent US 6645492.
ACCESSION   AR429446
VERSION     AR429446.1  GI:40189653
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Levitt,R.C., Maloy,W.L., Kari,U.P. and Nicolaides,N.C.
  TITLE     Methods of treating asthma with interleukin-9 receptor antibodies
  JOURNAL   Patent: US 6645492-A 35 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1641 TTAAAGAGCCTTCACT 1656
              ||||||||| ||||||
Db          5 TTAAAGAGCATTCACT 20


RESULT 2697
AX709266/c
LOCUS       AX709266                 20 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 1 from Patent WO02064822.
ACCESSION   AX709266
VERSION     AX709266.1  GI:29564834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kuhn,M. and Mergemeier,S.
  TITLE     Method and kit for animal species-specific dna identification of a
            sample
  JOURNAL   Patent: WO 02064822-A 1 22-AUG-2002;
            Congen Biotechnologie GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2682 GGGTGAAATGGAGATTTG 2699
              |||||:||||||  ||||
Db         20 GGGTGRAATGGAATTTTG 3


RESULT 2698
AX804881
LOCUS       AX804881                 20 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 1049 from Patent WO03060160.
ACCESSION   AX804881
VERSION     AX804881.1  GI:38522022
KEYWORDS    .
SOURCE      Oreochromis niloticus (Nile tilapia)
  ORGANISM  Oreochromis niloticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Labroidei; Cichlidae; Oreochromis.
REFERENCE   1
  AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
  TITLE     Verification of food origin based on nucleic acid pattern
            recognition
  JOURNAL   Patent: WO 03060160-A 1049 24-JUL-2003;
            Genomar ASA (NO)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oreochromis niloticus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:8128"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1453 CCCTGGAGACCAGAGT 1468
              ||||||||| ||||||
Db          1 CCCTGGAGAACAGAGT 16


RESULT 2699
BD185433/c
LOCUS       BD185433                 20 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Reversible nucleus inheritance system for male sterile in
            transgenic plant.
ACCESSION   BD185433
VERSION     BD185433.1  GI:31877633
KEYWORDS    JP 2002354954-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cignan,A.M. and Albertson,M.C.
  TITLE     Reversible nucleus inheritance system for male sterile in
            transgenic plant
  JOURNAL   Patent: JP 2002354954-A 5 10-DEC-2002;
            PIONEER HI BRED INTERNATIONAL INC
COMMENT     OS   Unidentified
            PN   JP 2002354954-A/5
            PD   10-DEC-2002
            PF   11-MAR-2002 JP 2002066072
            PR   08-DEC-1994 US    08/351899,07-JUN-1995 US    08/474556 PI
            ANDREW M CIGNAN,MARC C ALBERTSON
            PC   A01H5/00,A01H1/06,C12N15/09,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Reversible nucleus inheritance system for male sterile in  CC
                      transgenic plant
            FH   Key             Location/Qualifiers
            FT   source          1. .20
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 5320 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2543 TTAAGAATTAAGAGGA 2558
              ||||||| ||||||||
Db          2 TTAAGAAGTAAGAGGA 17


RESULT 2691
AR299773
LOCUS       AR299773                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 11508 from patent US 6537751.
ACCESSION   AR299773
VERSION     AR299773.1  GI:31687057
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 11508 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2160 TTCTCCTTTTTTTTTT 2175
              ||||||| ||||||||
Db          1 TTCTCCTCTTTTTTTT 16


RESULT 2692
AR312135
LOCUS       AR312135                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2672 from patent US 6559294.
ACCESSION   AR312135
VERSION     AR312135.1  GI:31705561
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2672 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1481 AACAAAACCCTGGAGA 1496
              ||||| ||||||||||
Db          5 AACAATACCCTGGAGA 20


RESULT 2693
AR312308/c
LOCUS       AR312308                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2845 from patent US 6559294.
ACCESSION   AR312308
VERSION     AR312308.1  GI:31705734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2845 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        898 GGCTGAAGTACAGAGG 913
              ||||||||||||||  |
Db         20 GGCTGAAGTACAGAAG 5


RESULT 2694
AR314291/c
LOCUS       AR314291                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4828 from patent US 6559294.
ACCESSION   AR314291
VERSION     AR314291.1  GI:31707717
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 4828 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1567 AAAAATCCTTCTCCAC 1582
              ||||||||| ||||||
Db         20 AAAAATCCTCCTCCAC 5


RESULT 2695
AR315574
LOCUS       AR315574                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6111 from patent US 6559294.
ACCESSION   AR315574
VERSION     AR315574.1  GI:31709000
KEYWORDS    .
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DEFINITION  Sequence 5 from patent US 5689051.
ACCESSION   I75233
VERSION     I75233.1  GI:3011374
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Transgenic plants and DNA comprising anther specific promoter 5126
            and gene to achieve male sterility
  JOURNAL   Patent: US 5689051-A 5 18-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAAC 658
              ||||||||||||||| |
Db         17 GGGCCTGGCCGAGATC 2


RESULT 2686
I92333
LOCUS       I92333                  20 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 10 from patent US 5728412.
ACCESSION   I92333
VERSION     I92333.1  GI:3936803
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fujii,T., Iwamatsu,A., Yoshimoto,H., Minetoki,T., Bogaki,T. and
            Nagasawa,N.
  TITLE     Alcohol acetyltransferase genes and use thereof
  JOURNAL   Patent: US 5728412-A 10 17-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        194 AAGTACGAAGAGGACTGCGA 213
              ||:||:||:||:||:| : |
Db          1 AARTAYGARGARGAYTAYCA 20


RESULT 2687
AR212517/c
LOCUS       AR212517                20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 5 from patent US 6399856.
ACCESSION   AR212517
VERSION     AR212517.1  GI:21516113
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Reversible nuclear genetic system for male sterility in transgenic
            plants
  JOURNAL   Patent: US 6399856-A 5 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAAC 658
              ||||||||||||||| |
Db         17 GGGCCTGGCCGAGATC 2


RESULT 2688
AR221115
LOCUS       AR221115                20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 168 from patent US 6426188.
ACCESSION   AR221115
VERSION     AR221115.1  GI:23328000
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of phosphorylase kinase alpha 1 expression
  JOURNAL   Patent: US 6426188-A 168 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1462 CCAGAGTCCAGCTGAT 1477
              |||||||||||||| ||
Db          3 CCAGAGTCCAGCTCAT 18


RESULT 2689
AR226005
LOCUS       AR226005                20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 68 from patent US 6444465.
ACCESSION   AR226005
VERSION     AR226005.1  GI:27264159
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wyatt,J. and Freier,S.M.
  TITLE     Antinsense modulation of Her-1 expression
  JOURNAL   Patent: US 6444465-A 68 03-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1424 CTGATTGTCATAGACA 1439
              |||||||| |||||||
Db          3 CTGATTGTGATAGACA 18


RESULT 2690
AR293585
LOCUS       AR293585                20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5320 from patent US 6537751.
ACCESSION   AR293585
VERSION     AR293585.1  GI:31680869
```

```
ACCESSION   I21402
VERSION     I21402.1  GI:1601756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fujii,T., Iwamatsu,A., Yoshimoto,H., Minetoki,T., Bogaki,T. and
            Nagasawa,N.
  TITLE     Alcohol acetyltransferase genes and use thereof
  JOURNAL   Patent: US 5521088-A 10 28-MAY-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        194 AAGTACGAAGAGGACTGCGA 213
              ||:||:||:||:||:| : |
Db          1 AARTAYGARGARGAYTAYCA 20


RESULT 2681
I28931
LOCUS       I28931                   20 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 5 from patent US 5576178.
ACCESSION   I28931
VERSION     I28931.1  GI:1819722
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Emanuel,B.S., Budarf,M.L. and Driscoll,D.
  TITLE     Method of detecting genetic deletions and mutations associated with
            DiGeorge syndrome, Velocardiofacial syndrome, charge association,
            conotruncal cardiac defect, and cleft palate and probes useful
            therefor
  JOURNAL   Patent: US 5576178-A 5 19-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        257 CACCTCTCCTCCGCCG 272
              ||||| ||||||||||
Db          5 CACCTATCCTCCGCCG 20


RESULT 2682
I61432
LOCUS       I61432                   20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 10 from patent US 5658777.
ACCESSION   I61432
VERSION     I61432.1  GI:2479380
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fujii,T., Iwamatsu,A., Yoshimoto,H., Minetoki,T., Bogaki,T. and
            Nagasawa,N.
  TITLE     Alcohol acetyltransferase genes and use thereof
  JOURNAL   Patent: US 5658777-A 10 19-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        194 AAGTACGAAGAGGACTGCGA 213
              ||:||:||:||:||:| : |
Db          1 AARTAYGARGARGAYTAYCA 20


RESULT 2683
I73367
LOCUS       I73367                   20 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 10 from patent US 5686284.
ACCESSION   I73367
VERSION     I73367.1  GI:3009508
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Fujii,T., Iwamatsu,A., Yoshimoto,H., Minetoki,T., Bogaki,T. and
            Nagasawa,N.
  TITLE     Alcohol acetyltransferase genes and use thereof
  JOURNAL   Patent: US 5686284-A 10 11-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 2.7e+03;
  Matches   12;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        194 AAGTACGAAGAGGACTGCGA 213
              ||:||:||:||:||:| : |
Db          1 AARTAYGARGARGAYTAYCA 20


RESULT 2684
I75208/c
LOCUS       I75208                   20 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 5 from patent US 5689049.
ACCESSION   I75208
VERSION     I75208.1  GI:3011349
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Transgenic plant and method for producing male sterility using
            anther specific promoter 5126
  JOURNAL   Patent: US 5689049-A 5 18-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAAC 658
              |||||||||||||| |
Db         17 GGGCCTGGCCGAGATC 2


RESULT 2685
I75233/c
LOCUS       I75233                   20 bp    DNA     linear   PAT 03-APR-1998
```

```
VERSION     AR158933.1  GI:16221345
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 555 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
              |||||| |||||||||
Db          4 TTTTTTCTTTTTTAAC 19


RESULT 2676
AR158934
LOCUS       AR158934                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 556 from patent US 6251588.
ACCESSION   AR158934
VERSION     AR158934.1  GI:16221347
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 556 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
              |||||| |||||||||
Db          3 TTTTTTCTTTTTTAAC 18


RESULT 2677
AR158935
LOCUS       AR158935                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 557 from patent US 6251588.
ACCESSION   AR158935
VERSION     AR158935.1  GI:16221349
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 557 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
              |||||| |||||||||
Db          2 TTTTTTCTTTTTTAAC 17


RESULT 2678
AR166719/c
LOCUS       AR166719                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 5 from patent US 6281348.
ACCESSION   AR166719
VERSION     AR166719.1  GI:16242162
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Reversible nuclear genetic system for male sterility in transgenic
            plants
  JOURNAL   Patent: US 6281348-A 5 28-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAAC 658
              ||||||||||||||| |
Db         17 GGGCCTGGCCGAGATC 2


RESULT 2679
AR172162
LOCUS       AR172162                  20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 5 from patent US 6303294.
ACCESSION   AR172162
VERSION     AR172162.1  GI:17911653
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Emanuel,B.S., Budarf,M.L. and Driscoll,D.
  TITLE     Methods of detecting genetic deletions and mutations associated
            with Digeorge syndrome, Velocardiofacial syndrome, CHARGE
            association, conotruncal cardiac defect, and cleft palate and
            probes useful therefore
  JOURNAL   Patent: US 6303294-A 5 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        257 CACCTCTCCTCCGCCG 272
              ||||| ||||||||||
Db          5 CACCTATCCTCCGCCG 20


RESULT 2680
I21402
LOCUS       I21402                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 10 from patent US 5521088.
```

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ACCESSION   AR052628
VERSION     AR052628.1  GI:5975992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Reed,J.C.
  TITLE     Regulation of bcl-2 gene expression
  JOURNAL   Patent: US 5831066-A 28 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         54 GCGGGGGCGGCGGCAG 69
              |||| ||||||||||
Db          2 GCGGCGGCGGCGGCAG 17


RESULT 2671
AR059046/c
LOCUS       AR059046                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5837851.
ACCESSION   AR059046
VERSION     AR059046.1  GI:5984623
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     DNA promoter 5126 and constructs useful in a reversible nuclear
            genetic system for male sterility in transgenic plants
  JOURNAL   Patent: US 5837851-A 5 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAAC 658
              |||||||||||||| |
Db         17 GGGCCTGGCCGAGATC 2


RESULT 2672
AR070884
LOCUS       AR070884                 20 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 35 from patent US 5908839.
ACCESSION   AR070884
VERSION     AR070884.1  GI:7221772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Levitt,R.Clifford. and Nicolaides,N.C.
  TITLE     Asthma associated factors as targets for treating atopic allergies
            including asthma and related disorders
  JOURNAL   Patent: US 5908839-A 35 01-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1641 TTAAAGAGCCTTCACT 1656
              |||||||| ||||||
Db          5 TTAAAGAGCATTCACT 20


RESULT 2673
AR121329
LOCUS       AR121329                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 13 from patent US 6159718.
ACCESSION   AR121329
VERSION     AR121329.1  GI:14104905
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dalboege,H., Andersen,L.Nonboe., Kofoed,L.Venke.,
            Kauppinen,M.Sakari., Christgau,S., Heldt-Hansen,H.Peter. and
            Halkier,T.
  TITLE     Enzyme with polygalacturonase activity
  JOURNAL   Patent: US 6159718-A 13 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        731 GATCAGACAGTCATTC 746
              |||||||| ||||||
Db          2 GATCAGACACTCATTC 17


RESULT 2674
AR158932
LOCUS       AR158932                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 554 from patent US 6251588.
ACCESSION   AR158932
VERSION     AR158932.1  GI:16221343
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 554 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
              |||||| |||||||||
Db          5 TTTTTTCTTTTTTAAC 20


RESULT 2675
AR158933
LOCUS       AR158933                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 555 from patent US 6251588.
ACCESSION   AR158933
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DEFINITION  Sequence 48 from patent US 6451968.
ACCESSION   AR231311
VERSION     AR231311.1  GI:27272242
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6451968-A 48 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||| |||||||| || ||
Db         18 GAAGAAAAAAAAANAANAA 1


RESULT 2666
AR007532/c
LOCUS       AR007532                  20 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5750868.
ACCESSION   AR007532
VERSION     AR007532.1  GI:3967016
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Reversible nuclear genetic system for male sterility in transgenic
            plants
  JOURNAL   Patent: US 5750868-A 5 12-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAAC 658
              ||||||||||||||| |
Db         17 GGGCCTGGCCGAGATC 2


RESULT 2667
AR012192/c
LOCUS       AR012192                  20 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5763243.
ACCESSION   AR012192
VERSION     AR012192.1  GI:3970182
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Reversible nuclear genetic system for male sterility in transgenic
            plants
  JOURNAL   Patent: US 5763243-A 5 09-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAAC 658
              ||||||||||||||| |
Db         17 GGGCCTGGCCGAGATC 2


RESULT 2668
AR022607/c
LOCUS       AR022607                  20 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 5 from patent US 5792853.
ACCESSION   AR022607
VERSION     AR022607.1  GI:3976669
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Reversible nuclear genetic system for male sterility in transgenic
            plants
  JOURNAL   Patent: US 5792853-A 5 11-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAAC 658
              ||||||||||||||| |
Db         17 GGGCCTGGCCGAGATC 2


RESULT 2669
AR023880/c
LOCUS       AR023880                  20 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 5 from patent US 5795753.
ACCESSION   AR023880
VERSION     AR023880.1  GI:3977174
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cigan,A.M. and Albertsen,M.C.
  TITLE     Reversible nuclear genetic system for male sterility in transgenic
            plants
  JOURNAL   Patent: US 5795753-A 5 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAAC 658
              ||||||||||||||| |
Db         17 GGGCCTGGCCGAGATC 2


RESULT 2670
AR052628
LOCUS       AR052628                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 28 from patent US 5831066.
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                    Sequenz:Erkennungssystem"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAA 2188
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTCAA 16


RESULT 2661
AX048440/c
LOCUS       AX048440                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 39 from Patent WO0071747.
ACCESSION   AX048440
VERSION     AX048440.1  GI:12225604
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 39 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              || |||||||||||||
Db         16 TTTAAAAAAAAAAAAA 1


RESULT 2662
AX048441/c
LOCUS       AX048441                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 40 from Patent WO0071747.
ACCESSION   AX048441
VERSION     AX048441.1  GI:12225605
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 40 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              || |||||||||||||
Db         16 TTTAAAAAAAAAAAAA 1


RESULT 2663
AX048442/c
LOCUS       AX048442                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 41 from Patent WO0071747.
ACCESSION   AX048442
VERSION     AX048442.1  GI:12225606
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 41 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              || |||||||||||||
Db         16 TTTAAAAAAAAAAAAA 1


RESULT 2664
AX048443/c
LOCUS       AX048443                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 42 from Patent WO0071747.
ACCESSION   AX048443
VERSION     AX048443.1  GI:12225607
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 42 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match              0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              || |||||||||||||
Db         16 TTTAAAAAAAAAAAAA 1


RESULT 2665
AR231311/c
LOCUS       AR231311                 20 bp    DNA     linear   PAT 20-DEC-2002
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                    ||||||| ||||||||
Db          17 CGAGGTGAAGAATGTC 2


RESULT 2656
AX587498
LOCUS       AX587498                  19 bp    DNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 8 from Patent WO0236751.
ACCESSION   AX587498
VERSION     AX587498.1  GI:27656314
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wernet,P.
  TITLE     Human cord blood derived unrestricted somatic stem cells (ussc)
  JOURNAL   Patent: WO 0236751-A 8 10-MAY-2002;
            Kourion Therapeuthics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3 primer for the neuofilament gene"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2024 CTGGTAGGAGGCAAAG 2039
                ||||||||||||| |
Db          2 CTGGTAGGAGGCAATG 17


RESULT 2657
AX699138/c
LOCUS       AX699138                  19 bp    DNA     linear   PAT 29-MAY-2003
DEFINITION  Sequence 79 from Patent WO03000727.
ACCESSION   AX699138
VERSION     AX699138.1  GI:29499787
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Zhang,Y., Moffatt,M., Cookson,W. and Tinsley,J.O.
  TITLE     Atopy
  JOURNAL   Patent: WO 03000727-A 79 03-JAN-2003;
            ISIS INNOVATION LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1483 CAAAACCCTGGAGAAA 1498
                |||| ||||||||||||
Db         19 CAAAGCCCTGGAGAAA 4


RESULT 2658
AR093063/c
LOCUS       AR093063                  20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 158 from patent US 5998383.
ACCESSION   AR093063
VERSION     AR093063.1  GI:10019815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wright,J.A. and Young,A.H.
  TITLE     Antitumor antisense sequences directed against ribonucleotide
            reductase
  JOURNAL   Patent: US 5998383-A 158 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
                ||||| ||||||||||
Db         20 AAAAAGAAAAAAAAAA 5


RESULT 2659
AR359565/c
LOCUS       AR359565                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 158 from patent US 6593305.
ACCESSION   AR359565
VERSION     AR359565.1  GI:33766288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wright,J.A.
  TITLE     Antitumor antisense sequences directed against R1 and R2 components
            of ribonucleotide reductase
  JOURNAL   Patent: US 6593305-A 158 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
                ||||| ||||||||||
Db         20 AAAAAGAAAAAAAAAA 5


RESULT 2660
AX048447
LOCUS       AX048447                  20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 46 from Patent WO0071747.
ACCESSION   AX048447
VERSION     AX048447.1  GI:12225611
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 46 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
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                hybridization of
CC   the probe with a target nucleic acid.
FH   Key             Location/Qualifiers
FT   source          1. .18
FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2177
              | ||||||||||||||
Db          3 CCCCTTTTTTTTTTT 18


RESULT 2653
BD166063
LOCUS       BD166063                 18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166063
VERSION     BD166063.1  GI:27871875
KEYWORDS    JP 2002191372-A/43.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 43 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/43
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                       examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2177
              | ||||||||||||||
Db          3 CCCCTTTTTTTTTTT 18


RESULT 2654
BD217400/c
LOCUS       BD217400                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of TNFR1 expression.
ACCESSION   BD217400
VERSION     BD217400.1  GI:33027170
KEYWORDS    JP 2002519015-A/23.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense modulation of TNFR1 expression
  JOURNAL   Patent: JP 2002519015-A 23 02-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002519015-A/23
            PD   02-JUL-2002
            PF   17-JUN-1999 JP 2000557265
            PR   26-JUN-1998 US    09/106038
            PI   BRENDA F BAKER,LEX M COWSERT
            PC
            C12N15/09,A61K31/7105,A61K31/711,A61K48/00,A61P29/00,A61P43/00, PC
             C12Q1/68,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense modulation of TNFR1 expression
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        605 GACCTGCTGCTGCCCC 620
              |||||||||||||| |
Db         17 GACCTGCTGCTGCCGC 2


RESULT 2655
I25108/c
LOCUS       I25108                   19 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 14 from patent US 5547868.
ACCESSION   I25108
VERSION     I25108.1  GI:1604978
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Miller,W.L., Harikrishna,J.A. and Black,S.M.
  TITLE     Cholesterol disposal fusion enzymes
  JOURNAL   Patent: US 5547868-A 14 20-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        691 CGAGGTGCAGAATGTC 706
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                  |||||||||||||| ||
Db         18 TTTAAATACATTCACT 3


RESULT 2650
BD072904
LOCUS       BD072904                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072904
VERSION     BD072904.1  GI:22618507
KEYWORDS    JP 2001286300-A/42.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 42 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/42
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTT 2177
              | ||||||||||||||
Db          3 CCCCTTTTTTTTTTTT 18


RESULT 2651
BD107531
LOCUS       BD107531                  18 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107531
VERSION     BD107531.1  GI:23202349
KEYWORDS    JP 2002000275-A/40.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 40 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/40
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTT 2177
              | ||||||||||||||
Db          3 CCCCTTTTTTTTTTTT 18


RESULT 2652
BD145063
LOCUS       BD145063                  18 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145063
VERSION     BD145063.1  GI:27850821
KEYWORDS    JP 2002119291-A/44.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 44 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/44
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
```

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  AUTHORS   Distler,J., Model,F. and Taubert,H.
  TITLE     Method and nucleic acids for the analysis of colon cancer
  JOURNAL   Patent: WO 03014388-A 211 20-FEB-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for p16"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1832 TTTAAATACATTCCCT 1847
                ||||||||||||| ||
Db         18 TTTAAATACATTCACT 3


RESULT 2646
AX705544
LOCUS       AX705544                  18 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 213 from Patent WO03014388.
ACCESSION   AX705544
VERSION     AX705544.1  GI:29562209
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Distler,J., Model,F. and Taubert,H.
  TITLE     Method and nucleic acids for the analysis of colon cancer
  JOURNAL   Patent: WO 03014388-A 213 20-FEB-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for p16"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1832 TTTAAATACATTCCCT 1847
                ||||||||||||| ||
Db          1 TTTAAATACATTCACT 16


RESULT 2647
AX796234/c
LOCUS       AX796234                  18 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 577 from Patent WO03052135.
ACCESSION   AX796234
VERSION     AX796234.1  GI:37516900
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
            and Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lung cell
            proliferative disorder
  JOURNAL   Patent: WO 03052135-A 577 26-JUN-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CDKN2a"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1832 TTTAAATACATTCCCT 1847
                ||||||||||||| ||
Db         18 TTTAAATACATTCACT 3


RESULT 2648
AX822736/c
LOCUS       AX822736                  18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 628 from Patent EP1340818.
ACCESSION   AX822736
VERSION     AX822736.1  GI:39749372
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferative disorder
  JOURNAL   Patent: EP 1340818-A 628 03-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CDKN2a"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1832 TTTAAATACATTCCCT 1847
                ||||||||||||| ||
Db         18 TTTAAATACATTCACT 3


RESULT 2649
AX826376/c
LOCUS       AX826376                  18 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 628 from Patent WO03072821.
ACCESSION   AX826376
VERSION     AX826376.1  GI:39751890
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
  TITLE     Method and nucleic acids for the analysis of a colon cell
            proliferactive disorder
  JOURNAL   Patent: WO 03072821-A 628 04-SEP-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CDKN2a"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1832 TTTAAATACATTCCCT 1847
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  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGG 66
              ||||||| ||||||||
Db         18 GCGGCGGCGGCGGCGG 3


RESULT 2641
AR264959
LOCUS       AR264959                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 43 from patent US 6492121.
ACCESSION   AR264959
VERSION     AR264959.1  GI:29693346
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 43 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2177
              | |||||||||||||
Db          3 CCCCTTTTTTTTTTT 18


RESULT 2642
AR264963/c
LOCUS       AR264963                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 47 from patent US 6492121.
ACCESSION   AR264963
VERSION     AR264963.1  GI:29693350
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 47 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2177
              | |||||||||||||
Db         16 CCCCTTTTTTTTTTT 1


RESULT 2643
AR266207/c
LOCUS       AR266207                 18 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 19 from patent US 6492173.
ACCESSION   AR266207
VERSION     AR266207.1  GI:29695053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of cyclin D2 expression
  JOURNAL   Patent: US 6492173-A 19 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        491 CAGGAGGGAGCGGGGC 506
              |||||||||| |||||
Db         17 CAGGAGGGAGAGGGGC 2


RESULT 2644
AX599370/c
LOCUS       AX599370                 18 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 710 from Patent WO02077272.
ACCESSION   AX599370
VERSION     AX599370.1  GI:28399514
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 710 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection oligonucleotide for CDKN2a"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1832 TTTAAATACATTCCCT 1847
              |||||||||||| ||
Db         18 TTTAAATACATTCACT 3


RESULT 2645
AX705542/c
LOCUS       AX705542                 18 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 211 from Patent WO03014388.
ACCESSION   AX705542
VERSION     AX705542.1  GI:29562207
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 4546 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
                ||||  ||||||||||
Db          2 ATCTATTAAATACATT 17


RESULT 2637
BD067572/c
LOCUS       BD067572                  17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067572
VERSION     BD067572.1  GI:22613175
KEYWORDS    JP 2001511003-A/412.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 412 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/412
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1424 CTGATTGTCATAGACA 1439
                ||||||| |||||||
Db         17 CTGATTGTGATAGACA 2


RESULT 2638
AR096352/c
LOCUS       AR096352                  18 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 23 from patent US 6007995.
ACCESSION   AR096352
VERSION     AR096352.1  GI:10025086
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F. and Cowsert,L.M.
  TITLE     Antisense inhibition of TNFR1 expression
  JOURNAL   Patent: US 6007995-A 23 28-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        605 GACCTGCTGCTGCCCC 620
              ||||||||||||||| |
Db         17 GACCTGCTGCTGCCGC 2


RESULT 2639
I18339
LOCUS       I18339                    18 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 12 from patent US 5495009.
ACCESSION   I18339
VERSION     I18339.1  GI:1598694
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Matteucci,M., Jones,B. and Lin,K.-Y.
  TITLE     Oligonucleotide analogs containing thioformacetal linkages
  JOURNAL   Patent: US 5495009-A 12 27-FEB-1996;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTT 2170
              ||| |||||||||||||
Db          2 TTTCTTTCTCCTTTTT 17


RESULT 2640
AR196700/c
LOCUS       AR196700                  18 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1165 from patent US 6350934.
ACCESSION   AR196700
VERSION     AR196700.1  GI:20246137
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
            Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
  TITLE     Nucleic acid encoding delta-9 desaturase
  JOURNAL   Patent: US 6350934-A 1165 26-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db         16 TCAAAAAAAAAAAAAA 1


RESULT 2632
AX728115/c
LOCUS       AX728115                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 5802 from Patent WO03025176.
ACCESSION   AX728115
VERSION     AX728115.1  GI:30507458
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 5802 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        110 GGGGGCTGGGGGGATC 125
              ||||| ||||||||||
Db         16 GGGGGGTGGGGGGATC 1


RESULT 2633
AX729041/c
LOCUS       AX729041                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 675 from Patent WO03025175.
ACCESSION   AX729041
VERSION     AX729041.1  GI:30508384
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 675 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2263 CATATTTATTTCAGAT 2278
              ||| ||||||||||||
Db         17 CATTTTTATTTCAGAT 2


RESULT 2634
AX744259
LOCUS       AX744259                  17 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 224 from Patent WO03031621.
ACCESSION   AX744259
VERSION     AX744259.1  GI:30722926
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 224 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2110 CCTTCTGGTTTTAGGA 2125
              ||||||||| ||||||
Db          2 CCTTCTGGTCTTAGGA 17


RESULT 2635
AX744260
LOCUS       AX744260                  17 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 225 from Patent WO03031621.
ACCESSION   AX744260
VERSION     AX744260.1  GI:30722927
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 225 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2110 CCTTCTGGTTTTAGGA 2125
              ||||||||| ||||||
Db          1 CCTTCTGGTCTTAGGA 16


RESULT 2636
AX761225
LOCUS       AX761225                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 4546 from Patent WO03040369.
ACCESSION   AX761225
VERSION     AX761225.1  GI:32255841
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 2790 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2465 AATTTTAATATTAACT 2480
                ||||||||||||| |
Db         17 AATTTTAATATTAAGT 2


RESULT 2628
AX692522
LOCUS       AX692522                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5254 from Patent EP1281758.
ACCESSION   AX692522
VERSION     AX692522.1  GI:29415480
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5254 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTT 2178
              | |||||||||||||||
Db          2 TTCTTTTTTTTTTTTT 17


RESULT 2629
AX692522/c
LOCUS       AX692522                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5254 from Patent EP1281758.
ACCESSION   AX692522
VERSION     AX692522.1  GI:29415480
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5254 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              |||||||||||||| ||
Db         17 AAAAAAAAAAAAAGAA 2


RESULT 2630
AX692528
LOCUS       AX692528                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5260 from Patent EP1281758.
ACCESSION   AX692528
VERSION     AX692528.1  GI:29415486
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5260 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              ||||||||||||||| |
Db          1 TTTTTTTTTTTTTGA 16


RESULT 2631
AX692528/c
LOCUS       AX692528                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5260 from Patent EP1281758.
ACCESSION   AX692528
VERSION     AX692528.1  GI:29415486
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5260 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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AR402072/c
LOCUS       AR402072                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 412 from patent US 6623962.
ACCESSION   AR402072
VERSION     AR402072.1  GI:40149522
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and McSwiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases of conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: US 6623962-A 412 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

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  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1424 CTGATTGTCATAGACA 1439
              ||||||| |||||||
Db         17 CTGATTGTGATAGACA 2


RESULT 2623
AR434232
LOCUS       AR434232                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 655 from patent US 6656700.
ACCESSION   AR434232
VERSION     AR434232.1  GI:40197075
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 655 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

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  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAG 466
              |||||| ||||||||
Db          2 CACAGGTAGCCAGCAG 17


RESULT 2624
AR434233
LOCUS       AR434233                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 656 from patent US 6656700.
ACCESSION   AR434233
VERSION     AR434233.1  GI:40197076
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 656 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAG 466
              |||||| ||||||||
Db          1 CACAGGTAGCCAGCAG 16


RESULT 2625
AR435298
LOCUS       AR435298                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1721 from patent US 6656700.
ACCESSION   AR435298
VERSION     AR435298.1  GI:40198141
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1721 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2315 ATTTGTTGCTGCTTGT 2330
              | |||||||||||||||
Db          2 AGTTGTTGCTGCTTGT 17


RESULT 2626
AR435299
LOCUS       AR435299                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1722 from patent US 6656700.
ACCESSION   AR435299
VERSION     AR435299.1  GI:40198142
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1722 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2315 ATTTGTTGCTGCTTGT 2330
              | |||||||||||||||
Db          1 AGTTGTTGCTGCTTGT 16


RESULT 2627
AX217348/c
LOCUS       AX217348                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 2790 from Patent WO0159103.
ACCESSION   AX217348
VERSION     AX217348.1  GI:15527409
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RESULT 2617
AR323667
LOCUS       AR323667                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1069 from patent US 6566127.
ACCESSION   AR323667
VERSION     AR323667.1  GI:33709475
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1069 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTT 2176
              ||| ||||||||||||
Db          2 TCTACTTTTTTTTTTT 17


RESULT 2618
AR323677/c
LOCUS       AR323677                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1079 from patent US 6566127.
ACCESSION   AR323677
VERSION     AR323677.1  GI:33709485
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1079 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              ||| ||||||||||||
Db         16 TTGGAAAAAAAAAAAA 1


RESULT 2619
AR324345
LOCUS       AR324345                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1747 from patent US 6566127.
ACCESSION   AR324345
VERSION     AR324345.1  GI:33710153
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1747 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1511 AGGAAATAAAATTGGA 1526
              |||||||||||||| |
Db          2 AGGAAATAAAATTGAA 17


RESULT 2620
AR328223
LOCUS       AR328223                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 5625 from patent US 6566127.
ACCESSION   AR328223
VERSION     AR328223.1  GI:33714031
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 5625 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1339 TCATTTCAGCCTGATT 1354
              |||||||||||||| |
Db          2 TCATTTCAGCCTGAAT 17


RESULT 2621
AR398091
LOCUS       AR398091                  17 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 472 from patent US 6617438.
ACCESSION   AR398091
VERSION     AR398091.1  GI:40135620
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Oligoribonucleotides with enzymatic activity
  JOURNAL   Patent: US 6617438-A 472 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        603 CCGACCTGCTGCTGCC 618
              |||||||||| ||||
Db          2 CCGACCTGCTGGTGCC 17


RESULT 2622
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            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTTTG 2193
              ||||||||||| ||||
Db          1 TTTTTTTTTAATTTTG 16


RESULT 2613
AR187057
LOCUS       AR187057                17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2545 from patent US 6346398.
ACCESSION   AR187057
VERSION     AR187057.1  GI:20233022
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2545 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTT 2176
              ||| ||||||||||||
Db          2 TCTACTTTTTTTTTTT 17


RESULT 2614
AR187067/c
LOCUS       AR187067                17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2555 from patent US 6346398.
ACCESSION   AR187067
VERSION     AR187067.1  GI:20233032
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2555 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              ||| ||||||||||||
Db         16 TTGGAAAAAAAAAAAA 1


RESULT 2615
AR188492
LOCUS       AR188492                17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 3980 from patent US 6346398.
ACCESSION   AR188492
VERSION     AR188492.1  GI:20234457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 3980 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1511 AGGAAATAAAATTGGA 1526
              |||||||||||||| |
Db          2 AGGAAATAAAATTGAA 17


RESULT 2616
AR286101
LOCUS       AR286101                17 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 473 from patent US 6528640.
ACCESSION   AR286101
VERSION     AR286101.1  GI:29723697
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 473 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        603 CCGACCTGCTGCTGCC 618
              |||||||||| ||||
Db          2 CCGACCTGCTGGTGCC 17
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            PN   JP 2002541795-A/2608
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1040 GGGAGGCGGAAAGCCG 1055
              ||||||||||| |||||
Db         17 GGGAGGCGGACAGCCG 2


RESULT 2610
BD258525/c
LOCUS       BD258525                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258525
VERSION     BD258525.1  GI:33068295
KEYWORDS    JP 2002541795-A/6318.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6318 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6318
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1970 TTTACCTTGAAAAAAA 1985
              |||||||||| ||||
Db         17 TTTACCTTGAATAAAA 2


RESULT 2611
BD258578
LOCUS       BD258578                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258578
VERSION     BD258578.1  GI:33068348
KEYWORDS    JP 2002541795-A/6371.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6371 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6371
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
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                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTTTG 2193
              |||||||||| ||||
Db          2 TTTTTTTTTAATTTTG 17


RESULT 2612
BD258579
LOCUS       BD258579                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD258579
VERSION     BD258579.1  GI:33068349
KEYWORDS    JP 2002541795-A/6372.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 6372 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/6372
            PD   10-DEC-2002
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VERSION     AX202013.1  GI:15391821
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y., Ullman,C.G. and Moore,M.
  TITLE     Molecular switches ii
  JOURNAL   Patent: WO 0153479-A 79 26-JUL-2001;
            Gendaq Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Binding sequence"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 2606
AR029854/c
LOCUS       AR029854                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 43 from patent US 5861244.
ACCESSION   AR029854
VERSION     AR029854.1  GI:5943068
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 43 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTTT 2173
              ||||||||| ||||||
Db         16 TTTTCTCCTCTTTTTT 1


RESULT 2607
AR029855
LOCUS       AR029855                 17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 44 from patent US 5861244.
ACCESSION   AR029855
VERSION     AR029855.1  GI:5943069
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 44 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||||||| ||||
Db          1 TTTTTTCTCCTCTTTT 16


RESULT 2608
BD254621
LOCUS       BD254621                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD254621
VERSION     BD254621.1  GI:33064391
KEYWORDS    JP 2002541795-A/2414.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2414 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/2414
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key              Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2734 TAATTGTTGTGTGTAT 2749
              |||||||||| |||||
Db          2 TAATTGTTGTTTGTAT 17


RESULT 2609
BD254815/c
LOCUS       BD254815                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD254815
VERSION     BD254815.1  GI:33064585
KEYWORDS    JP 2002541795-A/2608.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2608 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
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            Gendaq Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 2601
AX059786/c
LOCUS       AX059786                 16 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 18 from Patent WO0100815.
ACCESSION   AX059786
VERSION     AX059786.1  GI:12405491
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y.M. and Ullman,C.G.
  TITLE     Molecular switches
  JOURNAL   Patent: WO 0100815-A 18 04-JAN-2001;
            Gendaq Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Selection target"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 2602
AX059827/c
LOCUS       AX059827                 16 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 59 from Patent WO0100815.
ACCESSION   AX059827
VERSION     AX059827.1  GI:12405501
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y.M. and Ullman,C.G.
  TITLE     Molecular switches
  JOURNAL   Patent: WO 0100815-A 59 04-JAN-2001;
            Gendaq Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 2603
AX201949/c
LOCUS       AX201949                 16 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 15 from Patent WO0153479.
ACCESSION   AX201949
VERSION     AX201949.1  GI:15391796
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y., Ullman,C.G. and Moore,M.
  TITLE     Molecular switches ii
  JOURNAL   Patent: WO 0153479-A 15 26-JUL-2001;
            Gendaq Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Selection target"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 2604
AX201990/c
LOCUS       AX201990                 16 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 56 from Patent WO0153479.
ACCESSION   AX201990
VERSION     AX201990.1  GI:15391808
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y., Ullman,C.G. and Moore,M.
  TITLE     Molecular switches ii
  JOURNAL   Patent: WO 0153479-A 56 26-JUL-2001;
            Gendaq Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 2605
AX202013/c
LOCUS       AX202013                 16 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 79 from Patent WO0153479.
ACCESSION   AX202013
```

```
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 861 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 25;
  Best Local Similarity   81.0%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||  ||  ||
Db          1 TTTTTTTTTTTTCATTCCTT 21


RESULT 2597
AX043259
LOCUS       AX043259                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 825 from Patent WO0065088.
ACCESSION   AX043259
VERSION     AX043259.1  GI:11341867
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 825 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 25;
  Best Local Similarity   81.0%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||| ||  | |
Db          1 TTTTTTTTTTTTTGTTCCAGT 21


RESULT 2598
BD082357/c
LOCUS       BD082357                 26 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
            corresponding polynucleotide molecules.
ACCESSION   BD082357
VERSION     BD082357.1  GI:22627967
KEYWORDS    JP 2001523954-A/64.
SOURCE      Mastadenovirus
  ORGANISM  Mastadenovirus
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kleanthous,H., Lissolo,L., Tomb,J.F., Miller,C. and Garawi,A.A.
  TITLE     76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
            corresponding polynucleotide molecules
  JCURNAL   Patent: JP 2001523954-A 64 27-NOV-2001;
            MERIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET
            VACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA,
            HUMAN GENOME SCIENCES INC
COMMENT     PN   JP 2001523954-A/64
            PD   27-NOV-2001
            PF   31-MAR-1998 JP 1998541962
            PI   HAROLD KLEANTHOUS,LING LISSOLO,JEAN FRANCOIS TOMB,CHARLES  PI
             MILLER,
            PI   AMAL AL GARAWI
            PC   A01N43/04,A01N59/16,A61K9/48,A61K31/70,A61K31/715,A61K39/02,
            PC   A61K39/40,
            PC   G01N33/554,G01N33/569
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mastadenovirus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10509"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 26;
  Best Local Similarity   81.0%;  Pred. No. 3.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              ||||||| ||||||| || |
Db         24 TTTTTTTCGTTTTTTTGAATT 4


RESULT 2599
AX053187/c
LOCUS       AX053187                 16 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 15 from Patent WO0073434.
ACCESSION   AX053187
VERSION     AX053187.1  GI:12227537
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y. and Ullman,C.G.
  TITLE     Gene switches
  JOURNAL   Patent: WO 0073434-A 15 07-DEC-2000;
            Gendaq Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Selection target"

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 2600
AX053228/c
LOCUS       AX053228                 16 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 56 from Patent WO0073434.
ACCESSION   AX053228
VERSION     AX053228.1  GI:12227547
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y. and Ullman,C.G.
  TITLE     Gene switches
  JOURNAL   Patent: WO 0073434-A 56 07-DEC-2000;
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2352 GTTCTGTATTTTAAGAAACAG 2372
              || ||| || || ||||||||
Db         22 GTCCTGAATCTTGAGAAACAG 2

RESULT 2592
AX803836/c
LOCUS       AX803836                 24 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 4 from Patent WO03060160.
ACCESSION   AX803836
VERSION     AX803836.1  GI:38520971
KEYWORDS    .
SOURCE      Salmo salar (Atlantic salmon)
  ORGANISM  Salmo salar
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
REFERENCE   1
  AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
  TITLE     Verification of food origin based on nucleic acid pattern
            recognition
  JOURNAL   Patent: WO 03060160-A 4 24-JUL-2003;
            Genomar ASA (NO)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Salmo salar"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:8030"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 24;
  Best Local Similarity   81.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACTT 2191
              ||||||| ||||||  || ||
Db         21 TTTTTTTGTTTTTTCCAATTT 1

RESULT 2593
AX043563/c
LOCUS       AX043563                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1129 from Patent WO0065088.
ACCESSION   AX043563
VERSION     AX043563.1  GI:11342171
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1129 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 25;
  Best Local Similarity   81.0%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAA 2797
              ||| ||   ||||||||||||
Db         21 TTACAAGCTAAAAAAAAAAAA 1

RESULT 2594
AX042571
LOCUS       AX042571                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 137 from Patent WO0065088.
ACCESSION   AX042571
VERSION     AX042571.1  GI:11341179
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 137 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 25;
  Best Local Similarity   81.0%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTT 2192
              |||||||||||||  || | |
Db          1 TTTTTTTTTTTTTCCAAGTCT 21

RESULT 2595
AX042652/c
LOCUS       AX042652                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 218 from Patent WO0065088.
ACCESSION   AX042652
VERSION     AX042652.1  GI:11341260
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 218 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DRB1 Homozygote Primer Sequence"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 25;
  Best Local Similarity   81.0%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAA 2797
              | |||  | ||||||||||||
Db         21 TCAGACGTAAAAAAAAAAAAA 1

RESULT 2596
AX043295
LOCUS       AX043295                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 861 from Patent WO0065088.
ACCESSION   AX043295
VERSION     AX043295.1  GI:11341903
KEYWORDS    .
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  JOURNAL   Patent: WO 02057450-A 150 25-JUL-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically synthesized"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2673 AGTGTGTGTGGGTGAAATGGA 2693
              | | ||| ||| |||||||||
Db         21 ACTTTGTATGGCTGAAATGGA 1


RESULT 2588
AX708078
LOCUS       AX708078                  22 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 14 from Patent WO03014387.
ACCESSION   AX708078
VERSION     AX708078.1  GI:29564029
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wojnowski,L. and Presecan-Siedel,E.
  TITLE     Polymorphisms in the human gene for cyp1a2 and their use in
            diagnostic and therapeutic applications
  JOURNAL   Patent: WO 03014387-A 14 20-FEB-2003;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1675 CCTGGACTTCTTAGTTGTTTC 1695
              ||||| | || |||||| |||
Db          2 CCTGGCCATCCTAGTTGATTC 22


RESULT 2589
AX763895/c
LOCUS       AX763895                  22 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 50 from Patent WO03040407.
ACCESSION   AX763895
VERSION     AX763895.1  GI:32258257
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ruiz,P., Grzweskowiak,R., Drungowski,M., Witt,H., Osterziel,K.,
            Perrot,A. and Saleh,A.
  TITLE     Novel markers for cardiopathies
  JOURNAL   Patent: WO 03040407-A 50 15-MAY-2003;
            MAX-PLANCK-GESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer ZASP_R"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        753 GTCCCATTTCCATGACCAAGA 773
              |||||||| ||||  ||| ||
Db         21 GTCCCATTCCCATCTCCACGA 1


RESULT 2590
AX798061
LOCUS       AX798061                  22 bp    DNA     linear   PAT 08-OCT-2003
DEFINITION  Sequence 5 from Patent WO03054182.
ACCESSION   AX798061
VERSION     AX798061.1  GI:37604345
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Karatzas,C., Huang,Y.J. and Lazaris,A.
  TITLE     Production of butyrylcholinesterases in transgenic mammals
  JOURNAL   Patent: WO 03054182-A 5 03-JUL-2003;
            Nexia Biotechnologies, Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer Acb710"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2598 TGAAACTCTCTGTTCAGAAAG 2618
              || |||||||| |  ||||||
Db          2 TGTAACTCTCTTTGGAGAAAG 22


RESULT 2591
BD133307/c
LOCUS       BD133307                  22 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Process for producing threonine and isoleucine.
ACCESSION   BD133307
VERSION     BD133307.1  GI:23228252
KEYWORDS    JP 2002051787-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Miyata,Y., Nakai,Y., Nakanishi,K., Ito,H., Kojima,H. and
            Kurahashi,O.
  TITLE     Process for producing threonine and isoleucine
  JOURNAL   Patent: JP 2002051787-A 5 19-FEB-2002;
            AJINOMOTO CO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002051787-A/5
            PD   19-FEB-2002
            PF   11-AUG-2000 JP 2000244921
            PI   YURI MIYATA,YUTA NAKAI,KAZUO NAKANISHI,HISAO ITO,HIROYUKI  PI
             KOJIMA,
            PI   OSAMU KURAHASHI
            PC
            C12N15/09,C12N1/21,C12N9/02,C12N9/18,C12N9/88,C12P13/06,C12P13/ PC
             08//
            PC   (C12N1/21,C12R1:19),(C12P13/06,C12R1:19),(C12P13/08,C12R1:19),
            PC   C12N15/00
            CC   Description of Artificial Sequence:primer
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
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              ||| |||||| ||||| || |
Db          2 TTTCTTTCTCTTTTTTCTTCT 22


RESULT 2583
AX370701/c
LOCUS       AX370701                  22 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 5 from Patent EP1179597.
ACCESSION   AX370701
VERSION     AX370701.1  GI:19168858
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Miyata,Y., Nakai,Y., Nakanishi,K., Ito,H., Kojima,H. and
            Kurahashi,O.
  TITLE     Method for producing threonine and isoleucine
  JOURNAL   Patent: EP 1179597-A 5 13-FEB-2002;
            Ajinomoto Co., Ltd. (JP)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2352 GTTCTGTATTTTAAGAAACAG 2372
              || ||| || || ||||||||
Db         22 GTCCTGAATCTTGAGAAACAG 2

RESULT 2584
AX380339
LOCUS       AX380339                  22 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 22 from Patent WO0198514.
ACCESSION   AX380339
VERSION     AX380339.1  GI:19575303
KEYWORDS    .
SOURCE      Feline leukemia virus
  ORGANISM  Feline leukemia virus
            Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
REFERENCE   1
  AUTHORS   Roth,M.J. and Bupp,K.
  TITLE     Targeting viral vectors to specific cells
  JOURNAL   Patent: WO 0198514-A 22 27-DEC-2001;
            UNIVERSITY OF MEDICINE AND DENTISTRY OF NEW JERSEY (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Feline leukemia virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11768"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1614 GGAAGAGTTTGTTACCTACCT 1634
              ||| ||||||  ||||||| |
Db          2 GGAGGAGTTTTATACCTACAT 22


RESULT 2585
AX488277
LOCUS       AX488277                  22 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 5577 from Patent WO02053728.
ACCESSION   AX488277
VERSION     AX488277.1  GI:22322357
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 5577 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Candida albicans"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:5476"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2479 CTTTTAATGGTGATGGGGTAA 2499
              | | ||||| ||| |||||||
Db          2 CGTATAATGCTGACGGGGTAA 22


RESULT 2586
AX601153/c
LOCUS       AX601153                  22 bp    DNA     linear   PAT 17-FEB-2003
DEFINITION  Sequence 248 from Patent WO02092851.
ACCESSION   AX601153
VERSION     AX601153.1  GI:28401226
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Binns,M.M. and Swinburne,J.E.
  TITLE     Genetic typing
  JOURNAL   Patent: WO 02092851-A 248 21-NOV-2002;
            ANIMAL HEALTH TRUST (GB) ; The British Horseracing Board (GB)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2412 GGGGTCTGTAAATACTGGTGC 2432
              || |||| |||| | ||||||
Db         21 GGAGTCTATAAACATTGGTGC 1


RESULT 2587
AX686594/c
LOCUS       AX686594                  22 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 150 from Patent WO02057450.
ACCESSION   AX686594
VERSION     AX686594.1  GI:29372201
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Edinger,S., Macdougall,J.R., Millet,I., Ellerman,K., Stone,D.J.,
            Gerlach,V., Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Rieger,D.,
            Burgess,C.E., Casman,S.J., Spytek,K.A., Boldog,F.L., Li,L.,
            Padigaru,M., Mishra,V., Patturajan,M., Shenoy,S., Rastelli,L.,
            Tchernev,V.T., Vernet,C.A., Zerhusen,B.D., Malyankar,U.M., Guo,Y.,
            Miller,C.E. and Gangolli,E.A.
  TITLE     Proteins and nucleic acids encoding same
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  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 6649742-A 58 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGCGGGT 252
              ||||||||||| |||  || |
Db         22 CAGCAATGGGATTCCATGGCT 2


RESULT 2579
AX040633/c
LOCUS       AX040633                 22 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 10 from Patent WO0064480.
ACCESSION   AX040633
VERSION     AX040633.1  GI:11340361
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bicknell,R. and Zhan,H.T.
  TITLE     Treatment, imaging and diagnosis of disease using an agent which b
            inds alfa5-integrin
  JOURNAL   Patent: WO 0064480-A 10 02-NOV-2000;
            IMPERIAL CANCER RESEARCH TECHNOLOGY LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR Primer"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2546 AGAATTAAGAGGATGCTGGGC 2566
              ||| | |||| |||| |||||
Db         21 AGACTGAAGAAGATGTTGGGC 1


RESULT 2580
AX058985/c
LOCUS       AX058985                 22 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 24 from Patent WO0075326.
ACCESSION   AX058985
VERSION     AX058985.1  GI:12311255
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Auernhammer,C.J. and Shlomo,M.
  TITLE     Suppressor of cytokine signaling (socs)-3 promoter and methods for
            its use
  JOURNAL   Patent: WO 0075326-A 24 14-DEC-2000;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PRIMER"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2100 CAAACGGGGGCCTTCTGGTTT 2120
              || || |||||| || |||||
Db         22 CAGACTGGGGCCCTCGGGTTT 2


RESULT 2581
AX267016
LOCUS       AX267016                 22 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 5 from Patent WO0173001.
ACCESSION   AX267016
VERSION     AX267016.1  GI:16515801
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Seidman,M.M. and Majumdar,A.
  TITLE     Establishment of cellular manipulations which enhance
            oligo-mediated gene targeting
  JOURNAL   Patent: WO 0173001-A 5 04-OCT-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic"
     misc_feature    5. .6
                     /note="The residue between C at position 5 and T at
                     position 6 is pyrene"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTT 2175
              ||| |||||| ||||| || |
Db          2 TTTCTTTCTCTTTTTTCTTCT 22


RESULT 2582
AX267017
LOCUS       AX267017                 22 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 6 from Patent WO0173001.
ACCESSION   AX267017
VERSION     AX267017.1  GI:16515802
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Seidman,M.M. and Majumdar,A.
  TITLE     Establishment of cellular manipulations which enhance
            oligo-mediated gene targeting
  JOURNAL   Patent: WO 0173001-A 6 04-OCT-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic"
     misc_feature    5. .6
                     /note="The residue between C at position 5 and T at
                     position 6 is acridi ne"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTT 2175
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REFERENCE   1  (bases 1 to 22)
  AUTHORS   Auernhammer,C.J. and Melmed,S.
  TITLE     Suppressor of cytokine signaling (SOCS)-3 promoter and methods for
            its use in genetic therapy in humans
  JOURNAL   Patent: US 6541244-A 24 01-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2100 CAAACGGGGGCCTTCTGGTTT 2120
              || || |||||| || |||||
Db         22 CAGACTGGGGCCCTCGGGTTT 2


RESULT 2574
AR368003/c
LOCUS       AR368003                 22 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 58 from patent US 6376217.
ACCESSION   AR368003
VERSION     AR368003.1  GI:34601514
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D. and Carroll,S.F.
  TITLE     Fusion proteins and polynucleotides encoding gelonin sequences
  JOURNAL   Patent: US 6376217-A 58 23-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGCGGGT 252
              |||||||||| ||| || |
Db         22 CAGCAATGGGATTCCATGGCT 2


RESULT 2575
AR399102
LOCUS       AR399102                 22 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1483 from patent US 6617438.
ACCESSION   AR399102
VERSION     AR399102.1  GI:40137500
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Oligoribonucleotides with enzymatic activity
  JOURNAL   Patent: US 6617438-A 1483 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        245 CCGCGGGTCCCCCACCTCTCC 265
              ||||||||  | ||||| |||
Db          2 CCGCGGGTTGCACACCTTTCC 22


RESULT 2576
AR409904
LOCUS       AR409904                 22 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 17 from patent US 6635422.
ACCESSION   AR409904
VERSION     AR409904.1  GI:40161039
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 17 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| |||| | | |||||
Db          1 TTTTTTATTTTCTGTATTTTT 21


RESULT 2577
AR409906
LOCUS       AR409906                 22 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 19 from patent US 6635422.
ACCESSION   AR409906
VERSION     AR409906.1  GI:40161041
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 19 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||| |||| | | |||||
Db          1 TTTTTTATTTTCTGTATTTTT 21


RESULT 2578
AR430984/c
LOCUS       AR430984                 22 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 58 from patent US 6649742.
ACCESSION   AR430984
VERSION     AR430984.1  GI:40192815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Bernhard,S.L., Better,M.D., Carroll,S.F., Lane,J.A. and Lei,S.-P.
  TITLE     Materials comprising and methods of preparation and use for
            ribosome-inactivating proteins
  JOURNAL   Patent: US 5416202-A 60 16-MAY-1995;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGCGGGT 252
              ||||||||||| |||  || |
Db         22 CAGCAATGGGATTCCATGGCT 2


RESULT 2569
I29984
LOCUS       I29984                  22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 16 from patent US 5578493.
ACCESSION   I29984
VERSION     I29984.1  GI:1820775
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Gilliam,T.Conrad. and Tanzi,R.E.
  TITLE     Wilson's disease gene
  JOURNAL   Patent: US 5578493-A 16 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        346 TCCCCCTCCCTACCAGCAGCT 366
              |||||||| | || ||| ||
Db          2 TCCCCCTCCTTGCCTGCAACT 22


RESULT 2570
I40519/c
LOCUS       I40519                  22 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 58 from patent US 5621083.
ACCESSION   I40519
VERSION     I40519.1  GI:2082811
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 5621083-A 58 15-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGCGGGT 252
              ||||||||||| |||  || |
Db         22 CAGCAATGGGATTCCATGGCT 2


RESULT 2571
AR217804
LOCUS       AR217804                22 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 4 from patent US 6416988.
ACCESSION   AR217804
VERSION     AR217804.1  GI:23317687
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Conklin,D.C., Yamamoto,G., Jaspers,S.R. and Gao,Z.
  TITLE     Beta-1,3-galactosyltransferase homologs
  JOURNAL   Patent: US 6416988-A 4 09-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        793 TCAGAAGGAGCTGGTGGGGGC 813
              ||||| |||||||  || |||
Db          2 TCAGAGGGAGCTGAGGGAGGC 22


RESULT 2572
AR287112
LOCUS       AR287112                22 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1484 from patent US 6528640.
ACCESSION   AR287112
VERSION     AR287112.1  GI:29724708
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
            Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
  TITLE     Synthetic ribonucleic acids with RNAse activity
  JOURNAL   Patent: US 6528640-A 1484 04-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        245 CCGCGGGTCCCCCACCTCTCC 265
              ||||||||  | ||||| |||
Db          2 CCGCGGGTTGCACACCTTTCC 22


RESULT 2573
AR302530/c
LOCUS       AR302530                22 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 24 from patent US 6541244.
ACCESSION   AR302530
VERSION     AR302530.1  GI:31690827
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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```
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Sato,T.
  TITLE     TREX, a novel gene of TRAF-interacting EXT gene family and
            diagnostic and therapeutic uses thereof
  JOURNAL   Patent: JP 2002525126-A 22 13-AUG-2002;
            THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT     OS   Linear
            PN   JP 2002525126-A/22
            PD   13-AUG-2002
            PF   17-SEP-1999 JP 2000572406
            PR   17-SEP-1998 US    09/156191
            PI   TAKAAKI SATO
            PC
            C12N15/09,A61K31/711,A61K39/395,A61K39/395,A61K45/00,A61K48/00, PC
             A61P35/00,
            PC   A61P35/04,A61P37/02,C07K14/47,C07K16/18,C12P21/02,C12Q1/68, PC
              G01N33/15,
            PC
            G01N33/50,G01N33/566,G01N33/574//C12P21/08,(C12P21/02,C12R1:91) PC
             ,C12N15/00
            CC   TREX, a novel gene of TRAF-interacting EXT gene family and  CC
                      diagnostic and
            CC   therapeutic uses thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Linear'.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1469 CCAGCTGATTCTAACAAAACC 1489
              |||||| || || ||| ||||
Db         21 CCAGCTAATACTGACAGAACC 1


RESULT 2566
BD264571
LOCUS       BD264571                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Beta-1,3-galactosyltransferase homologs.
ACCESSION   BD264571
VERSION     BD264571.1  GI:33074339
KEYWORDS    JP 2002531131-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Conklin,D.C., Yamamoto,G., Jaspers,S.R. and Gao,Z.
  TITLE     Beta-1,3-galactosyltransferase homologs
  JOURNAL   Patent: JP 2002531131-A 3 24-SEP-2002;
            ZYMOGENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002531131-A/3
            PD   24-SEP-2002
            PF   10-DEC-1999 JP 2000586918
            PR   10-DEC-1998 US    09/208970
            PI   DARRELL C CONKLIN,GAYLE YAMAMOTO,STEPHEN R JASPERS,ZEREN GAO
            PC   C12N15/09,A61K38/00,A61P1/00,A61P1/18,A61P3/10,A61P35/00, PC
            A61P37/02,
            PC   C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/06,C12N5/10,C12N9/
            PC   10,C12P21/08,
            PC   C12Q1/48,G01N33/15,G01N33/50,G01N33/53,G01N33/577,C12N15/00,
            PC   C12N5/00,
            PC   C12N5/00,A61K37/02
            CC   Oligonucleotide primer, ZC18227
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.

FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        793 TCAGAAGGAGCTGGTGGGGGC 813
              ||||| ||||||| || |||
Db          2 TCAGAGGGAGCTGAGGGAGGC 22


RESULT 2567
E10721/c
LOCUS       E10721                    22 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer for gaining part of ilvGMEDA operon.
ACCESSION   E10721
VERSION     E10721.1  GI:22027814
KEYWORDS    JP 1996047397-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hashiguchi,K., Kishino,H., Tsujimoto,N. and Matsui,Y.
  TITLE     PRODUCTION OF L-ISOLEUCINE BY FERMENTATION METHTOD
  JOURNAL   Patent: JP 1996047397-A 4 20-FEB-1996;
            AJINOMOTO CO INC
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996047397-A/4
            PD   20-FEB-1996
            PF   26-MAY-1995 JP 1995127990
            PR   30-MAY-1994 JP 94P   116340
            PI   HASHIGUCHI KENICHI, KISHINO HIROKO, TSUJIMOTO NOBUHARU, PI
            MATSUI YUTAKA
            PC   C12P13/06,C12N1/21,C12N9/06,C12N9/12,C12N15/09,(C12P13/06, PC
             C12R1:19),
            PC   (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N15/09,C12R1:19);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .22
            FT                   /organism='Artificial sequences' FT
            misc_feature    1. .22
            FT                   /note='PCR primer for gaining fragment B which
             FT                   is part of
            FT                   ilvGMEDA operon'.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2352 GTTCTGTATTTTAAGAAACAG 2372
              || ||| || || ||||||||
Db         22 GTCCTGAATCTTGAGAAACAG 2


RESULT 2568
I11948/c
LOCUS       I11948                    22 bp    DNA     linear   PAT 26-JUL-1995
DEFINITION  Sequence 60 from Patent US 5416202.
ACCESSION   I11948
VERSION     I11948.1  GI:909391
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D. and Carroll,S.F.
  TITLE     Proteins encoding gelonin sequences
  JOURNAL   Patent: US 6146850-A 58 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGCGGGT 252
              ||||||||||| |||  || |
Db         22 CAGCAATGGGATTCCATGGCT 2


RESULT 2562
AR178553/c
LOCUS       AR178553                 22 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 10 from patent US 6319696.
ACCESSION   AR178553
VERSION     AR178553.1  GI:20219691
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kishino,H., Izui,M., Ono,Y., Ito,H. and Kurahashi,O.
  TITLE     Process for producing L-amino acids
  JOURNAL   Patent: US 6319696-A 10 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2352 GTTCTGTATTTTAAGAAACAG 2372
              || ||| || || ||||||||
Db         22 GTCCTGAATCTTGAGAAACAG 2


RESULT 2563
BD230926
LOCUS       BD230926                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Total genome radiation hybrid map of canine genome and its use for
            identification of interesting genes.
ACCESSION   BD230926
VERSION     BD230926.1  GI:33040696
KEYWORDS    JP 2002530091-A/795.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Galibert,F. and Andre,C.
  TITLE     Total genome radiation hybrid map of canine genome and its use for
            identification of interesting genes
  JOURNAL   Patent: JP 2002530091-A 795 17-SEP-2002;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
COMMENT     OS   Canis familiaris (dog)
            PN   JP 2002530091-A/795
            PD   17-SEP-2002
            PF   15-NOV-1999 JP 2000582596
            PR   13-NOV-1998 US    60/108193
            PI   FRANCIS GALIBERT,CATHERINE ANDRE
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   FH2347
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Canis familiaris (dog)'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        829 TGAGGTCTTCTGCTCAGTCCC 849
              | || ||||||| || |||||
Db          1 TTAGCTCTTCTGATCTGTCCC 21


RESULT 2564
BD235583/c
LOCUS       BD235583                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Formation of modified molecule having elevated serum half life.
ACCESSION   BD235583
VERSION     BD235583.1  GI:33045353
KEYWORDS    JP 2002522063-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Gallo,M., Junghans,R. and Foord,O.
  TITLE     Formation of modified molecule having elevated serum half life
  JOURNAL   Patent: JP 2002522063-A 5 23-JUL-2002;
            ABGENIX INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002522063-A/5
            PD   23-JUL-2002
            PF   17-AUG-1999 JP 2000565006
            PR   17-AUG-1998 US    60/096868
            PI   MICHAEL GALLO,RICHARD JUNGHANS,ORIT FOORD
            PC   C12N15/02,A61K39/395,A61K39/395,A61K39/395,A61K39/395,A61P43/
            PC   00,C07K16/24,
            PC   C12P21/08,C12N15/00
            CC   Description of Artificial Sequence: PCR Primer FH   Key
                 Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        508 GCCCTCGCACCACGGGCGCCC 528
              |||||||||| || | | ||
Db         22 GCCCTCGCACCCCGTGGGTCC 2


RESULT 2565
BD243946/c
LOCUS       BD243946                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  TREX, a novel gene of TRAF-interacting EXT gene family and
            diagnostic and therapeutic uses thereof.
ACCESSION   BD243946
VERSION     BD243946.1  GI:33053716
KEYWORDS    JP 2002525126-A/22.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
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DEFINITION  Sequence 58 from patent US 5756699.
ACCESSION   AR010102
VERSION     AR010102.1  GI:3968907
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 5756699-A 58 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGCGGGT 252
              ||||||||||| |||  || |
Db         22 CAGCAATGGGATTCCATGGCT 2


RESULT 2557
AR029876
LOCUS       AR029876                 22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 65 from patent US 5861244.
ACCESSION   AR029876
VERSION     AR029876.1  GI:5943090
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 65 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTTTTTTT 2178
              |||||| || ||||| ||| |
Db          2 TTTTCTTCTCTTTTTATTTCT 22


RESULT 2558
AR055308/c
LOCUS       AR055308                 22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 58 from patent US 5837491.
ACCESSION   AR055308
VERSION     AR055308.1  GI:5980885
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Polynucleotides encoding gelonin sequences
  JOURNAL   Patent: US 5837491-A 58 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGCGGGT 252
              ||||||||||| |||  || |
Db         22 CAGCAATGGGATTCCATGGCT 2


RESULT 2559
AR092611/c
LOCUS       AR092611                 22 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 6 from patent US 5998178.
ACCESSION   AR092611
VERSION     AR092611.1  GI:10019364
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hashiguchi,K.-i., Kishino,H., Tsujimoto,N. and Matsui,H.
  TITLE     L-isoleucine-producing bacterium and method for preparing
            L-isoleucine through fermentation
  JOURNAL   Patent: US 5998178-A 6 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2352 GTTCTGTATTTTAAGAAACAG 2372
              || ||| || || ||||||||
Db         22 GTCCTGAATCTTGAGAAACAG 2


RESULT 2560
AR141237/c
LOCUS       AR141237                 22 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 58 from patent US 6146631.
ACCESSION   AR141237
VERSION     AR141237.1  GI:15100754
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 6146631-A 58 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGCGGGT 252
              ||||||||||| |||  || |
Db         22 CAGCAATGGGATTCCATGGCT 2


RESULT 2561
AR141474/c
LOCUS       AR141474                 22 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 58 from patent US 6146850.
ACCESSION   AR141474
VERSION     AR141474.1  GI:15100990
KEYWORDS    .
SOURCE      Unknown.
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          derived sequences were removed. Information to order the
          corresponding mutant line and a link to a database providing a
          graphical display of the insertion site are available at
          http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
          been generated in the framework of the French plant genomics
          program 'Genoplante' (http://www.genoplante.com and
          http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="097A05"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .21
                     /note="T-DNA flanking sequence
                     left border"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2731 AAATAATTGTTGTGTGTATGA 2751
              |||||| || ||| ||||| |
Db         21 AAATAAATGATGTATGTATAA 1


RESULT 2553
AB015844
LOCUS       AB015844                 21 bp    mRNA    linear   ROD 27-MAR-2002
DEFINITION  Mus musculus mRNA for T cell receptor (TCR) beta chain (CDR3
            region), partial cds.
ACCESSION   AB015844
VERSION     AB015844.1  GI:3986238
KEYWORDS    T cell receptor (TCR) beta chain.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Sai,T., Mine,M., Fukuoka,M., Koarada,S. and Kimoto,M.
  TITLE     A mutational analysis of the Abetaz/Aalphad major
            histocompatibility complex class II molecule that restricts
            autoreactive T cells in (NZBxNZW)F1 mice. The critical influence of
            alanine at position 69 in the Aalphad chain
  JOURNAL   Immunology 96 (3), 325-332 (1999)
  MEDLINE   99250309
   PUBMED   10233712
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Kimoto,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1998) Masao Kimoto, Saga Medical School,
            Department of Immunology; Nabeshima 5-1-1, Saga, Saga 849-8501,
            Japan (E-mail:kimoto@post.saga-med.ac.jp, Tel:0952-34-2255,
            Fax:0952-34-2049)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /cell_type="T cell"
                     /tissue_type="lymph node"
     CDS             <1. .>21
                     /note="CDR3 region; a part of an beta chain comprising
                     BV4S1, CDR3 and J beta 2.3"
                     /codon_start=1
                     /product="T cell receptor (TCR) beta chain"
                     /protein_id="BAA34968.1"
                     /db_xref="GI:3986239"
                     /db_xref="IMGT/LIGM:AB015844"
                     /translation="SQEGLGL"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        488 AGCCAGGAGGGAGCGGGGCTG 508
              ||||| |||||| ||| |||
Db          1 AGCCAAGAGGGACTGGGCCTG 21


RESULT 2554
A63568
LOCUS       A63568                   22 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 9 from Patent WO9720924.
ACCESSION   A63568
VERSION     A63568.1  GI:3717223
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Scaggiante,B. and Quadrifoglio,F.
  TITLE     A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMOURAL
            AGENTS
  JOURNAL   Patent: WO 9720924-A 9 12-JUN-1997;
            SAICOM S R L (IT)
COMMENT     Other publication IT MI952539 19970604
            Other publication AU 1175497 19970627.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              || || ||||| |||| ||||
Db          2 TTGTTGTTTTTGTTTTGTTTT 22


RESULT 2555
AR003766/c
LOCUS       AR003766                 22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 58 from patent US 5744580.
ACCESSION   AR003766
VERSION     AR003766.1  GI:3965025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Better,M.D., Carroll,S.F. and Studnicka,G.M.
  TITLE     Immunotoxins comprising ribosome-inactivating proteins
  JOURNAL   Patent: US 5744580-A 58 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGCGGGT 252
              |||||||||||| |||  || |
Db         22 CAGCAATGGGATTCCATGGCT 2


RESULT 2556
AR010102/c
LOCUS       AR010102                 22 bp    DNA     linear   PAT 04-DEC-1998
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                  | ||| |||||| || |||||
Db          1 GATGGCCAAGATGGGCTTGAA 21


RESULT 2550
BD081038
LOCUS       BD081038                 21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Coding sequence haplotypes of the human BRCA2 gene.
ACCESSION   BD081038
VERSION     BD081038.1  GI:22626641
KEYWORDS    JP 2001514887-A/46.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Murphy,P.D., White,M.B., Rabin,M.B., Olson,S.J., Yoshikawa,M.,
            Jackson,G.M., Eskandari,T., Schryer,B. and Park,M.
  TITLE     Coding sequence haplotypes of the human BRCA2 gene
  JOURNAL   Patent: JP 2001514887-A 46 18-SEP-2001;
            ONCORMED INC
COMMENT     OS   Unidentified
            PN   JP 2001514887-A/46
            PD   18-SEP-2001
            PF   14-AUG-1998 JP 2000509828
            PR   15-AUG-1997 US    60/055784,07-NOV-1997 US    60/064926 PR
            12-NOV-1997 US    60/065367,01-MAY-1998 US    09/071715 PR
            22-MAY-1998 US    09/084471
            PI   PATRICIA D MURPHY,MARGA B WHITE,MARK B RABIN,SHERI J OLSON, PI
              MATTHEW YOSHIKAWA,GEOFFREY M JACKSON,TARA ESKANDARI,BRENDA  PI
            SCHRYER,
            PI   MICHAEL PARK
            PC   C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00,C07K14/47,
            PC   C07K16/18,
            PC
            C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68//C12P21/02,C12P21/ PC
             08,
            PC   C12N15/00,A61K37/02,C12N5/00
            CC   11IF primer
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1401 TGCAGAACTACATCAAAGAAG 1421
              |||||| |||||| || |||
Db          1 TGCAGAGGTACATCCAATAAG 21


RESULT 2551
ATH525271/c
LOCUS       ATH525271                21 bp    DNA     linear   PLN 29-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            092B08.
ACCESSION   AJ525271
VERSION     AJ525271.1  GI:26793507
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="092B08"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .21
                     /note="T-DNA flanking sequence
                     left border"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2731 AAATAATTGTTGTGTGTATGA 2751
              |||||| || ||| ||||| |
Db         21 AAATAAATGATGTATGTATAA 1


RESULT 2552
ATH525445/c
LOCUS       ATH525445                21 bp    DNA     linear   PLN 29-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            097A05.
ACCESSION   AJ525445
VERSION     AJ525445.1  GI:26793681
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
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  Query Match              0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTT 2185
              || ||||| | ||||| ||||
Db          1 CTATTTTTCTATTTTTCTTTT 21


RESULT 2546
AX539546/c
LOCUS       AX539546                  21 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 333 from Patent WO02059142.
ACCESSION   AX539546
VERSION     AX539546.1  GI:25273063
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
  TITLE     Polymorphisms in the human gene for the multidrug
            resistance-associated protein 1 (mrp-1) and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 02059142-A 333 01-AUG-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        289 CCCCGCGCCACCCCTCTCCCA 309
              |||||||||| |||   ||||
Db         21 CCCCGCGCCATCCCCACCCCA 1


RESULT 2547
AX539547
LOCUS       AX539547                  21 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 334 from Patent WO02059142.
ACCESSION   AX539547
VERSION     AX539547.1  GI:25273064
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
  TITLE     Polymorphisms in the human gene for the multidrug
            resistance-associated protein 1 (mrp-1) and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 02059142-A 334 01-AUG-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        289 CCCCGCGCCACCCCTCTCCCA 309
              |||||||||| |||   ||||
Db          1 CCCCGCGCCATCCCCACCCCA 21


RESULT 2548
AX718122/c
LOCUS       AX718122                  21 bp    DNA     linear   PAT 15-APR-2003
DEFINITION  Sequence 380 from Patent WO02081518.
ACCESSION   AX718122
VERSION     AX718122.1  GI:29890882
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Pena,C.E., Shimkets,R.A., Li,L., Shenoy,S.G., Kekuda,R.,
            Spytek,K.A., Vernet,C.A., Malyankar,U.L., Guo,X., Gusev,V.Y.,
            Casman,S.J., Boldog,F.L., Furtak,K., Tchernev,V.T., Patturajan,M.,
            Gangolli,E.A., Padigaru,M., Liu,X., Baumgartner,J.C., Gerlach,V.L.,
            Spaderna,S.K. and Zerhusen,B.D.
  TITLE     Proteins, polynucleotides encoding them and methods of using the
            same
  JOURNAL   Patent: WO 02081518-A 380 17-OCT-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR Primer Sequence"

  Query Match              0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        827 ACTGAGGTCTTCTGCTCAGTC 847
              |||| |||  ||| |||||||
Db         21 ACTGTGGTGCTCTCCTCAGTC 1


RESULT 2549
BD057322
LOCUS       BD057322                  21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Peptide having a function regulating transcription of gene.
ACCESSION   BD057322
VERSION     BD057322.1  GI:22602928
KEYWORDS    JP 2001269178-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Takagi,M., Shinji,H. and Ota,K.
  TITLE     Peptide having a function regulating transcription of gene
  JOURNAL   Patent: JP 2001269178-A 2 02-OCT-2001;
            AGENCY OF IND SCIENCE & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2001269178-A/2
            PD   02-OCT-2001
            PF   27-MAR-2000 JP 2000087556
            PI   MASARU TAKAGI,HIDEAKI SHINJI,KEN OTA
            PC   C12N15/09,C07K14/415,C12N1/15,C12N1/19,C12N1/21,C12N5/10// PC
             C12P21/02,
            PC   C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: Synthetic primer DNA FH
            Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1009 GTTGGACAAGATCGGGTTGAA 1029
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RESULT 2541
AR429681
LOCUS       AR429681                  21 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 24 from patent US 6645736.
ACCESSION   AR429681
VERSION     AR429681.1  GI:40189999
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Jones,S. and Tang,J.
  TITLE     Calcium independent cytosolic phospholipase A2/B enzymes
  JOURNAL   Patent: US 6645736-A 24 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1283 CATGGGACCAGCAGGCTCGCC 1303
              ||||||||| || ||||  ||
Db          1 CATGGGACCCGCTGGCTTTCC 21


RESULT 2542
AX023419
LOCUS       AX023419                  21 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 34 from Patent WO0014217.
ACCESSION   AX023419
VERSION     AX023419.1  GI:10183819
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lipford,G.B., Heeg,K. and Wagner,H.
  TITLE     G-motif oligonucleotides and uses thereof
  JOURNAL   Patent: WO 0014217-A 34 16-MAR-2000;
            LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;
            CPG IMMUNOPHARMACEUTICALS GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic, no natural origin"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTT 2182
              ||||| ||||||||||  | |
Db          1 CTCCTATTTTTTTTTCCTAT 21


RESULT 2543
AX032696
LOCUS       AX032696                  21 bp    DNA     linear   PAT 20-SEP-2000
DEFINITION  Sequence 142 from Patent EP1016715.
ACCESSION   AX032696
VERSION     AX032696.1  GI:10279634
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
            Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
            Wyatt,J.R.
  TITLE     Oligonucleotides having a conserved g4 core sequence
  JOURNAL   Patent: EP 1016715-A 142 05-JUL-2000;
            ISIS PHARMACEUTICALS INC (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||    ||||
Db          1 TTTTTTTTTTTTTGGGGTTTT 21


RESULT 2544
AX154462/c
LOCUS       AX154462                  21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 560 from Patent WO0138576.
ACCESSION   AX154462
VERSION     AX154462.1  GI:14536076
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0138576-A 560 31-MAY-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        139 GCGACTGTTTTGGGGGACGCC 159
              ||| |||||  |||||||| |
Db         21 GCGGCTGTTGSGGGGGACGTC 1


RESULT 2545
AX521617
LOCUS       AX521617                  21 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 123 from Patent WO0222874.
ACCESSION   AX521617
VERSION     AX521617.1  GI:23572664
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Utermohlen,J.G. and Connaughton,J.
  TITLE     Oligonucleotides for labeling oligonucleotide probes and proteins
  JOURNAL   Patent: WO 0222874-A 123 21-MAR-2002;
            VENTANA MEDICAL SYSTEMS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide probe"
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  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||    ||||
Db          1 TTTTTTTTTTTTTGGGGTTTT 21


RESULT 2536
AR083394
LOCUS       AR083394                 21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 24 from patent US 5976854.
ACCESSION   AR083394
VERSION     AR083394.1  GI:10010184
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Jones,S. and Tang,J.
  TITLE     Calcium independent cytosolic phospholipase A.sub.2 /B enzymes
  JOURNAL   Patent: US 5976854-A 24 02-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1283 CATGGGACCAGCAGGCTCGCC 1303
              ||||||||| || ||||  ||
Db          1 CATGGGACCCGCTGGCTTTCC 21


RESULT 2537
AR164503
LOCUS       AR164503                 21 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 24 from patent US 6274140.
ACCESSION   AR164503
VERSION     AR164503.1  GI:16237552
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Jones,S. and Tang,J.
  TITLE     Calcium independent cytosolic phospholipase A2/B enzymes
  JOURNAL   Patent: US 6274140-A 24 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1283 CATGGGACCAGCAGGCTCGCC 1303
              ||||||||| || ||||  ||
Db          1 CATGGGACCCGCTGGCTTTCC 21


RESULT 2538
I21708
LOCUS       I21708                   21 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 4 from patent US 5523389.
ACCESSION   I21708
VERSION     I21708.1  GI:1602062
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Ecker,D.J., Wyatt,J.R. and Imbach,J.L.
  TITLE     Inhibitors of human immunodeficiency virus
  JOURNAL   Patent: US 5523389-A 4 04-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||    ||||
Db          1 TTTTTTTTTTTTTGGGGTTTT 21


RESULT 2539
AR241709/c
LOCUS       AR241709                 21 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 16 from patent US 6472153.
ACCESSION   AR241709
VERSION     AR241709.1  GI:27287521
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dempcy,R.O., Afonina,I.A. and Vermeulen,N.M.J.
  TITLE     Hybridization-triggered fluorescent detection of nucleic acids
  JOURNAL   Patent: US 6472153-A 16 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              ||||||| |||| || ||| |
Db         21 ATTGAAAGAAAAGAAGAAAGA 1


RESULT 2540
AR297482/c
LOCUS       AR297482                 21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 9217 from patent US 6537751.
ACCESSION   AR297482
VERSION     AR297482.1  GI:31684766
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 9217 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2674 GTGTGTGTGGGTGAAATGGAG 2694
              |||| ||||| ||| ||| ||
Db         21 GTGTATGTGGTTGAGATGAAG 1
```

```
LOCUS       AR409915                27 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 28 from patent US 6635422.
ACCESSION   AR409915
VERSION     AR409915.1  GI:40161050
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 28 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||| | ||||||
Db         24 GAAAAAAAAGAGAAAAAA 7


RESULT 2532
AX181697
LOCUS       AX181697                29 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 54 from Patent WO0146231.
ACCESSION   AX181697
VERSION     AX181697.1  GI:15133035
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burgess,C.E.
  TITLE     Novel proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0146231-A 54 28-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 29;
  Best Local Similarity   73.1%;  Pred. No. 3.9e+03;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | || | ||| |||| |||| || ||
Db          2 AAAAATAAAACAAAACAAAAGAATAA 27


RESULT 2533
AX674922
LOCUS       AX674922                21 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 49 from Patent WO03005034.
ACCESSION   AX674922
VERSION     AX674922.1  GI:29333255
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Macdonald,M.L., Zeisler,J.M., Samuels,M., Goldberg,Y.P.,
            Robataille,J.M. and Hayden,M.R.
  TITLE     Processes for identifying therapeutic agents useful in treating
            diseases involving fzd4 gene
  JOURNAL   Patent: WO 03005034-A 49 16-JAN-2003;
            Xenon Genetics, Inc. (CA) ; The University of British Columbia (CA)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCATT 1791
              ||||||||||| || | || |
Db          1 TTTTTTTTTTTCAATCACACT 21


RESULT 2534
A49016
LOCUS       A49016                  21 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 28 from Patent WO9604374.
ACCESSION   A49016
VERSION     A49016.1  GI:2302627
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Toulme,J. and Mishra,R.
  TITLE     OLIGONUCLEOTIDE RECOGNISING A NON LINEAR NUCLEIC ACID SEQUENCE,
            THERAPEUTIC APPLICATIONS THEREOF AND METHOD FOR PREPARING SAME
  JOURNAL   Patent: WO 9604374-A 28 15-FEB-1996;
            INST NAT SANTE RECH MED (FR)
COMMENT     Other publication FR 2723371 960209.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2099 TCAAACGGGGGCCTTCTGGTT 2119
              || |||||| |||| || |||
Db          1 TCTAACGGGTGCCTACTCGTT 21


RESULT 2535
AR074334
LOCUS       AR074334                21 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 142 from patent US 5952490.
ACCESSION   AR074334
VERSION     AR074334.1  GI:10001089
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
            Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
            Imbach,J.Louis.
  TITLE     Oligonucleotides having a conserved G4 core sequence
  JOURNAL   Patent: US 5952490-A 142 14-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.8e+03;
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```
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 611 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 25;
  Best Local Similarity   88.9%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
              ||  ||||||||||||||||
Db         18 TGTTAAAAAAAAAAAAAA 1


RESULT 2527
AX043647/c
LOCUS       AX043647                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1213 from Patent WO0065088.
ACCESSION   AX043647
VERSION     AX043647.1  GI:11342262
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1213 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 25;
  Best Local Similarity   88.9%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAA 2796
              ||||  | ||||||||||||
Db         18 AGAAGTAAAAAAAAAAAA 1


RESULT 2528
AX042952
LOCUS       AX042952                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 518 from Patent WO0065088.
ACCESSION   AX042952
VERSION     AX042952.1  GI:11341560
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 518 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 25;
  Best Local Similarity   88.9%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAAC 2189
              ||||||||||||| |||
Db          1 TTTTTTTTTTTTTACAAC 18


RESULT 2529
AX043374/c
LOCUS       AX043374                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 940 from Patent WO0065088.
ACCESSION   AX043374
VERSION     AX043374.1  GI:11341982
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 940 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 25;
  Best Local Similarity   88.9%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              || || ||||||||||||
Db         18 TTAAACAAAAAAAAAAAA 1


RESULT 2530
AX043481/c
LOCUS       AX043481                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1047 from Patent WO0065088.
ACCESSION   AX043481
VERSION     AX043481.1  GI:11342089
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1047 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DRB345 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 25;
  Best Local Similarity   88.9%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              || || ||||||||||||
Db         18 GAGTTCAAAAAAAAAAAA 1


RESULT 2531
AR409915/c
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/db_xref="taxon:32630"
/note="Detection primer for BAK1"

Query Match 0.5%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       340 CTACTTTCCCCCTCCCTA 357
             ||||||| ||| ||||||
Db        21 CTACTTTTCCCATCCCTA 4
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RESULT 2523
BD106467
LOCUS BD106467 22 bp DNA linear PAT 18-SEP-2002
DEFINITION Rat ST38.2 chemokine.
ACCESSION BD106467
VERSION BD106467.1 GI:23201285
KEYWORDS JP 2002500509-A/8.
SOURCE Chlamydia sp.
ORGANISM Chlamydia sp.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE 1 (bases 1 to 22)
AUTHORS Lesslauer,W. and Schneitz,U.U.
TITLE Rat ST38.2 chemokine
JOURNAL Patent: JP 2002500509-A 8 08-JAN-2002;
F HOFFMANN LA ROCHE AG
COMMENT PN JP 2002500509-A/8
PD 08-JAN-2002
PF 23-APR-1998 JP 1998546575
PR 30-APR-1997 EP 97107135.2
PI WERNER LESSLAUER,ULRIKE UTANS SCHNEITZ
PC C12N15/19,C07K14/52,C12N5/08,C12N5/10,C12Q1/68,C07K19/00, PC
C07K16/24,
PC A61K38/19,G01N33/50,G01N33/53
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'primer'
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1. .22
/organism="Chlamydia sp."
/mol_type="genomic DNA"
/db_xref="taxon:35827"

Query Match 0.5%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       611 CTGCTGCCCCACGCACAC 628
             |||||||| |||| ||||
Db         5 CTGCTGCCTCACGTACAC 22
```

RESULT 2524
BD226410/c
LOCUS BD226410 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Use of triplex structure DNA sequences for transferring nucleotide
sequences.
ACCESSION BD226410
VERSION BD226410.1 GI:33036180
KEYWORDS JP 2002512804-A/20.
SOURCE Visna virus
ORGANISM Visna virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Ovine/caprine
lentivirus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Charneau,P., Zennou,V. and Firat,H.
TITLE Use of triplex structure DNA sequences for transferring nucleotide
sequences
JOURNAL Patent: JP 2002512804-A 20 08-MAY-2002;
INSTITUT PASTEUR
COMMENT OS Visna virus
PN JP 2002512804-A/20
PD 08-MAY-2002
PF 23-APR-1999 JP 2000546035
PR 24-APR-1998 FR 98/05197
PI PIERRE CHARNEAU,VERONIQUE ZENNOU,HUESEYIN FIRAT PC
C12N15/09,A61K48/00,C12N5/10,C12N7/00//A61K35/12,C07K14/16, PC
C12N15/00,
PC C12N5/00
CC Strandedness: Double;
CC A can be T
CC G can be T
CC Sequence of double strand
FH Key Location/Qualifiers
FT misc_feature (4)
FT misc_feature (6)
FT misc_feature complement(1. .22).
FEATURES Location/Qualifiers
source 1. .22
/organism="Visna virus"
/mol_type="genomic DNA"
/db_xref="taxon:11741"

Query Match 0.5%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      2164 CCTTTTTTTTTTTTTTT 2181
             ||||| |||||| |||||
Db        18 CCTTTCTTTTTTCTTTTT 1
```

RESULT 2525
AX043291/c
LOCUS AX043291 24 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 857 from Patent WO0065088.
ACCESSION AX043291
VERSION AX043291.1 GI:11341899
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 857 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES Location/Qualifiers
source 1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DQA1 Heterozygote Primer Sequence"

Query Match 0.5%; Score 14.8; DB 1; Length 24;
Best Local Similarity 88.9%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      2779 AGAATTGAAAAAAAAAAA 2796
             ||| || ||||||||||||
Db        18 AGAGTTAAAAAAAAAAAA 1
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RESULT 2526
AX043045/c
LOCUS AX043045 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 611 from Patent WO0065088.
ACCESSION AX043045
VERSION AX043045.1 GI:11341653
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1

```
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Lesslauer,W. and Utans-Schneitz,U.
  TITLE     Chemokine
  JOURNAL   Patent: US 6537794-A 10 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 22;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        611 CTGCTGCCCCACGCACAC 628
              ||||||||| |||| ||||
Db          5 CTGCTGCCTCACGTACAC 22


RESULT 2519
AX011523/c
LOCUS       AX011523                 22 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 20 from Patent WO9955892.
ACCESSION   AX011523
VERSION     AX011523.1  GI:9998073
KEYWORDS    .
SOURCE      Visna virus
  ORGANISM  Visna virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Ovine/caprine
            lentivirus.
REFERENCE   1
  AUTHORS   Charneau,P., Firat,H. and Zennou,V.
  TITLE     Use of triplex structure dna sequences for transferring nucleotide
            sequences
  JOURNAL   Patent: WO 9955892-A 20 04-NOV-1999;
            CHARNEAU PIERRE (FR); FIRAT HUESEYIN (FR); PASTEUR INSTITUT (FR);
            ZENNOU VERONIQUE (FR)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Visna virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11741"
     misc_feature    complement(1. .22)
                     /note="Sequence a double brin"
     misc_feature    4
                     /note="A peut etre T"
     misc_feature    6
                     /note="G peut etre T"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 22;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2181
              ||||| |||||| |||||
Db         18 CCTTTCTTTTTTCTTTT 1


RESULT 2520
AX599143/c
LOCUS       AX599143                 22 bp    DNA     linear   PAT 14-FEB-2003
DEFINITION  Sequence 483 from Patent WO02077272.
ACCESSION   AX599143
VERSION     AX599143.1  GI:28399285
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pelet,C. and Ziebarth,H.
  TITLE     Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
  JOURNAL   Patent: WO 02077272-A 483 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Detection primer for BAK1"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 22;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        340 CTACTTTCCCCCTCCCTA 357
              ||||||| ||| ||||||
Db         21 CTACTTTTCCCATCCCTA 4


RESULT 2521
AX743292/c
LOCUS       AX743292                 22 bp    DNA     linear   PAT 12-MAY-2003
DEFINITION  Sequence 52 from Patent WO03029451.
ACCESSION   AX743292
VERSION     AX743292.1  GI:30577218
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zelent,A., Petrie,K. and Guidez,F.
  TITLE     Histone deacetylase 9
  JOURNAL   Patent: WO 03029451-A 52 10-APR-2003;
            The Institute of Cancer Research (GB) ; Zelent, Arthur (GB) ;
            Petrie, Kevin (GB) ; Guidez, Fabien (GB)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 22;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        919 GTCCCCACCTGAATGCTT 936
              || || ||||||||||||
Db         18 GTACCAACCTGAATGCTT 1


RESULT 2522
AX767637/c
LOCUS       AX767637                 22 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 285 from Patent WO03044226.
ACCESSION   AX767637
VERSION     AX767637.1  GI:32436242
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
            Nimmrich,I.
  TITLE     Method and nucleic acids for the analysis of a lymphoid cell
            proliferative disorder
  JOURNAL   Patent: WO 03044226-A 285 30-MAY-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        951 TGGGAGGTGTTCTCAGAAGA 970
              | | ||||||: ||||||||
Db          1 TTGAAGGTGTYTTCAGAAGA 20


RESULT 2515
AX096473
LOCUS       AX096473                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 1651 from Patent WO0118250.
ACCESSION   AX096473
VERSION     AX096473.1  GI:13512727
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1651 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         71 CGCCTGGTCACCGTGACCCC 90
              ||||||| |:||| ||| ||
Db          2 CGCCTGGACWCCGAGACTCC 21


RESULT 2516
ATH527468
LOCUS       ATH527468                21 bp    DNA     linear   PLN 29-MAR-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            140F08.
ACCESSION   AJ527468
VERSION     AJ527468.1  GI:26795728
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="140F08"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .21
                     /note="T-DNA flanking sequence
                     left border"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTT 2173
              ||||| || |||||||||
Db          3 TTTTTGCTTCTTTTTTTT 20


RESULT 2517
A83654
LOCUS       A83654                   22 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 10 from Patent WO9849309.
ACCESSION   A83654
VERSION     A83654.1  GI:6732904
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Utans-Schneitz,U. and Lesslauer,W.
  TITLE     RAT ST38.2 CHEMOKINE
  JOURNAL   Patent: WO 9849309-A 10 05-NOV-1998;
            HOFFMANN LA ROCHE (CH)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 22;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        611 CTGCTGCCCCACGCACAC 628
              |||||||| |||| ||||
Db          5 CTGCTGCCTCACGTACAC 22


RESULT 2518
AR300568
LOCUS       AR300568                 22 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 10 from patent US 6537794.
ACCESSION   AR300568
VERSION     AR300568.1  GI:31688073
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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Qy       1282 CCATGGGACCAGCAGGCT 1299
              ||||||| ||| ||||||
Db         19 CCATGGGTCCACCAGGCT 2


RESULT 2510
A96974/c
LOCUS       A96974                    21 bp    DNA     linear   PAT 26-JAN-2000
DEFINITION  Sequence 52 from Patent WO9922023.
ACCESSION   A96974
VERSION     A96974.1  GI:6780415
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Epping,B. and Leiser,M.
  TITLE     METHOD FOR IDENTIFYING MICRO-ORGANISMS
  JOURNAL   Patent: WO 9922023-A 52 06-MAY-1999;
            MIRA DIAGNOSTICA GMBH (DE); EPPING BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        168 TGTTGTGGAAAATAACCG 185
              ||||||||  ||||||||
Db         21 TGTTGTGGTTAATAACCG 4


RESULT 2511
AR080176/c
LOCUS       AR080176                  21 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 109 from patent US 5968734.
ACCESSION   AR080176
VERSION     AR080176.1  GI:10006911
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Aurias,A., Delattre,O., Desmaze,C., Melot,T., Peter,M.,
            Plougastel,B., Thomas,G. and Zucman,J.
  TITLE     Nucleic acid corresponding to a gene of chromosome 22 involved in
            recurrent chromosomal translocations associated with the
            development of cancerous tumors, and nucleic acids of fusion
            resulting from said translocations
  JOURNAL   Patent: US 5968734-A 109 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1282 CCATGGGACCAGCAGGCT 1299
              ||||||| ||| ||||||
Db         19 CCATGGGTCCACCAGGCT 2


RESULT 2512
AR364260
LOCUS       AR364260                  21 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 1 from patent US 5256775.
ACCESSION   AR364260
VERSION     AR364260.1  GI:34426645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Froehler,B.C.
  TITLE     Exonuclease-resistant oligonucleotides
  JOURNAL   Patent: US 5256775-A 1 26-OCT-1993;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTT 2167
              | ||||||||||||||| |
Db          4 AGTGATTTTTTTCTCCAT 21


RESULT 2513
AX094992/c
LOCUS       AX094992                  21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 170 from Patent WO0118250.
ACCESSION   AX094992
VERSION     AX094992.1  GI:13511195
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 170 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         26 GTGACCCGGACAGCAAGGCC 45
              ||| || ||:|||| |||||
Db         20 GTGTCCTGGMCAGCCAGGCC 1


RESULT 2514
AX095108
LOCUS       AX095108                  21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 286 from Patent WO0118250.
ACCESSION   AX095108
VERSION     AX095108.1  GI:13511311
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 286 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
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  TITLE     Method for identifying/detecting eucaryote with II type
            topoisomerase gene as indication
  JOURNAL   Patent: JP 2000125873-A 2 09-MAY-2000;
            MARINE BIOTECHNOLOGY INST CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000125873-A/2
            PD   09-MAY-2000
            PF   24-SEP-1998 JP 1998270337
            PR
            PI   SATOSHI YAMAMOTO,MIKA ATAMI,HIROAKI KASAI,SACHIKO NAKAMURA, PI
              TORU HAMADA
            PC   C12N15/09,C12Q1/00,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   68.4%;  Pred. No. 2.4e+03;
  Matches   13;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTT 2180
              | ||:|| ||:||:||:||
Db         19 CNCCYTTRTTYTTYTTYTT 1


RESULT 2507
BD170376
LOCUS       BD170376                20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel formate dehydrogenase and process for producing the same.
ACCESSION   BD170376
VERSION     BD170376.1  GI:27876188
KEYWORDS    WO 0246427-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Takaoka,Y. and Namba,H.
  TITLE     Novel formate dehydrogenase and process for producing the same
  JOURNAL   Patent: WO 0246427-A 6 13-JUN-2002;
            KANEKA CORP,YASUKO TAKAOKA,HIROKAZU NAMBA
COMMENT     OS   Artificial Sequence
            PN   WO 0246427-A/6
            PD   13-JUN-2002
            PF   04-DEC-2001 WO 2001JP010569
            PR   04-DEC-2000 JP 00P   368838
            PI   YASUKO TAKAOKA,HIROKAZU NAMBA
            PC   C12N15/53,C12N9/04,C12N1/21
            CC   Description of Artificial Sequence: primer-4
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1084 AGAAGGTGAAGCTGTTCA 1101
              ||| | ||||||||||||
Db          2 AGACGCTGAAGCTGTTCA 19


RESULT 2508
BD225115
LOCUS       BD225115                20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD225115
VERSION     BD225115.1  GI:33034885
KEYWORDS    JP 2002526095-A/250.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 250 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/250
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        483 GCCAGAGCCAGGAGGGAG 500
              ||||| |||||| |||||
Db          2 GCCAGGGCCAGGTGGGAG 19


RESULT 2509
A36543/c
LOCUS       A36543                  21 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 84 from Patent WO9323549.
ACCESSION   A36543
VERSION     A36543.1  GI:2293854
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Aurias,A., Delattre,O., Desmaze,C., Melot,T., Peter,M.,
            Plougastel,B., Thomas,G. and Zucman,J.
  TITLE     NUCLEIC ACID CORRESPONDING TO A GENE OF CHROMOSOME 22 INVOLVED IN
            RECURRENT CHROMOSOMAL TRANSLOCATIONS ASSOCIATED WITH THE
            DEVELOPMENT OF CANCEROUS TUMORS
  JOURNAL   Patent: WO 9323549-A 84 25-NOV-1993;
            CENTRE NAT RECH SCIENT (FR)
COMMENT     Other publication FR 2691475 931126
            Other publication JP 8500964T 960206.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        775 CCCTCTGAACCTCCCCTG 792
              || ||||||| |||||||
Db         19 CCTTCTGAACGTCCCCTG 2


RESULT 2502
AX557097
LOCUS       AX557097                  20 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 13 from Patent WO02059278.
ACCESSION   AX557097
VERSION     AX557097.1  GI:25900150
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Lumelsky,N.L., Blondel,O., mc Kay,R.D. and Kim,J.H.
  TITLE     Differentiation of stem cells to pancreatic endocrine cells
  JOURNAL   Patent: WO 02059278-A 13 01-AUG-2002;
            THE DEPARTMENT OF HEALTH & HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="Alpha-amylase-2A"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2317 TTGTTGCTGCTTGTCACC 2334
              |||||||  |||||||||
Db          3 TTGTTGCACCTTGTCACC 20


RESULT 2503
AX565527/c
LOCUS       AX565527                  20 bp    DNA     linear   PAT 29-NOV-2002
DEFINITION  Sequence 16 from Patent WO02077228.
ACCESSION   AX565527
VERSION     AX565527.1  GI:26000877
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   de Villartay,J.P., Moshous,D. and Fischer,A.
  TITLE     Gene involved in v(d)j recombination and/or dna repair
  JOURNAL   Patent: WO 02077228-A 16 03-OCT-2002;
            INSERM (E.P.S.T.) (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer Ex6R1"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2480 TTTTAATGGTGATGGGGT 2497
              ||||| ||| ||||||||
Db         20 TTTTAGTGGAGATGGGGT 3


RESULT 2504
AX573362/c
LOCUS       AX573362                  20 bp    DNA     linear   PAT 29-NOV-2002
DEFINITION  Sequence 16 from Patent WO02077026.
ACCESSION   AX573362
VERSION     AX573362.1  GI:26005245
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   de Villartay,J.P., Moshous,D. and Fischer,A.
  TITLE     Gene involved in v(d)j recombination and/or dna repair
  JOURNAL   Patent: WO 02077026-A 16 03-OCT-2002;
            INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
            (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer Ex6R1"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2480 TTTTAATGGTGATGGGGT 2497
              ||||| ||| ||||||||
Db         20 TTTTAGTGGAGATGGGGT 3


RESULT 2505
AX812129
LOCUS       AX812129                  20 bp    DNA     linear   PAT 02-DEC-2003
DEFINITION  Sequence 17 from Patent WO03062405.
ACCESSION   AX812129
VERSION     AX812129.1  GI:38635765
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Inoue,K., Kim,D., Gu,Y. and Ishii,M.
  TITLE     Method for inducing differentiation of embryonic stem cells into
            functioning cells
  JOURNAL   Patent: WO 03062405-A 17 31-JUL-2003;
            Inoue, Kazutomo (JP) ; Yugengaisha Okuma Contactlens Kenkyujo (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide Primer"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2317 TTGTTGCTGCTTGTCACC 2334
              |||||||  |||||||||
Db          3 TTGTTGCACCTTGTCACC 20


RESULT 2506
BD001838/c
LOCUS       BD001838                  20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for identifying/detecting eucaryote with II type
            topoisomerase  gene as indication.
ACCESSION   BD001838
VERSION     BD001838.1  GI:18628578
KEYWORDS    JP 2000125873-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Yamamoto,S., Atami,M., Kasai,H., Nakamura,S. and Hamada,T.
```

```
VERSION     AX383913.1  GI:19577484
KEYWORDS    .
SOURCE      Borrelia burgdorferi (Lyme disease spirochete)
  ORGANISM  Borrelia burgdorferi
            Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
            Borrelia burgdorferi group.
REFERENCE   1
  AUTHORS   Fritzsche,M.
  TITLE     Use of microbial dna sequences for the identification of human
            diseases
  JOURNAL   Patent: WO 0214546-A 16 21-FEB-2002;
            Fritzsche, Markus (CH)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Borrelia burgdorferi"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:139"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1505 AAACACAGGAAATAAAAT 1522
              |||| ||| |||||||||
Db          1 AAACTCAGAAAATAAAAT 18


RESULT 2498
AX383951
LOCUS       AX383951                  20 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 54 from Patent WO0214546.
ACCESSION   AX383951
VERSION     AX383951.1  GI:19577522
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Fritzsche,M.
  TITLE     Use of microbial dna sequences for the identification of human
            diseases
  JOURNAL   Patent: WO 0214546-A 54 21-FEB-2002;
            Fritzsche, Markus (CH)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1505 AAACACAGGAAATAAAAT 1522
              |||| ||| |||||||||
Db          1 AAACTCAGAAAATAAAAT 18


RESULT 2499
AX394078/c
LOCUS       AX394078                  20 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 53 from Patent WO0214366.
ACCESSION   AX394078
VERSION     AX394078.1  GI:19702028
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Groot,P.C., van Bergenhenegouwen,B.J. and van Oosterhout,A.J.
  TITLE     Genes involved in immune related responses observed with asthma
  JOURNAL   Patent: WO 0214366-A 53 21-FEB-2002;
            Universiteit Utrecht (NL)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sense primer R1-OS-B1-B2"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1290 CCAGCAGGCTCGCCCCAG 1307
              |||||||||| || |||
Db         18 CCAGCAGGCTCCCCTCAG 1


RESULT 2500
AX487219/c
LOCUS       AX487219                  20 bp    DNA     linear   PAT 16-AUG-2002
DEFINITION  Sequence 4519 from Patent WO02053728.
ACCESSION   AX487219
VERSION     AX487219.1  GI:22321367
KEYWORDS    .
SOURCE      Candida albicans
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
  AUTHORS   Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
  TITLE     Gene disruption methodologies for drug target discovery
  JOURNAL   Patent: WO 02053728-A 4519 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Candida albicans"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:5476"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        533 GGCCTACTGCCCCACCTC 550
              | |||||| |||||||||
Db         20 GACCTACTCCCCCACCTC 3


RESULT 2501
AX525290/c
LOCUS       AX525290                  20 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 8 from Patent WO02066637.
ACCESSION   AX525290
VERSION     AX525290.1  GI:25170179
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mitsuhashi,M.
  TITLE     Method for collecting and using nuclear mrna
  JOURNAL   Patent: WO 02066637-A 8 29-AUG-2002;
            HITACHI CHEMICAL RESEARCH CENTER, INC. (US) ; HITACHI CHEMICAL
            COMPANY, LTD. (JP) ; Hitachi, Ltd. (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="jun-B reverse primer."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
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                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1175 CCTCATCTTGGAGGACGA 1192
              | |||||  ||||||||||
Db         20 CATCATCCTGGAGGACGA 3


RESULT 2493
AX085396/c
LOCUS       AX085396                  20 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 9 from Patent WO0112833.
ACCESSION   AX085396
VERSION     AX085396.1  GI:13275451
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Emptage,M., Haynie,S., Laffend,L., Pucci,J. and Whited,G.
  TITLE     Process for the biological production of 1,3-propanediol with high
            titer
  JOURNAL   Patent: WO 0112833-A 9 22-FEB-2001;
            E.I. DU PONT DE NEMOURS AND COMPANY (US) ; GENENCOR INTERNATIONAL,
            INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer-primer"

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTT 2167
              | ||||||||||||||| |
Db         18 AGTGATTTTTTTCTCCAT 1


RESULT 2494
AX111391
LOCUS       AX111391                  20 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 2124 from Patent WO0123604.
ACCESSION   AX111391
VERSION     AX111391.1  GI:13927683
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 2124 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2243 AGGTACTGAAGCTTTATT 2260
              ||||||||  ||  ||||||
Db          2 AGGTACTGTAGGTTTATT 19


RESULT 2495
AX293227
LOCUS       AX293227                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 4989 from Patent WO0179548.
ACCESSION   AX293227
VERSION     AX293227.1  GI:17054910
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 4989 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         26 GTGACCCGGACAGCAAGG 43
              ||||||  ||||||||  ||
Db          3 GTGACCAGGACAGCACGG 20


RESULT 2496
AX296876
LOCUS       AX296876                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 8638 from Patent WO0179548.
ACCESSION   AX296876
VERSION     AX296876.1  GI:17058565
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 8638 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1046 CGGAAAGCCGCTCATGTG 1063
              ||||||||  ||||  ||||
Db          2 CGGAAAGCAGCTCGTGTG 19


RESULT 2497
AX383913
LOCUS       AX383913                  20 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 16 from Patent WO0214546.
ACCESSION   AX383913
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  JOURNAL   Patent: US 5543509-A 3 06-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1113 ACTTTGCCTATGTCTGTG 1130
              |||| ||||||| |||||
Db          3 ACTTCGCCTATGACTGTG 20


RESULT 2488
I83424
LOCUS       I83424                   20 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 5 from patent US 5714318.
ACCESSION   I83424
VERSION     I83424.1  GI:3406954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sagner,G., Kessler,C., Blum,H. and Domdey,H.
  TITLE     Simultaneous sequencing of nucleic acids
  JOURNAL   Patent: US 5714318-A 5 03-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2530 TATATACAGGGTATTAAG 2547
              |||||| ||||||||| |
Db          1 TATATATAGGGTATTAGG 18


RESULT 2489
AR216033
LOCUS       AR216033                 20 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 80 from patent US 6410518.
ACCESSION   AR216033
VERSION     AR216033.1  GI:23314321
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P.
  TITLE     Antisense oligonucleotide inhibition of raf gene expression
  JOURNAL   Patent: US 6410518-A 80 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        505 GCTGCCCTCGCACCACGG 522
              ||||||||| |||||| |
Db          3 GCTGCCCTCACACCACTG 20


RESULT 2490
AR230706/c
LOCUS       AR230706                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 3 from patent US 6451595.
ACCESSION   AR230706
VERSION     AR230706.1  GI:27271487
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,S., Yu,S.S. and Kim,J.-m.
  TITLE     High efficiency retroviral vectors that contain none of viral
            coding sequences
  JOURNAL   Patent: US 6451595-A 3 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTT 2167
              | ||||||||||||||| |
Db         20 AGTGATTTTTTTCTCCAT 3


RESULT 2491
AR231311
LOCUS       AR231311                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 48 from patent US 6451968.
ACCESSION   AR231311
VERSION     AR231311.1  GI:27272242
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6451968-A 48 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              || || |||||||| || ||
Db          1 TTNTTNTTTTTTTTCTTCTT 20


RESULT 2492
AR271177/c
LOCUS       AR271177                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 120 from patent US 6503152.
ACCESSION   AR271177
VERSION     AR271177.1  GI:29702480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Pelz,D.T.
  TITLE     Putting trainer
  JOURNAL   Patent: US 6503152-A 120 07-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        894 CAGTGGCTGAAGTACAGA 911
              || ||||||||| |||||
Db         19 CATTGGCTGAAGGACAGA 2
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RESULT 2484
BD231609/c
LOCUS BD231609 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Chromosome 17q-linked prostate cancer susceptibility gene.
ACCESSION BD231609
VERSION BD231609.1 GI:33041379
KEYWORDS JP 2002529065-A/161.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tavtigian,S.V., Teng,D.H.F., Simard,J. and Rommens,J.M.
TITLE Chromosome 17q-linked prostate cancer susceptibility gene
JOURNAL Patent: JP 2002529065-A 161 10-SEP-2002;
MYRIAD GENETICS INC,THE HOSPITAL FOR SICK CHILDREN
COMMENT OS Homo sapiens (human)
PN JP 2002529065-A/161
PD 10-SEP-2002
PF 05-NOV-1999 JP 2000581041
PR 06-NOV-1998 US 60/107468
PI SEAN V TAVTIGIAN,DAVID H F TENG,JACQUES SIMARD,JOHANNA M PI
ROMMENS
PC C12N15/09,A61K31/713,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
PC A61P35/00,
PC
C07K14/47,C07K16/18,C07K16/44,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566,
PC G01N33/577,
PC G01N37/00,C12N15/00,A61K37/02,C12N5/00
CC Chromosome 17q-linked prostate cancer susceptibility gene FH
Key Location/Qualifiers
FT source 1. .20
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
source 1. .20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        894 CAGTGGCTGAAGTACAGA 911
              || ||||||||| |||||
Db         19 CATTGGCTGAAGGACAGA 2
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RESULT 2485
BD242596/c
LOCUS BD242596 20 bp DNA linear PAT 17-JUL-2003
DEFINITION High efficiency retroviral vectors that contain none of viralcoding
sequences.
ACCESSION BD242596
VERSION BD242596.1 GI:33052366
KEYWORDS JP 2002519037-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,S., Yu,S.S. and Kim,J.M.
TITLE High efficiency retroviral vectors that contain none of viralcoding
sequences
JOURNAL Patent: JP 2002519037-A 3 02-JUL-2002;
VIROMED LTD
COMMENT OS Artificial Sequence
PN JP 2002519037-A/3
PD 02-JUL-2002
PF 24-JUN-1999 JP 2000557382
PR 26-JUN-1998 KR 1998/24478,22-JUN-1999 KR 1999/23398 PI
SUNYOUNG KIM,SEUNG SHIN YU,JONG MOOK KIM
PC C12N15/09,C12N1/21//(C12N1/21,C12R1:19),C12N15/00 CC CATATGN
primer
FH Key Location/Qualifiers
FT source 1. .20
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2150 ATTGATTTTTTTCTCCTT 2167
              | ||||||||||||||| |
Db         20 AGTGATTTTTTTCTCCAT 3
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RESULT 2486
I18340/c
LOCUS I18340 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 13 from patent US 5495009.
ACCESSION I18340
VERSION I18340.1 GI:1598695
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Matteucci,M., Jones,B. and Lin,K.-Y.
TITLE Oligonucleotide analogs containing thioformacetal linkages
JOURNAL Patent: US 5495009-A 13 27-FEB-1996;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2156 TTTTTTCTCCTTTTTTTT 2173
              ||||| ||||||| ||||
Db         19 TTTTTCCTCCTTTCTTTT 2
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RESULT 2487
I24514
LOCUS I24514 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 3 from patent US 5543509.
ACCESSION I24514
VERSION I24514.1 GI:1604384
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Klotman,P.E., Bruggeman,L.A. and Horikoshi,S.
TITLE Method for quantifying laminin and .beta.-actin messenger RNA

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ACCESSION   AR152574
VERSION     AR152574.1  GI:15120106
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baird,D.Martin., Royle,N.Jane. and Jeffreys,A.John.
  TITLE     Method for characterising variability in telomere DNA by PCR
  JOURNAL   Patent: US 6235468-A 2 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1800 CTCTGAAAGTGGTGCTAT 1817
              ||||||||||||  ||||
Db          3 CTCTGAAAGTGGACCTAT 20


RESULT 2480
AR157139
LOCUS       AR157139                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 56 from patent US 6242590.
ACCESSION   AR157139
VERSION     AR157139.1  GI:15125843
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense modulation of zinc finger protein-217 expression
  JOURNAL   Patent: US 6242590-A 56 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2115 TGGTTTTAGGAAACTTGT 2132
              |||||||||||||| | |
Db          1 TGGTTTTAGGAAACATCT 18


RESULT 2481
AR172933
LOCUS       AR172933                 20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 58 from patent US 6303374.
ACCESSION   AR172933
VERSION     AR172933.1  GI:17912424
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zhang,H. and Cowsert,L.M.
  TITLE     Antisense modulation of caspase 3 expression
  JOURNAL   Patent: US 6303374-A 58 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2394 ATTTATGCGTAATTTAAT 2411
              ||||||  | |||||||||
Db          1 ATTTATTCCTAATTTAAT 18


RESULT 2482
AR173880
LOCUS       AR173880                 20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 78 from patent US 6306606.
ACCESSION   AR173880
VERSION     AR173880.1  GI:17914200
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Weber,M.J., Wyatt,J. and Cowsert,L.M.
  TITLE     Antisense modulation of MP-1 expression
  JOURNAL   Patent: US 6306606-A 78 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2379 GAGTGTACAGATTTTATT 2396
              || |||||  |||||||||
Db          1 GATTGTACTGATTTTATT 18


RESULT 2483
BD231605/c
LOCUS       BD231605                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Chromosome 17q-linked prostate cancer susceptibility gene.
ACCESSION   BD231605
VERSION     BD231605.1  GI:33041375
KEYWORDS    JP 2002529065-A/157.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tavtigian,S.V., Teng,D.H.F., Simard,J. and Rommens,J.M.
  TITLE     Chromosome 17q-linked prostate cancer susceptibility gene
  JOURNAL   Patent: JP 2002529065-A 157 10-SEP-2002;
            MYRIAD GENETICS INC,THE HOSPITAL FOR SICK CHILDREN
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002529065-A/157
            PD   10-SEP-2002
            PF   05-NOV-1999 JP 2000581041
            PR   06-NOV-1998 US    60/107468
            PI   SEAN V TAVTIGIAN,DAVID H F TENG,JACQUES SIMARD,JOHANNA M  PI
            ROMMENS
            PC   C12N15/09,A61K31/713,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
            PC   A61P35/00,
            PC
            C07K14/47,C07K16/18,C07K16/44,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566,
            PC   G01N33/577,
            PC   G01N37/00,C12N15/00,A61K37/02,C12N5/00
            CC   Chromosome 17q-linked prostate cancer susceptibility gene FH
            Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
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KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Vasseur,M., Blumenfeld,M., Meguenni,S. and Poddevin,B.
  TITLE     STAPLE AND SEMI-STAPLE OLIGONUCLEOTIDES, METHOD OF PREPARATION AND
            APPLICATIONS
  JOURNAL   Patent: WO 9423026-A 2 13-OCT-1994;
            GENSET (FR)
COMMENT     Other publication AU 6432094 941024
            Other publication FR 2703053 940930.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTT 2176
              |||| | ||||||||||
Db         18 TTTCGCTTTTTTTTTTTT 1


RESULT 2475
A50098
LOCUS       A50098                  20 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 2 from Patent WO9612821.
ACCESSION   A50098
VERSION     A50098.1  GI:2303259
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baird,D.M., Royle,N.J. and Jeffreys,A.J.
  TITLE     METHOD FOR CHARACTERISING VARIABILITY IN TELOMERE DNA BY PCR
  JOURNAL   Patent: WO 9612821-A 2 02-MAY-1996;
            ZENECA LTD (GB)
COMMENT     Other publication GB 2294322 960424.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1800 CTCTGAAAGTGGTGCTAT 1817
              |||||||||||  ||||
Db          3 CTCTGAAAGTGGACCTAT 20


RESULT 2476
AR107644/c
LOCUS       AR107644                20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 84 from patent US 6110664.
ACCESSION   AR107644
VERSION     AR107644.1  GI:12823131
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 84 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAAA 1520
              ||||||| | ||||||||
Db         18 AGAAACAAATGAAATAAA 1


RESULT 2477
AR107645
LOCUS       AR107645                20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 85 from patent US 6110664.
ACCESSION   AR107645
VERSION     AR107645.1  GI:12823132
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 85 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2266 ATTTATTTCAGATGTTTC 2283
              ||||||||||  ||||||
Db          1 ATTTATTTCATTTGTTTC 18


RESULT 2478
AR107645/c
LOCUS       AR107645                20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 85 from patent US 6110664.
ACCESSION   AR107645
VERSION     AR107645.1  GI:12823132
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 85 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAAA 1520
              ||||||| | ||||||||
Db         19 AGAAACAAATGAAATAAA 2


RESULT 2479
AR152574
LOCUS       AR152574                20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6235468.
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  Best Local Similarity   84.2%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||| |||||||| || ||
Db          1 AAAACAAAAAAAAGAANAA 19


RESULT 2470
AX048432/c
LOCUS       AX048432                  20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 31 from Patent WO0071747.
ACCESSION   AX048432
VERSION     AX048432.1  GI:12225596
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 31 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1973 ACCTTGAAAAAAAGAAAA 1990
              ||||| ||||||| ||||
Db         18 ACCTTAAAAAAAAAAAAA 1


RESULT 2471
AX048431/c
LOCUS       AX048431                  20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 30 from Patent WO0071747.
ACCESSION   AX048431
VERSION     AX048431.1  GI:12225595
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 30 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1973 ACCTTGAAAAAAAGAAAA 1990
              ||||| ||||||| ||||
Db         18 ACCTTAAAAAAAAAAAAA 1


RESULT 2472
AX048434/c
LOCUS       AX048434                  20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 33 from Patent WO0071747.
ACCESSION   AX048434
VERSION     AX048434.1  GI:12225598
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 33 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1973 ACCTTGAAAAAAAGAAAA 1990
              ||||| ||||||| ||||
Db         18 ACCTTAAAAAAAAAAAAA 1


RESULT 2473
AX048446/c
LOCUS       AX048446                  20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 45 from Patent WO0071747.
ACCESSION   AX048446
VERSION     AX048446.1  GI:12225610
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 45 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              | ||| ||||||||||||
Db         18 GCATTAAAAAAAAAAAAA 1


RESULT 2474
A40126/c
LOCUS       A40126                    20 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 2 from Patent WO9423026.
ACCESSION   A40126
VERSION     A40126.1  GI:2296284
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RESULT 2465
AR371269
LOCUS       AR371269                  20 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 5 from patent US 6395474.
ACCESSION   AR371269
VERSION     AR371269.1  GI:34608201
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 5 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              || || ||||||||||||
Db          1 AAGAAGAAAAAAAAAAAA 18


RESULT 2466
A40129
LOCUS       A40129                    20 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 5 from Patent WO9423026.
ACCESSION   A40129
VERSION     A40129.1  GI:2296287
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Vasseur,M., Blumenfeld,M., Meguenni,S. and Poddevin,B.
  TITLE     STAPLE AND SEMI-STAPLE OLIGONUCLEOTIDES, METHOD OF PREPARATION AND
            APPLICATIONS
  JOURNAL   Patent: WO 9423026-A 5 13-OCT-1994;
            GENSET (FR)
COMMENT     Other publication AU 6432094 941024
            Other publication FR 2703053 940930.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||||||||| | |||
Db          1 AAAAAAAAAAAATAGAAA 18


RESULT 2467
AR107646/c
LOCUS       AR107646                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 86 from patent US 6110664.
ACCESSION   AR107646
VERSION     AR107646.1  GI:12823133
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 86 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAAA 1520
              ||||||| | ||||||||
Db         20 AGAAACAAATGAAATAAA 3


RESULT 2468
AX184029
LOCUS       AX184029                  20 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 1782 from Patent WO0142511.
ACCESSION   AX184029
VERSION     AX184029.1  GI:15135365
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
  TITLE     Ibd-related polymorphisms
  JOURNAL   Patent: WO 0142511-A 1782 14-JUN-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
            Biotherapeutics Corporation (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||| ||||| ||| |||
Db          1 AAAAAGAAAAANAAAGAAA 19


RESULT 2469
AX495922
LOCUS       AX495922                  20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 1687 from Patent WO02059256.
ACCESSION   AX495922
VERSION     AX495922.1  GI:23341532
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 1687 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
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RESULT 2461
AX323371
LOCUS       AX323371                  19 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 6 from Patent WO0192511.
ACCESSION   AX323371
VERSION     AX323371.1  GI:18094133
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
  TITLE     Purification of a triple helix formation with an immobilized
            oligonucleotide
  JOURNAL   Patent: WO 0192511-A 6 06-DEC-2001;
            Aventis Pharma (FR)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 2462
AX359990
LOCUS       AX359990                  19 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 18 from Patent WO0200938.
ACCESSION   AX359990
VERSION     AX359990.1  GI:18675626
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kurn,N.
  TITLE     Methods and compositions for transcription-based nucleic acid
            amplification
  JOURNAL   Patent: WO 0200938-A 18 03-JAN-2002;
            Nugen Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Primer: Chimeric RNA/DNA Primer."

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GCCGATGCGTGTCCAGTG 28
              | |||||||| |||||||
Db          1 GACGATGCGTCTCCAGTG 18


RESULT 2463
AX686841
LOCUS       AX686841                  19 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 6 from Patent EP1281774.
ACCESSION   AX686841
VERSION     AX686841.1  GI:29372382
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Couzet,J., Scherman,D. and Wils,P.
  TITLE     Purification of a triple helix formation with an immobilized
            oligonucleotide
  JOURNAL   Patent: EP 1281774-A 6 05-FEB-2003;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 2464
BD135015
LOCUS       BD135015                  19 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Vector having nucleic acid transferred thereinto, compositions
            containing the vector and utilization thereof.
ACCESSION   BD135015
VERSION     BD135015.1  GI:23229960
KEYWORDS    JP 2002507429-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Siorina,C., Sherman,D. and Wills,P.
  TITLE     Vector having nucleic acid transferred thereinto, compositions
            containing the vector and utilization thereof
  JOURNAL   Patent: JP 2002507429-A 4 12-MAR-2002;
            AVENTIS PHARMA SA
COMMENT     OS   Unidentified
            PN   JP 2002507429-A/4
            PD   12-MAR-2002
            PF   19-MAR-1999 JP 2000538027
            PR   24-MAR-1998 FR     98/03573,18-MAY-1998 US   60/085 848 PI
            CAROL SIORINA,DANIEL SHERMAN,PIERRE WILLS
            PC   C12N15/09,A61K39/39,A61K48/00,C12N1/15,C12N1/19,C12N5/10, PC
            C12N15/00,
            PC   C12N5/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Vector having nucleic acid transferred thereinto, compositions

            CC            containing
            CC   the vector and utilization thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19
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          Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
  TITLE     Purification of a triple helix formation with an immobilized
            oligonucleotide
  JOURNAL   Patent: US 6319672-A 6 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 2457
AR282316
LOCUS       AR282316                 19 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 75 from patent US 6521435.
ACCESSION   AR282316
VERSION     AR282316.1  GI:29718355
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Okubara,P.A., Blechl,A.E., Hohn,T.M. and Berka,R.M.
  TITLE     Nucleic acid sequences encoding cell wall-degrading enzymes and use
            to engineer resistance to Fusarium and other pathogens
  JOURNAL   Patent: US 6521435-A 75 18-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        849 CTGGAAGATTGTCGCTCC 866
              ||||||| ||||||| ||
Db          1 CTGGAAGTTTGTCGCACC 18


RESULT 2458
AX016237
LOCUS       AX016237                 19 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from Patent WO9949067.
ACCESSION   AX016237
VERSION     AX016237.1  GI:10041814
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wils,P., Ciolina,C. and Scherman,D.
  TITLE     Nucleic acid transfer vectors, compositions containing same and
            uses
  JOURNAL   Patent: WO 9949067-A 4 30-SEP-1999;
            WILS PIERRE (FR); CIOLINA CAROLE (FR); SCHERMAN DANIEL (FR); RHONE
            POULENC RORER SA (FR)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="misc_binding"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 2459
AX100011
LOCUS       AX100011                 19 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 5 from Patent WO0120035.
ACCESSION   AX100011
VERSION     AX100011.1  GI:13539017
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kurn,N.
  TITLE     Methods and compositions for linear isothermal amplification of
            polynucleotide sequences
  JOURNAL   Patent: WO 0120035-A 5 22-MAR-2001;
            Nugen Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Chimeric DNA/RNA primer"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GCCGATGCGTGTCCAGTG 28
              | |||||||| |||||||
Db          1 GACGATGCGTCTCCAGTG 18


RESULT 2460
AX129906
LOCUS       AX129906                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1124 from Patent WO0130362.
ACCESSION   AX129906
VERSION     AX129906.1  GI:14136211
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1124 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk-we-hu ribozyme binding site"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        714 AGCACCTGTTGCTGCACG 731
              || |||||||||||| ||
Db          1 AGGACCTGTTGCTGCCCG 18
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            Other publication FR 2728264 960621.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 2452
A57717/c
LOCUS       A57717                   19 bp    DNA     linear   PAT 03-MAR-1998
DEFINITION  Sequence 3 from Patent WO9632489.
ACCESSION   A57717
VERSION     A57717.1  GI:3713541
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Chen,R., Doiron,B. and Kahn,A.
  TITLE     GLUCOSE-INDUCIBLE RECOMBINANT VIRAL VECTOR
  JOURNAL   Patent: WO 9632489-A 3 17-OCT-1996;
            INST NAT SANTE RECH MED (FR)
COMMENT     Other publication AU 5652396 961030
            Other publication FR 2732978 961018.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1455 CTGGAGACCAGAGTCCAG 1472
              |||| | ||||||||||||
Db         18 CTGGGGGCCAGAGTCCAG 1


RESULT 2453
A65476
LOCUS       A65476                   19 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 4 from Patent WO9735002.
ACCESSION   A65476
VERSION     A65476.1  GI:4531211
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Wils,P. and Ollivier,M.
  TITLE     PURIFICATION OF PHARMACEUTICAL-GRADE PLASMID DNA
  JOURNAL   Patent: WO 9735002-A 4 25-SEP-1997;
            RHONE POULENC RORER SA (FR)
COMMENT     Other publication AU 2166197 19971010
            Other publication FR 2746412 19970926.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 2454
AR167579
LOCUS       AR167579                 19 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 6 from patent US 6287762.
ACCESSION   AR167579
VERSION     AR167579.1  GI:17903368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Crouzet,J., Scherman,D. and Wils,P.
  TITLE     Purification of a triple helix formation with an immobilized
            oligonucleotide
  JOURNAL   Patent: US 6287762-A 6 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 2455
AR175911/c
LOCUS       AR175911                 19 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 3 from patent US 6309878.
ACCESSION   AR175911
VERSION     AR175911.1  GI:17917210
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Chen,R., Doiron,B. and Kahn,A.
  TITLE     Glucose-inducible recombinant viral vector
  JOURNAL   Patent: US 6309878-A 3 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1455 CTGGAGACCAGAGTCCAG 1472
              |||| | ||||||||||||
Db         18 CTGGGGGCCAGAGTCCAG 1


RESULT 2456
AR178289
LOCUS       AR178289                 19 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 6 from patent US 6319672.
ACCESSION   AR178289
VERSION     AR178289.1  GI:20219427
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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 Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
 Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        847 CCCTGGAAGATTGTCGCT 864
              | |||| ||||||||||||
Db         18 CTCTGGTAGATTGTCGCT 1


RESULT 2448
BD224873/c
LOCUS       BD224873                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224873
VERSION     BD224873.1  GI:33034643
KEYWORDS    JP 2002526095-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 8 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/8
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        464 CAGCAGGCCTGGCCCGGC 481
              |||||| ||| |||||||
Db         18 CAGCAGTCCTCGCCCGGC 1


RESULT 2449
AB069627
LOCUS       AB069627                 18 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, reverse primer for human STS sts-N26127 at
            1p36.
ACCESSION   AB069627
VERSION     AB069627.1  GI:15130431
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 18)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .18
                     /note="reverse primer for human STS sts-N26127 at 1p36
                     sts-N26127 obtained from clones B68J10, B68H10, B30J5,
                     B358I24, B42C4, B151K19, B239O24, Human BAC library
                     RPCI-11"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1607 GCCTGGGGGAAGAGTTTG 1624
              || |||||||||||| ||
Db          1 GCATGGGGGAAGAGTGTG 18


RESULT 2450
A33509/c
LOCUS       A33509                   19 bp    DNA     linear   PAT 19-JUL-1996
DEFINITION  Synthetic IVS-1-6 GC clamp.
ACCESSION   A33509
VERSION     A33509.1  GI:1567949
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   .
  TITLE     PROCESS AND DEVICE FOR SEPARATING AND DETECTING CONSTITUENTS OF A
            MIXTURE OF SUBSTANCES BY TEMPERATURE GRADIENT GEL ELECTROPHORESIS
  JOURNAL   Patent: WO 9102815-A 3 07-MAR-1991;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         49 GCGCGGCGGGGGCGGCGG 66
              |||||| | |||||||||
Db         18 GCGCGGGGCGGGCGGCGG 1


RESULT 2451
A51700
LOCUS       A51700                   19 bp    DNA     linear   PAT 10-MAR-1997
DEFINITION  Sequence 6 from Patent WO9618744.
ACCESSION   A51700
VERSION     A51700.1  GI:2304504
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Crouzet,J., Scherman,D. and Wils,P.
  TITLE     PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN IMMOBILIZED
            OLIGONUCLEOTIDE
  JOURNAL   Patent: WO 9618744-A 6 20-JUN-1996;
            RHONE POULENC RORER SA (FR)
COMMENT     Other publication AU 4178996 960703
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  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        464 CAGCAGGCCTGGCCCGGC 481
              |||||| ||| |||||||
Db         18 CAGCAGTCCTCGCCCGGC 1


RESULT 2443
AR231295
LOCUS       AR231295                  18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 32 from patent US 6451968.
ACCESSION   AR231295
VERSION     AR231295.1  GI:27272226
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6451968-A 32 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||| |||||||| ||||
Db          1 TTTTGTTTTTTTTCTTTT 18


RESULT 2444
AR231295/c
LOCUS       AR231295                  18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 32 from patent US 6451968.
ACCESSION   AR231295
VERSION     AR231295.1  GI:27272226
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6451968-A 32 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||| |||||||| ||||
Db         18 AAAAGAAAAAAAACAAAA 1


RESULT 2445
AR231296
LOCUS       AR231296                  18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 33 from patent US 6451968.
ACCESSION   AR231296
VERSION     AR231296.1  GI:27272227
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6451968-A 33 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||| |||||||| ||||
Db          1 TTTTCTTTTTTTTCTTTT 18


RESULT 2446
AR231296/c
LOCUS       AR231296                  18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 33 from patent US 6451968.
ACCESSION   AR231296
VERSION     AR231296.1  GI:27272227
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6451968-A 33 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||| |||||||| ||||
Db         18 AAAAGAAAAAAAAGAAAA 1


RESULT 2447
AX006491/c
LOCUS       AX006491                  18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 6 from Patent WO0004143.
ACCESSION   AX006491
VERSION     AX006491.1  GI:9994616
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wrana,J.L. and Attisano,L.
  TITLE     Mammalian fast transcription factor
  JOURNAL   Patent: WO 0004143-A 6 27-JAN-2000;
            HSC RES DEV LP (CA); WRANA JEFFREY L (CA); ATTISANO LILIANA (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
```

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LOCUS       BD274799                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  CANCER CELL VACCINE.
ACCESSION   BD274799
VERSION     BD274799.1  GI:33084567
KEYWORDS    JP 2002531582-A/24.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kusu,M., Qiu,G. and Hunfrees,R.
  TITLE     CANCER CELL VACCINE
  JOURNAL   Patent: JP 2002531582-A 24 24-SEP-2002;
            ANTIGEN EXPRESS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002531582-A/24
            PD   24-SEP-2002
            PF   24-NOV-1999 JP 2000586901
            PR   04-DEC-1998 US    09/205995
            PI   minzhen kusu,gang qiu,robert hunfrees
            CC   Description of Artificial Sequence: antisense oligonucleotide
            CC   corresponding
            CC   to a specific region of the mouse Ii gene.
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2565 GCTCTGTTCTTGGCTTGG 2582
              |||||| |||||||| ||
Db         18 GCTCTGCTCTTGGCTGGG 1


RESULT 2439
I04805/c
LOCUS       I04805                   18 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 15 from Patent EP 0206783.
ACCESSION   I04805
VERSION     I04805.1  GI:591458
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Thill,G.P., Harpold,M.M. and Tschopp,J.F.
  TITLE     Expression and secretion of polypeptides from saccharomyces
            cerevisiae
  JOURNAL   Patent: EP 0206783-A2 15 30-DEC-1986;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1485 AAACCCTGGAGAAAATGG 1502
              || |||||||||||| |
Db         18 AAGCCCTGGAGAAAATAG 1


RESULT 2440
I18341/c
LOCUS       I18341                   18 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 14 from patent US 5495009.
ACCESSION   I18341
VERSION     I18341.1  GI:1598696
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Matteucci,M., Jones,B. and Lin,K.-Y.
  TITLE     Oligonucleotide analogs containing thioformacetal linkages
  JOURNAL   Patent: US 5495009-A 14 27-FEB-1996;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTT 2173
              ||||| ||||||| ||||
Db         18 TTTTTCCTCCTTTCTTTT 1


RESULT 2441
AR205265/c
LOCUS       AR205265                 18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 25 from patent US 6368855.
ACCESSION   AR205265
VERSION     AR205265.1  GI:21502805
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Xu,M., Qiu,G. and Humphreys,R.
  TITLE     MHC class II antigen presenting cells containing oligonucleotides
            which inhibit Ii protein expression
  JOURNAL   Patent: US 6368855-A 25 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2565 GCTCTGTTCTTGGCTTGG 2582
              |||||| |||||||| ||
Db         18 GCTCTGCTCTTGGCTGGG 1


RESULT 2442
AR211095/c
LOCUS       AR211095                 18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 8 from patent US 6399297.
ACCESSION   AR211095
VERSION     AR211095.1  GI:21514326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 8 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
```

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I36757/c
LOCUS       I36757                    26 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5608148.
ACCESSION   I36757
VERSION     I36757.1  GI:2086582
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.E.
  TITLE     Transgenic cotton plants producing heterologous peroxidase
  JOURNAL   Patent: US 5608148-A 1 04-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 2434
I40322/c
LOCUS       I40322                    26 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5620882.
ACCESSION   I40322
VERSION     I40322.1  GI:2082614
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.
  TITLE     Genetically engineering cotton plants for altered fiber
  JOURNAL   Patent: US 5620882-A 1 15-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 2435
I30206/c
LOCUS       I30206                    30 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 2 from patent US 5580731.
ACCESSION   I30206
VERSION     I30206.1  GI:1820997
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Chang,C.-A., Urdea,M.S. and Horn,T.
  TITLE     N-4 modified pyrimidine deoxynucleotides and oligonucleotide probes
            synthesized therewith
  JOURNAL   Patent: US 5580731-A 2 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         30 AAAAAAAAAAAAAAA 16


RESULT 2436
AX267026/c
LOCUS       AX267026                  30 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 15 from Patent WO0173001.
ACCESSION   AX267026
VERSION     AX267026.1  GI:16515811
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Seidman,M.M. and Majumdar,A.
  TITLE     Establishment of cellular manipulations which enhance
            oligo-mediated gene targeting
  JOURNAL   Patent: WO 0173001-A 15 04-OCT-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic"

  Query Match             0.5%;  Score 15;  DB 1;  Length 30;
  Best Local Similarity   78.3%;  Pred. No. 3.9e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAA 2803
              ||  |||| |||| || ||||||
Db         27 AAAAGAAAGAAAAGAAGAAAAAA 5


RESULT 2437
AR085574/c
LOCUS       AR085574                  18 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 10 from patent US 5981732.
ACCESSION   AR085574
VERSION     AR085574.1  GI:10012341
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense modulation of G-alpha-13 expression
  JOURNAL   Patent: US 5981732-A 10 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         50 CGCGGCGGGGGCGGCGGC 67
              || ||||| |||||||||
Db         18 CGAGGCGGCGGCGGCGGC 1


RESULT 2438
BD274799/c
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                    || ||  ||  ||||||||||||
Db         23 AGTATCAAAGGAAAAAAAAAAAA 1


RESULT 2428
AR034927/c
LOCUS       AR034927                  26 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5869720.
ACCESSION   AR034927
VERSION     AR034927.1  GI:5950532
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.E.
  TITLE     Transgenic cotton plants producing heterologous peroxidase
  JOURNAL   Patent: US 5869720-A 1 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 2429
AR145386/c
LOCUS       AR145386                  26 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 10 from patent US 6211430.
ACCESSION   AR145386
VERSION     AR145386.1  GI:15107253
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.E.
  TITLE     FbLate promoter
  JOURNAL   Patent: US 6211430-A 10 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 2430
I18346/c
LOCUS       I18346                    26 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5495070.
ACCESSION   I18346
VERSION     I18346.1  GI:1598701
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.
  TITLE     Genetically engineering cotton plants for altered fiber
  JOURNAL   Patent: US 5495070-A 1 27-FEB-1996;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 2431
I21333/c
LOCUS       I21333                    26 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5521078.
ACCESSION   I21333
VERSION     I21333.1  GI:1601687
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.
  TITLE     Genetically engineering cotton plants for altered fiber
  JOURNAL   Patent: US 5521078-A 1 28-MAY-1996;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 2432
I35739/c
LOCUS       I35739                    26 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5602321.
ACCESSION   I35739
VERSION     I35739.1  GI:2087590
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.
  TITLE     Transgenic cotton plants producing heterologous polyhydroxy(e)
            butyrate bioplastic
  JOURNAL   Patent: US 5602321-A 1 11-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 2433
```

```
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2424
AX043206/c
LOCUS       AX043206                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 772 from Patent WO0065088.
ACCESSION   AX043206
VERSION     AX043206.1  GI:11341814
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 772 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match              0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 3.4e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAA 2797
              |||   | || ||||||||||||
Db         23 TGTACCAGTTAAAAAAAAAAAA 1


RESULT 2425
AX043296
LOCUS       AX043296                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 862 from Patent WO0065088.
ACCESSION   AX043296
VERSION     AX043296.1  GI:11341904
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 862 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match              0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 3.4e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAACTT 2191
              |||||||||||| ||  |  |||
Db          1 TTTTTTTTTTTTCTTCCTCCCTT 23


RESULT 2426
BD075857
LOCUS       BD075857                  25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Standardized nucleic acid library and method of constructing the
            same.
ACCESSION   BD075857
VERSION     BD075857.1  GI:22621460
KEYWORDS    JP 2001517460-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Li,W.B., Jessee,J. and Nisson,P.E.
  TITLE     Standardized nucleic acid library and method of constructing the
  JOURNAL   Patent: JP 2001517460-A 2 09-OCT-2001;
            LIFE TECHNOLOGIES INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001517460-A/2
            PD   09-OCT-2001
            PF   24-SEP-1998 JP 2000512989
            PR   24-SEP-1997 US    60/059817,23-SEP-1998 US    09/159496 PI
            WU BO LI,JOEL JESSEE,PAUL E NISSON
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P19/34 PC
            ,C12Q1/68,C12N15/00,
            PC   C12N5/00
            CC   Description of artificial sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2427
AX042962/c
LOCUS       AX042962                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 528 from Patent WO0065088.
ACCESSION   AX042962
VERSION     AX042962.1  GI:11341570
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 528 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match              0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 3.4e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
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```
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACTTT 2192
                || ||| ||| |||||||  |||
Db         23 TTGTTTGTTTATTTTTTAGGTTT 1


RESULT 2419
A33476
LOCUS       A33476                   24 bp    DNA     linear   PAT 23-JUL-1996
DEFINITION  Synthetic pCAS7 poliovirus coding sequence 3' end.
ACCESSION   A33476
VERSION     A33476.1  GI:1567921
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   .
  TITLE     POLIOVIRUS CHIMAERAS
  JOURNAL   Patent: WO 9015145-A 33 13-DEC-1990;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2420
AX554007/c
LOCUS       AX554007                 24 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 30 from Patent WO02074799.
ACCESSION   AX554007
VERSION     AX554007.1  GI:25897944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Freyssinet,G., Rang,C. and Frutos,R.
  TITLE     Pepsin-sensitive modified bacillus thuringiensis insecticidal toxin
  JOURNAL   Patent: WO 02074799-A 30 26-SEP-2002;
            AVENTIS CROPSCIENCE S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="mutant 18"

  Query Match             0.5%;  Score 15;  DB 1;  Length 24;
  Best Local Similarity   78.3%;  Pred. No. 3.2e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAA 2802
              ||||  ||| || || |||||||
Db         24 GAATAAAAATAATAATAAAAAAA 2

RESULT 2421
AX043309
LOCUS       AX043309                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 875 from Patent WO0065088.
ACCESSION   AX043309
VERSION     AX043309.1  GI:11341917
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 875 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 3.4e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||   |  |||| |
Db          1 TTTTTTTTTTTTGCTACAACTCT 23


RESULT 2422
I56670/c
LOCUS       I56670                   25 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5650279.
ACCESSION   I56670
VERSION     I56670.1  GI:2477083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Nagpal,S. and Chandraratna,R.A.
  TITLE     Gene sequence induced in skin by retinoids
  JOURNAL   Patent: US 5650279-A 1 22-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         25 AAAAAAAAAAAAAAA 11


RESULT 2423
AR211579
LOCUS       AR211579                 25 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 2 from patent US 6399334.
ACCESSION   AR211579
VERSION     AR211579.1  GI:21514938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Li,W.-B., Nisson,P.E. and Jessee,J.
  TITLE     Normalized nucleic acid libraries and methods of production thereof
  JOURNAL   Patent: US 6399334-A 2 04-JUN-2002;
FEATURES             Location/Qualifiers
```

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VERSION     AX591818.1  GI:27950087
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Guo,X., Li,L., Patturajan,M., Shimkets,R.A., Casman,S.J.,
            Malyankar,U.M., Tchernev,V.T., Vernet,C.A., Spytek,K.A.,
            Shenoy,S.G., Alsobrook,J.P., Edinger,S., Peyman,J.A., Stone,D.J.,
            Ellerman,K., Gangolli,E.A., Boldog,F.L., Colman,S.D., Eisen,A.J.,
            Liu,X., Padigaru,M., Spaderna,S.K. and Zerhusen,B.D.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0246409-A 179 13-JUN-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="CHEMICALLY SYNTHESIZED"

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        714 AGCACCTGTTGCTGCACGATCAG 736
              ||||  || ||||||| | ||||
Db         23 AGCATGTGGTGCTGCAGGGTCAG 1


RESULT 2416
BD009266/c
LOCUS       BD009266                  23 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Recombinant plant genome, comprising specific chicory genes and a
            nucleotide sequence conferring male sterility, and its use.
ACCESSION   BD009266
VERSION     BD009266.1  GI:18637639
KEYWORDS    JP 2001502882-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Delesalle,L., Dhellemmes,C. and Desprez,M.
  TITLE     Recombinant plant genome, comprising specific chicory genes and a
            nucleotide sequence conferring male sterility, and its use
  JOURNAL   Patent: JP 2001502882-A 1 06-MAR-2001;
            FLORIMOND DESPREZ VEUVE ET FILS
COMMENT     OS   Unidentified
            PN   JP 2001502882-A/1
            PD   06-MAR-2001
            PF   30-MAY-1997 JP 1997541751
            PR   31-MAY-1996 FR     96/06725
            PI   LOUIS DELESALLE,CHARLES DHELLEMMES,MICHEL DESPREZ PC
            C12N15/82,C12N5/04//C07K14/415
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        482 CGCCAGAGCCAGGAGGGAGCGGG 504
              |||| || |||  |||||| |||
Db         23 CGCCGGATCCACCAGGGAGGGGG 1


RESULT 2417
BD188565/c
LOCUS       BD188565                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method for distinguishing specie of animal by SINE method.
ACCESSION   BD188565
VERSION     BD188565.1  GI:32998304
KEYWORDS    JP 2003009866-A/302.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Okada,N.
  TITLE     Method for distinguishing specie of animal by SINE method
  JOURNAL   Patent: JP 2003009866-A 302 14-JAN-2003;
            THE CIRCLE FOR THE PROMOTION OF SCIENCE AND ENGINEERING
COMMENT     OS   Artificial Sequence
            PN   JP 2003009866-A/302
            PD   14-JAN-2003
            PF   24-APR-2001 JP 2001126667
            PI   NORIHIRO OKADA
            PC   C12N15/09,C12Q1/68,G01N33/00,G01N33/50,G01N33/53,G01N33/566,
            PC   G06F17/30,
            PC   C12N15/00
            CC   Isi14 Isi14 F1 PCR primer
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1485 AAACCCTGGAGAAAATGGAGAAA 1507
              ||||| ||||||| || | | ||
Db         23 AAACCATGGAGAATATAGGGGAA 1


RESULT 2418
BD225572/c
LOCUS       BD225572                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Assay for methylation in the GST-Pi gene.
ACCESSION   BD225572
VERSION     BD225572.1  GI:33035342
KEYWORDS    JP 2002512810-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Clark,S.J., Millar,D.S. and Molloy,P.L.
  TITLE     Assay for methylation in the GST-Pi gene
  JOURNAL   Patent: JP 2002512810-A 17 08-MAY-2002;
            COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
COMMENT     OS   Artificial Sequence
            PN   JP 2002512810-A/17
            PD   08-MAY-2002
            PF   23-APR-1999 JP 2000546048
            PR   23-APR-1998 AU      PP 3129
            PI   SUSAN JOY CLARK,DOUGLAS S MILLAR,PETER LAURENCE MOLLOY PC
            C12Q1/68,C12N15/09,C12Q1/48,C12N15/00
            CC   Description of Artificial Sequence:Oligonucleotide which binds
            CC   bisulfite-converted human GST-Pi gene
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
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FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        415 CGCCGCCGCCATCAACCCCCTGC 437
              ||||||| |||| | ||||  ||
Db          1 CGCCGCCACCATGAGCCCCAGGC 23


RESULT 2411
AR409907
LOCUS       AR409907                  23 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 20 from patent US 6635422.
ACCESSION   AR409907
VERSION     AR409907.1  GI:40161042
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 20 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTT 2181
              ||| |  ||||||  ||||||||
Db          1 TTTTTAATTTTTTAATTTTTTTT 23


RESULT 2412
AX048427
LOCUS       AX048427                  23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 26 from Patent WO0071747.
ACCESSION   AX048427
VERSION     AX048427.1  GI:12225591
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 26 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match              0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||

Db          1 TTTTTTTTTTTTTTT 15


RESULT 2413
AX048427/c
LOCUS       AX048427                  23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 26 from Patent WO0071747.
ACCESSION   AX048427
VERSION     AX048427.1  GI:12225591
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 26 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match              0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2414
AX226182
LOCUS       AX226182                  23 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 101 from Patent WO0160856.
ACCESSION   AX226182
VERSION     AX226182.1  GI:15555494
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Vikkula,M.
  TITLE     vmglom gene and its mutations causing disorders with a vascular
            component
  JOURNAL   Patent: WO 0160856-A 101 23-AUG-2001;
            UNIVERSITE CATHOLIQUE DE LOUVAIN (BE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"

  Query Match              0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1924 TTTTTTCAGTGTTAAGGTAATGG 1946
              |||||  ||||| ||||||  | |
Db          1 TTTTTGTAGTGTCAAGGTATTAG 23


RESULT 2415
AX591818/c
LOCUS       AX591818                  23 bp    DNA     linear   PAT 27-JAN-2003
DEFINITION  Sequence 179 from Patent WO0246409.
ACCESSION   AX591818
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  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         33 GGACAGCAAGGCCCGCGCGCGGC 55
              || |||  ||||| ||||| |||
Db         23 GGCCAGTGAGGCCTGCGCGTGGC 1


RESULT 2407
BD250901
LOCUS       BD250901                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  A plant disease resistance signalling gene: materials and methods
            relating thereto.
ACCESSION   BD250901
VERSION     BD250901.1  GI:33060671
KEYWORDS    JP 2002524044-A/34.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Lefert,P.M.J.S., Shirasu,K. and Lahaye,T.
  TITLE     A plant disease resistance signalling gene: materials and methods
            relating thereto
  JOURNAL   Patent: JP 2002524044-A 34 06-AUG-2002;
            PLANT BIOSCIENCE LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002524044-A/34
            PD   06-AUG-2002
            PF   06-AUG-1999 JP 2000563785
            PR   06-AUG-1998 GB    9817169.7
            PI   PAUL MARIA JOSEF SCHULZE LEFERT,KEN SHIRASU,THOMAS LAHAYE PC
            C12N15/09,A01H5/00,C07K14/415,C07K16/16,C12N5/10,C12Q1/68, PC
            G01N33/53//
            PC   (C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) CC
             Description of Artificial Sequence: Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        310 CACTGGAGTCGCCGAATATCAGC 332
              | ||||||  ||||| | |||||
Db          1 CTCTGGAGGAGCCGAGTGTCAGC 23


RESULT 2408
BD260935
LOCUS       BD260935                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Galectin 11.
ACCESSION   BD260935
VERSION     BD260935.1  GI:33070705
KEYWORDS    JP 2002541832-A/6.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Ni,J., Rosen,C.A., Gentz,R.L. and Lui,F.T.
  TITLE     Galectin 11
  JOURNAL   Patent: JP 2002541832-A 6 10-DEC-2002;
            HUMAN GENOME SCIENCES INC, LA JOLLA INSTITUTE FOR ALLERGY AND
            IMMUNOLOGY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002541832-A/6
            PD   10-DEC-2002
            PF   21-APR-2000 JP 2000612311
            PR   21-APR-1999 US    60/130390,10-DEC-1999 US    60/169932 PI
            JIAN NI,CRAIG A ROSEN,REINER L GENTZ,FU TONG LUI PC
            C12N15/09,A61K38/00,A61P11/06,A61P29/00,A61P35/00,A61P37/00, PC
            A61P37/08,
            PC   C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/06 PC
            ,C12N5/10,C12P21/02,
            PC   G01N33/15,G01N33/50,G01N33/53,G01N33/68,C12N15/00,A61K37/02,
            PC   C12N5/00,
            PC   C12N5/00
            CC   Galectin 11
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        415 CGCCGCCGCCATCAACCCCCTGC 437
              ||||||| |||| | ||||  ||
Db          1 CGCCGCCACCATGAGCCCCAGGC 23


RESULT 2409
I12757/c
LOCUS       I12757                    23 bp    DNA     linear   PAT 26-JUL-1995
DEFINITION  Sequence 55 from patent US 5427930.
ACCESSION   I12757
VERSION     I12757.1  GI:910139
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Birkenmeyer,L.G., Carrino,J.J., Dille,B.J., Hu,H.-Y.,
            Kratochvil,J.D., Laffler,T.G., Marshall,R.L., Rinehardt,L.A. and
            Solomon,N.A.
  TITLE     Amplification of target nucleic acids using gap filling ligase
            chain reaction
  JOURNAL   Patent: US 5427930-A 55 27-JUN-1995;
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         92 ATTTTGGATTTACCGCTTGGGGG 114
              |||||| ||||   |||||| ||
Db         23 ATTTTGAATTTTTTGCTTGGAGG 1


RESULT 2410
AR374920
LOCUS       AR374920                  23 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 10 from patent US 6605699.
ACCESSION   AR374920
VERSION     AR374920.1  GI:40078078
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Ni,J., Gentz,R.L., Rosen,C.A. and Liu,F.-T.
  TITLE     Galectin-11 polypeptides
  JOURNAL   Patent: US 6605699-A 10 12-AUG-2003;
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            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                      Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES                Location/Qualifiers
     source             1. .22
                        /organism="Aspergillus oryzae"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:5062"

  Query Match              0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2403
AX053000
LOCUS       AX053000                23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 16 from Patent WO0071749.
ACCESSION   AX053000
VERSION     AX053000.1  GI:12227102
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 16 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES                Location/Qualifiers
     source             1. .23
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Komponente (b)-3"

  Query Match              0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2404
AX052992/c
LOCUS       AX052992                23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 8 from Patent WO0071749.
ACCESSION   AX052992
VERSION     AX052992.1  GI:12227094
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 8 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES                Location/Qualifiers
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                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Komponente (b)-1"

  Query Match              0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2405
A68080/c
LOCUS       A68080                  23 bp    DNA     linear   PAT 05-MAY-1999
DEFINITION  Sequence 1 from Patent WO9745548.
ACCESSION   A68080
VERSION     A68080.1  GI:4756880
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Delesalle,L., Dhellemmes,C. and Desprez,M.
  TITLE     RECOMBINANT PLANT GENOME, COMPRISING SPECIFIC CHICORY GENES AND A
            NUCLEOTIDE SEQUENCE CONFERRING MALE STERILITY, AND ITS USE
  JOURNAL   Patent: WO 9745548-A 1 04-DEC-1997;
            FLORIMOND DESPREZ VEUVE ET FIL (FR)
COMMENT     Other publication FR 2749321 19971205.
FEATURES                Location/Qualifiers
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  Query Match              0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        482 CGCCAGAGCCAGGAGGGAGCGGG 504
              ||||  ||  |||  ||||||  |||
Db         23 CGCCGGATCCACCAGGGAGGGGG 1


RESULT 2406
A79730/c
LOCUS       A79730                  23 bp    DNA     linear   PAT 20-OCT-1999
DEFINITION  Sequence 1 from Patent EP0778349.
ACCESSION   A79730
VERSION     A79730.1  GI:6092658
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Polack,A. and Muecke,S.
  TITLE     GENE CONSTRUCT AND THE USE THEREOF
  JOURNAL   Patent: EP 0778349-A 1 11-JUN-1997;
            GSF FORSCHUNGSZENTRUM UMWELT (DE)
FEATURES                Location/Qualifiers
     source             1. .23
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                        /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3e+03;
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            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 9 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/9
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                      Location/Qualifiers
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FEATURES             Location/Qualifiers
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  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2400
BD206197
LOCUS       BD206197                22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206197
VERSION     BD206197.1  GI:33015967
KEYWORDS    JP 2002515252-A/10.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 10 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/10
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                      Location/Qualifiers
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            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2401
BD206202
LOCUS       BD206202                22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206202
VERSION     BD206202.1  GI:33015972
KEYWORDS    JP 2002515252-A/15.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 15 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/15
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                      Location/Qualifiers
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FEATURES             Location/Qualifiers
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  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2402
BD206203
LOCUS       BD206203                22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206203
VERSION     BD206203.1  GI:33015973
KEYWORDS    JP 2002515252-A/16.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 16 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/16
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
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RESULT 2396
BD206193
LOCUS       BD206193                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206193
VERSION     BD206193.1  GI:33015963
KEYWORDS    JP 2002515252-A/6.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 6 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/6
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:5062"

  Query Match              0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2397
BD206194
LOCUS       BD206194                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206194
VERSION     BD206194.1  GI:33015964
KEYWORDS    JP 2002515252-A/7.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 7 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/7
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:5062"

  Query Match              0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2398
BD206195
LOCUS       BD206195                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206195
VERSION     BD206195.1  GI:33015965
KEYWORDS    JP 2002515252-A/8.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 8 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/8
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
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            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:5062"

  Query Match              0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2399
BD206196
LOCUS       BD206196                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206196
VERSION     BD206196.1  GI:33015966
KEYWORDS    JP 2002515252-A/9.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
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  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2392
I30201
LOCUS       I30201                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 30 from patent US 5580726.
ACCESSION   I30201
VERSION     I30201.1  GI:1820992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 30 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2393
AX048418
LOCUS       AX048418                  22 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 17 from Patent WO0071747.
ACCESSION   AX048418
VERSION     AX048418.1  GI:12225582
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 17 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2394
AX048418/c
LOCUS       AX048418                  22 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 17 from Patent WO0071747.
ACCESSION   AX048418
VERSION     AX048418.1  GI:12225582
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 17 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2395
BD206192
LOCUS       BD206192                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206192
VERSION     BD206192.1  GI:33015962
KEYWORDS    JP 2002515252-A/5.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 5 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/5
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                      Location/Qualifiers
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            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
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                     /db_xref="taxon:5062"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
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Db          5 AAGCTTTTTTTTTTT 19
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  JOURNAL   Patent: US 5580726-A 20 03-DEC-1996;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2387
I30192
LOCUS       I30192                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 21 from patent US 5580726.
ACCESSION   I30192
VERSION     I30192.1  GI:1820983
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 21 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2388
I30193
LOCUS       I30193                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 22 from patent US 5580726.
ACCESSION   I30193
VERSION     I30193.1  GI:1820984
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 22 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2389
I30194
LOCUS       I30194                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 23 from patent US 5580726.
ACCESSION   I30194
VERSION     I30194.1  GI:1820985
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 23 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2390
I30195
LOCUS       I30195                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 24 from patent US 5580726.
ACCESSION   I30195
VERSION     I30195.1  GI:1820986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 24 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2391
I30200
LOCUS       I30200                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 29 from patent US 5580726.
ACCESSION   I30200
VERSION     I30200.1  GI:1820991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 29 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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          senescence-related genes
  JOURNAL   Patent: US 5744300-A 6 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2382
AR003289
LOCUS       AR003289                22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 11 from patent US 5744300.
ACCESSION   AR003289
VERSION     AR003289.1  GI:3964548
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 11 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2383
AR003290
LOCUS       AR003290                22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 12 from patent US 5744300.
ACCESSION   AR003290
VERSION     AR003290.1  GI:3964549
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 12 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2384
AR043093
LOCUS       AR043093                22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5814445.
ACCESSION   AR043093
VERSION     AR043093.1  GI:5964101
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Belyavsky,A.V. and Ivanova,N.B.
  TITLE     Method of identification and cloning differentially expressed
            messenger RNAs
  JOURNAL   Patent: US 5814445-A 1 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              |||||||||||||||
Db          8 CCTTTTTTTTTTTTT 22


RESULT 2385
I30190
LOCUS       I30190                  22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 19 from patent US 5580726.
ACCESSION   I30190
VERSION     I30190.1  GI:1820981
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 19 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2386
I30191
LOCUS       I30191                  22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 20 from patent US 5580726.
ACCESSION   I30191
VERSION     I30191.1  GI:1820982
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
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                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2377
AR003280
LOCUS       AR003280                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 2 from patent US 5744300.
ACCESSION   AR003280
VERSION     AR003280.1  GI:3964539
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 2 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2378
AR003281
LOCUS       AR003281                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5744300.
ACCESSION   AR003281
VERSION     AR003281.1  GI:3964540
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 3 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2379
AR003282
LOCUS       AR003282                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 4 from patent US 5744300.
ACCESSION   AR003282
VERSION     AR003282.1  GI:3964541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 4 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2380
AR003283
LOCUS       AR003283                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 5 from patent US 5744300.
ACCESSION   AR003283
VERSION     AR003283.1  GI:3964542
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 5 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 2381
AR003284
LOCUS       AR003284                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5744300.
ACCESSION   AR003284
VERSION     AR003284.1  GI:3964543
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
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LOCUS       AX097204                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 2382 from Patent WO0118250.
ACCESSION   AX097204
VERSION     AX097204.1  GI:13513560
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 2382 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 2.5e+03;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1128 GTGAAGCCGAATTTCCT 1144
              || ||||||:||||||
Db         21 GTTAAGCCGARTTTCCT 5


RESULT 2373
AX133222/c
LOCUS       AX133222                 21 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 4440 from Patent WO0130362.
ACCESSION   AX133222
VERSION     AX133222.1  GI:14139532
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 4440 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="IL8 ribozyme recognition site"

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1852 CAACAGACCCACACA 1866
              |||||||||||||||
Db         16 CAACAGACCCACACA 2


RESULT 2374
AX154103/c
LOCUS       AX154103                 21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 201 from Patent WO0138576.
ACCESSION   AX154103
VERSION     AX154103.1  GI:14535717
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0138576-A 201 31-MAY-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   88.2%;  Pred. No. 2.5e+03;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2341 TCCCCGTGGAGGTTCTG 2357
              |||||||:|||| ||||
Db         18 TCCCCGTRGAGGCTCTG 2


RESULT 2375
AX674922/c
LOCUS       AX674922                 21 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 49 from Patent WO03005034.
ACCESSION   AX674922
VERSION     AX674922.1  GI:29333255
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Macdonald,M.L., Zeisler,J.M., Samuels,M., Goldberg,Y.P.,
            Robataille,J.M. and Hayden,M.R.
  TITLE     Processes for identifying therapeutic agents useful in treating
            diseases involving fzd4 gene
  JOURNAL   Patent: WO 03005034-A 49 16-JAN-2003;
            Xenon Genetics, Inc. (CA) ; The University of British Columbia (CA)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAA 2796
              |||||||||||||||
Db         15 ATTGAAAAAAAAAAA 1


RESULT 2376
AR003279
LOCUS       AR003279                 22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5744300.
ACCESSION   AR003279
VERSION     AR003279.1  GI:3964538
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 1 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
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```
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 43 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2368
AX048446
LOCUS       AX048446                  20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 45 from Patent WO0071747.
ACCESSION   AX048446
VERSION     AX048446.1  GI:12225610
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 45 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2369
AX498246
LOCUS       AX498246                  20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 2 from Patent WO0218951.
ACCESSION   AX498246
VERSION     AX498246.1  GI:23343165
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 2 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2370
AX498246/c
LOCUS       AX498246                  20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 2 from Patent WO0218951.
ACCESSION   AX498246
VERSION     AX498246.1  GI:23343165
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 2 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2371
AX498247/c
LOCUS       AX498247                  21 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from Patent WO0218951.
ACCESSION   AX498247
VERSION     AX498247.1  GI:23343166
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 3 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 2372
AX097204/c
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RESULT 2363
AX048440
LOCUS       AX048440                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 39 from Patent WO0071747.
ACCESSION   AX048440
VERSION     AX048440.1  GI:12225604
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 39 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2364
AX048441
LOCUS       AX048441                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 40 from Patent WO0071747.
ACCESSION   AX048441
VERSION     AX048441.1  GI:12225605
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 40 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2365
AX048442
LOCUS       AX048442                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 41 from Patent WO0071747.
ACCESSION   AX048442
VERSION     AX048442.1  GI:12225606
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 41 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2366
AX048443
LOCUS       AX048443                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 42 from Patent WO0071747.
ACCESSION   AX048443
VERSION     AX048443.1  GI:12225607
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 42 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2367
AX048444
LOCUS       AX048444                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 43 from Patent WO0071747.
ACCESSION   AX048444
VERSION     AX048444.1  GI:12225608
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
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  TITLE     Protein having interleukin 13 activity, recombinant DNA coding for
            this protein, transformed cells and microorganisms
  JOURNAL   Patent: US 5652123-A 19 29-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
             ||||||||||||||||
Db         15 CCTTTTTTTTTTTTT 1


RESULT 2359
AX038541/c
LOCUS       AX038541                 20 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 298 from Patent WO0061795.
ACCESSION   AX038541
VERSION     AX038541.1  GI:11227889
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   De Canck,I.D., Rossau,R. and Rombout,A.
  TITLE     Method for the amplification of hla class i alleles
  JOURNAL   Patent: WO 0061795-A 298 19-OCT-2000;
            CANCK ILSE DE (BE) ; ROSSAU RUDI (BE) ; INNOGENETICS NV (BE) ;
            ROMBOUT ANNELIES (BE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1055 GCTCATGTGACTCTCCTGA 1073
              |: ||||||||: ||||||
Db         20 GSCCATGTGACYATCCTGA 2


RESULT 2360
AX048431
LOCUS       AX048431                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 30 from Patent WO0071747.
ACCESSION   AX048431
VERSION     AX048431.1  GI:12225595
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 30 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              ||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2361
AX048434
LOCUS       AX048434                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 33 from Patent WO0071747.
ACCESSION   AX048434
VERSION     AX048434.1  GI:12225598
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 33 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              ||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2362
AX048435
LOCUS       AX048435                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 34 from Patent WO0071747.
ACCESSION   AX048435
VERSION     AX048435.1  GI:12225599
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 34 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              ||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Uematsu,C.
  TITLE     DNA fragment preparation method for gene expression profiling
  JOURNAL   Patent: US 6203988-A 7 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         20 TTTTTTTTTTTTTTT 6


RESULT 2355
AR164799/c
LOCUS       AR164799                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 6 from patent US 6274333.
ACCESSION   AR164799
VERSION     AR164799.1  GI:16237994
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Caput,D., Chalon,P., Ferrara,P. and Vita,N.
  TITLE     Type-2 neurotensin receptor (NT-R2)
  JOURNAL   Patent: US 6274333-A 6 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              |||||||||||||||
Db         15 CCTTTTTTTTTTTTT 1


RESULT 2356
E28096
LOCUS       E28096                   20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for analyzing DNA fragment.
ACCESSION   E28096
VERSION     E28096.1  GI:13018321
KEYWORDS    JP 1999196874-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hideki,K. and Senshu,U.
  TITLE     Method for analyzing DNA fragment
  JOURNAL   Patent: JP 1999196874-A 7 27-JUL-1999;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 1999196874-A/7
            PD   27-JUL-1999
            PF   14-JAN-1998 JP 1998005399
            PR
            PI   HIDEKI KAMIBARA,SENSHU UEMATSU
            PC   C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          6 AAAAAAAAAAAAAAA 20


RESULT 2357
E28096/c
LOCUS       E28096                   20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for analyzing DNA fragment.
ACCESSION   E28096
VERSION     E28096.1  GI:13018321
KEYWORDS    JP 1999196874-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hideki,K. and Senshu,U.
  TITLE     Method for analyzing DNA fragment
  JOURNAL   Patent: JP 1999196874-A 7 27-JUL-1999;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 1999196874-A/7
            PD   27-JUL-1999
            PF   14-JAN-1998 JP 1998005399
            PR
            PI   HIDEKI KAMIBARA,SENSHU UEMATSU
            PC   C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         20 TTTTTTTTTTTTTTT 6


RESULT 2358
I58491/c
LOCUS       I58491                   20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 19 from patent US 5652123.
ACCESSION   I58491
VERSION     I58491.1  GI:2477729
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Caput,D., Ferrara,P., Guillemot,J.-C., Kaghad,M., Labit-Le
            Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
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  JOURNAL   Patent: WO 0071747-A 32 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 2350
A17773/c
LOCUS       A17773                    20 bp    DNA     linear   PAT 30-SEP-1994
DEFINITION  Nucleotide sequence 12 from patent number EP0488900.
ACCESSION   A17773
VERSION     A17773.1  GI:641136
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Caput,D., Ferrara,P., Miloux,B., Minty,A. and Vita,N.
  TITLE     Protein with cytokine activity, recombinant DNA, expression vector
            and hosts for obtaining it
  JOURNAL   Patent: EP 0488900-A 12 03-JUN-1992;
            ELF SANOFI
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              |||||||||||||||
Db         15 CCTTTTTTTTTTTTT 1


RESULT 2351
A29944/c
LOCUS       A29944                    20 bp    DNA     linear   PAT 23-JUN-1995
DEFINITION  Oligonucleotide primer sequence.
ACCESSION   A29944
VERSION     A29944.1  GI:1249025
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le
            Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
  TITLE     Protein having cytokin type activity, recombinant DNA coding for
            this protein, transformed cells and microorganisms
  JOURNAL   Patent: EP 0506574-A 17 30-SEP-1992;
            ELF SANOFI
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              |||||||||||||||
Db         15 CCTTTTTTTTTTTTT 1


RESULT 2352
AR094462/c
LOCUS       AR094462                  20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 20 from patent US 6001649.
ACCESSION   AR094462
VERSION     AR094462.1  GI:10021407
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Caput,D., Ferrara,P., Miloux,B., Minty,A. and Vita,N.
  TITLE     Chemokine NC28 (monocyte chemotactic protein-3, MCP-3) polypeptides
            and their recombinant production
  JOURNAL   Patent: US 6001649-A 20 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2178
              |||||||||||||||
Db         15 CCTTTTTTTTTTTTT 1


RESULT 2353
AR142677
LOCUS       AR142677                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6203988.
ACCESSION   AR142677
VERSION     AR142677.1  GI:15103963
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Uematsu,C.
  TITLE     DNA fragment preparation method for gene expression profiling
  JOURNAL   Patent: US 6203988-A 7 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          6 AAAAAAAAAAAAAAA 20


RESULT 2354
AR142677/c
LOCUS       AR142677                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6203988.
ACCESSION   AR142677
VERSION     AR142677.1  GI:15103963
KEYWORDS    .
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     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              ||||||  |  |  |  ||||||
Db          1 TTTTTTNTNTNTNTTTTTT 19


RESULT 2346
BD140103/c
LOCUS       BD140103                 19 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Enzyme-specific cleavable polynucleotide substrate and assay
            method.
ACCESSION   BD140103
VERSION     BD140103.1  GI:23235048
KEYWORDS    JP 2002508935-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Wei,A.P. and Mach,P.A.
  TITLE     Enzyme-specific cleavable polynucleotide substrate and assay method
  JOURNAL   Patent: JP 2002508935-A 3 26-MAR-2002;
            MINNESOTA MINING AND MANUFACTURING CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002508935-A/3
            PD   26-MAR-2002
            PF   20-AUG-1998 JP 2000527669
            PR   09-JAN-1998 US    09/005260
            PI   AI PING WEI,PATRICK A MACH
            PC   C12N15/09,C12Q1/68,G01N21/75,G01N33/50,G01N33/533,C12N15/00 CC
              amine-modified C6 derivative of deoxythymidine CC
            amine-modified C6 derivative of deoxythymidine CC   amine-modified
            C6 derivative of deoxythymidine CC   amine-modified C6 derivative
            of deoxythymidine FH   Key             Location/Qualifiers
            FT   misc_feature    7
            FT   misc_feature    9
            FT   misc_feature    11
            FT   misc_feature    13.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||  |  |  ||||||
Db         19 AAAAAANANANANAAAAAA 1


RESULT 2347
AR086111
LOCUS       AR086111                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from patent US 5985556.
ACCESSION   AR086111
VERSION     AR086111.1  GI:10012877
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Okano,K.
  TITLE     DNA sequencing method and DNA sample preparation method
  JOURNAL   Patent: US 5985556-A 5 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2348
E13189
LOCUS       E13189                   20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide.
ACCESSION   E13189
VERSION     E13189.1  GI:3251994
KEYWORDS    JP 1997140400-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okano,K. and Kanbara,H.
  TITLE     DETERMINATION OF BASE SEQUENCE
  JOURNAL   Patent: JP 1997140400-A 3 03-JUN-1997;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997140400-A/3
            PD   03-JUN-1997
            PF   13-SEP-1996 JP 1996242929
            PR   18-SEP-1995 JP 95P   238141
            PI   OKANO KAZUNOBU, KANBARA HIDEKI
            PC   C12Q1/68,G01N27/447,G01N33/58//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2349
AX048433
LOCUS       AX048433                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 32 from Patent WO0071747.
ACCESSION   AX048433
VERSION     AX048433.1  GI:12225597
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
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  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAA 2794
              |||||||||||||||
Db         15 GAATTGAAAAAAAAA 1


RESULT 2342
AR360418/c
LOCUS       AR360418                 18 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6596490.
ACCESSION   AR360418
VERSION     AR360418.1  GI:33767448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 6 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAA 2794
              |||||||||||||||
Db         15 GAATTGAAAAAAAAA 1


RESULT 2343
AX441502/c
LOCUS       AX441502                 18 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 6 from Patent WO0206531.
ACCESSION   AX441502
VERSION     AX441502.1  GI:21690463
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 6 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Immobilized oligonucleotide"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAA 2794
              |||||||||||||||
Db         15 GAATTGAAAAAAAAA 1


RESULT 2344
BD096968
LOCUS       BD096968                 18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  SAG:apoptosis sensitivity gene.
ACCESSION   BD096968
VERSION     BD096968.1  GI:22642556
KEYWORDS    JP 2001526063-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Sun,Y.
  TITLE     SAG:apoptosis sensitivity gene
  JOURNAL   Patent: JP 2001526063-A 3 18-DEC-2001;
            WARNER LAMBERT CO
COMMENT     OS   Unidentified
            PN   JP 2001526063-A/3
            PD   18-DEC-2001
            PF   15-DEC-1998 JP 2000525451
            PR   19-DEC-1997 US    60/068179,11-SEP-1998 US    60/099840 PI
            YI SUN
            PC   C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
            PC   A61P39/06,
            PC   A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12Q1/68,
            PC   G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   /desc = 'oligonucleotide P1 downstream primer' FH   Key
                 Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2345
BD140103
LOCUS       BD140103                 19 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Enzyme-specific cleavable polynucleotide substrate and assay
            method.
ACCESSION   BD140103
VERSION     BD140103.1  GI:23235048
KEYWORDS    JP 2002508935-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Wei,A.P. and Mach,P.A.
  TITLE     Enzyme-specific cleavable polynucleotide substrate and assay method
  JOURNAL   Patent: JP 2002508935-A 3 26-MAR-2002;
            MINNESOTA MINING AND MANUFACTURING CO
COMMENT     OS   Artificial Sequence
            PN   JP 2002508935-A/3
            PD   26-MAR-2002
            PF   20-AUG-1998 JP 2000527669
            PR   09-JAN-1998 US    09/005260
            PI   AI PING WEI,PATRICK A MACH
            PC   C12N15/09,C12Q1/68,G01N21/75,G01N33/50,G01N33/533,C12N15/00 CC
              amine-modified C6 derivative of deoxythymidine CC
            amine-modified C6 derivative of deoxythymidine CC   amine-modified
            C6 derivative of deoxythymidine CC   amine-modified C6 derivative
            of deoxythymidine FH   Key             Location/Qualifiers
            FT   misc_feature    7
            FT   misc_feature    9
            FT   misc_feature    11
            FT   misc_feature    13.
FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2338
E32451
LOCUS       E32451                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32451
VERSION     E32451.1  GI:13018687
KEYWORDS    JP 2000037190-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 11 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/11
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2339
E32451/c
LOCUS       E32451                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32451
VERSION     E32451.1  GI:13018687
KEYWORDS    JP 2000037190-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 11 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/11
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2340
AR293748
LOCUS       AR293748                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 5483 from patent US 6537751.
ACCESSION   AR293748
VERSION     AR293748.1  GI:31681032
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 5483 25-MAR-2003;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2410 ATGGGGTCTGTAAAT 2424
              |||||||||||||||
Db          3 ATGGGGTCTGTAAAT 17


RESULT 2341
AR360391/c
LOCUS       AR360391                  18 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6596489.
ACCESSION   AR360391
VERSION     AR360391.1  GI:33767421
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 6 22-JUL-2003;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
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            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2335
E32452
LOCUS       E32452                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32452
VERSION     E32452.1  GI:13018688
KEYWORDS    JP 2000037190-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 12 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/12
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2336
E32461
LOCUS       E32461                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32461
VERSION     E32461.1  GI:13018697
KEYWORDS    JP 2000037190-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 21 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/21
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2337
E32460
LOCUS       E32460                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32460
VERSION     E32460.1  GI:13018696
KEYWORDS    JP 2000037190-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 20 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/20
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
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          CC            anchor
          CC   primer sequence
          FH   Key             Location/Qualifiers
          FT   source          1. .17
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2332
BD171179
LOCUS       BD171179                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171179
VERSION     BD171179.1  GI:27876991
KEYWORDS    WO 0250269-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 4 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/4
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15G', an artificially
            CC            synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2333
BD171179/c
LOCUS       BD171179                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171179
VERSION     BD171179.1  GI:27876991
KEYWORDS    WO 0250269-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 4 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/4
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15G', an artificially
            CC            synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2334
E32450/c
LOCUS       E32450                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32450
VERSION     E32450.1  GI:13018686
KEYWORDS    JP 2000037190-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 10 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/10
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
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  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2329
BD167909/c
LOCUS       BD167909                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167909
VERSION     BD167909.1  GI:27873721
KEYWORDS    WO 0226962-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 8 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/8
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2330
BD168113
LOCUS       BD168113                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168113
VERSION     BD168113.1  GI:27873925
KEYWORDS    WO 0233069-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 20 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/20
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
            A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2331
BD168113/c
LOCUS       BD168113                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168113
VERSION     BD168113.1  GI:27873925
KEYWORDS    WO 0233069-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 20 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/20
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
            A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
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LOCUS       BD167837                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167837
VERSION     BD167837.1  GI:27873649
KEYWORDS    WO 0233122-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 4 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/4
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2327
BD167837/c
LOCUS       BD167837                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167837
VERSION     BD167837.1  GI:27873649
KEYWORDS    WO 0233122-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 4 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/4
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
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FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2328
BD167909
LOCUS       BD167909                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167909
VERSION     BD167909.1  GI:27873721
KEYWORDS    WO 0226962-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 8 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/8
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
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  JOURNAL    Patent: WO 0224903-A 4 28-MAR-2002;
             GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
             NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
             OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
             TAKAHASHI
COMMENT      OS   Artificial Sequence
             PN   WO 0224903-A/4
             PD   28-MAR-2002
             PF   21-SEP-2001 WO 2001JP008246
             PR   25-SEP-2000 JP 00P   291318
             PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
             TAKESHI NAGASU,
             PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
             PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
              C12Q1/68,
             PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
             PC   G01N33/15,
             PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
             CC   Description of Artificial Sequence:an artificially synthesized

             CC            primer
             CC   sequence
             FH   Key             Location/Qualifiers
             FT   source          1. .17
             FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2324
BD143836
LOCUS       BD143836                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143836
VERSION     BD143836.1  GI:27849594
KEYWORDS    JP 2002095500-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 4 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/4
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
             C12N15/00
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2325
BD143836/c
LOCUS       BD143836                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143836
VERSION     BD143836.1  GI:27849594
KEYWORDS    JP 2002095500-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 4 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/4
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
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            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
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FEATURES             Location/Qualifiers
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
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Db         16 AAAAAAAAAAAAAAA 2


RESULT 2326
BD167837
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            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/7
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
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                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2321
BD097336/c
LOCUS       BD097336                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097336
VERSION     BD097336.1  GI:22642910
KEYWORDS    WO 0165259-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 7 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/7
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
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FEATURES              Location/Qualifiers
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  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2322
BD142810
LOCUS       BD142810                  17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142810
VERSION     BD142810.1  GI:23237755
KEYWORDS    WO 0224903-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 4 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/4
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
              C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
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FEATURES              Location/Qualifiers
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  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2323
BD142810/c
LOCUS       BD142810                  17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142810
VERSION     BD142810.1  GI:23237755
KEYWORDS    WO 0224903-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
```

Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi,A.
TITLE 465, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073439-A 4 07-DEC-2000; GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI
COMMENT OS Artificial Sequence
PN WO 0073439-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003191
PR 27-MAY-1999 JP 99P 148784
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC Description of Artificial Sequence:Artificially Synthesized CC Primer Sequence
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1. .17
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Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 2318
BD091775
LOCUS BD091775 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 787, a novel gene related to pollen allergy.
ACCESSION BD091775
VERSION BD091775.1 GI:22637386
KEYWORDS WO 0073440-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi,A.
TITLE 787, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073440-A 4 07-DEC-2000; GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI
COMMENT OS Artificial Sequence
PN WO 0073440-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC Description of Artificial Sequence:Artificially Synthesized CC Primer Sequence
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Query Match 0.5%; Score 15; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 TTTTTTTTTTTTTTT 16

RESULT 2319
BD091775/c
LOCUS BD091775 17 bp DNA linear PAT 27-AUG-2002
DEFINITION 787, a novel gene related to pollen allergy.
ACCESSION BD091775
VERSION BD091775.1 GI:22637386
KEYWORDS WO 0073440-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi,A.
TITLE 787, a novel gene related to pollen allergy
JOURNAL Patent: WO 0073440-A 4 07-DEC-2000; GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA, TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI, YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI
COMMENT OS Artificial Sequence
PN WO 0073440-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC Description of Artificial Sequence:Artificially Synthesized CC Primer Sequence
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/mol_type="genomic DNA"
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Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
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Db 16 AAAAAAAAAAAAAAA 2

RESULT 2320
BD097336
LOCUS BD097336 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for examination for allergosis.
ACCESSION BD097336
VERSION BD097336.1 GI:22642910
KEYWORDS WO 0165259-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0165259-A 7 07-SEP-2001; GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA

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KEYWORDS    WO 0073435-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
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  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2315
BD091744/c
LOCUS       BD091744                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091744
VERSION     BD091744.1  GI:22637355
KEYWORDS    WO 0073435-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2316
BD091752
LOCUS       BD091752                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091752
VERSION     BD091752.1  GI:22637363
KEYWORDS    WO 0073439-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 4 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/4
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
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FEATURES              Location/Qualifiers
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                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2317
BD091752/c
LOCUS       BD091752                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091752
VERSION     BD091752.1  GI:22637363
KEYWORDS    WO 0073439-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
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  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1739 GGTGACAAGTACTGG 1753
             |||||||||||||||
Db         15 GGTGACAAGTACTGG 1


RESULT 2311
AX723850
LOCUS       AX723850                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 1537 from Patent WO03025176.
ACCESSION   AX723850
VERSION     AX723850.1  GI:30503193
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 1537 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTT 2177
             |||||||||||||||
Db          3 TCCTTTTTTTTTTTT 17


RESULT 2312
BD011732
LOCUS       BD011732                 17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011732
VERSION     BD011732.1  GI:22091921
KEYWORDS    WO 0065050-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 4 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/4
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2313
BD011732/c
LOCUS       BD011732                 17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011732
VERSION     BD011732.1  GI:22091921
KEYWORDS    WO 0065050-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 4 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/4
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2314
BD091744
LOCUS       BD091744                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091744
VERSION     BD091744.1  GI:22637355
```

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RESULT 2306
AX146684
LOCUS       AX146684                  17 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 26 from Patent WO0134834.
ACCESSION   AX146684
VERSION     AX146684.1  GI:14285077
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 26 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2307
AX146685
LOCUS       AX146685                  17 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 27 from Patent WO0134834.
ACCESSION   AX146685
VERSION     AX146685.1  GI:14285078
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 27 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2308
AX475808/c
LOCUS       AX475808                  17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1029 from Patent WO0224750.
ACCESSION   AX475808
VERSION     AX475808.1  GI:22215093
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 1029 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1739 GGTGACAAGTACTGG 1753
              |||||||||||||||
Db         17 GGTGACAAGTACTGG 3


RESULT 2309
AX475809/c
LOCUS       AX475809                  17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1030 from Patent WO0224750.
ACCESSION   AX475809
VERSION     AX475809.1  GI:22215094
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 1030 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1739 GGTGACAAGTACTGG 1753
              |||||||||||||||
Db         16 GGTGACAAGTACTGG 2


RESULT 2310
AX475810/c
LOCUS       AX475810                  17 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1031 from Patent WO0224750.
ACCESSION   AX475810
VERSION     AX475810.1  GI:22215095
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     Human kidney tumor overexpressed membrane protein 1
  JOURNAL   Patent: WO 0224750-A 1031 28-MAR-2002;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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DEFINITION  Sequence 730 from patent US 6566127.
ACCESSION   AR323328
VERSION     AR323328.1  GI:33709136
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 730 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
              |||||||||||||||
Db          3 GCTTTTTTTTTTTGA 17


RESULT 2302
AR323329
LOCUS       AR323329                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 731 from patent US 6566127.
ACCESSION   AR323329
VERSION     AR323329.1  GI:33709137
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 731 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
              |||||||||||||||
Db          2 GCTTTTTTTTTTTGA 16


RESULT 2303
AR323330
LOCUS       AR323330                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 732 from patent US 6566127.
ACCESSION   AR323330
VERSION     AR323330.1  GI:33709138
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 732 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
              |||||||||||||||
Db          1 GCTTTTTTTTTTTGA 15


RESULT 2304
AX146680
LOCUS       AX146680                 17 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 22 from Patent WO0134834.
ACCESSION   AX146680
VERSION     AX146680.1  GI:14285073
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 22 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2305
AX146681
LOCUS       AX146681                 17 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 23 from Patent WO0134834.
ACCESSION   AX146681
VERSION     AX146681.1  GI:14285074
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 23 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15
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LOCUS       AR186699                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2187 from patent US 6346398.
ACCESSION   AR186699
VERSION     AR186699.1  GI:20232664
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2187 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
              |||||||||||||||
Db          1 GCTTTTTTTTTTTGA 15


RESULT 2297
AR256849
LOCUS       AR256849                  17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 3 from patent US 6485916.
ACCESSION   AR256849
VERSION     AR256849.1  GI:27306475
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Muramatsu,T., Fujita,T., Kiyama,M., Irie,T. and Okano,K.
  TITLE     Preparation method of nucleic acid sample for rare expressed genes
            and analyzing method using the prepared nucleic acid samples
            thereby
  JOURNAL   Patent: US 6485916-A 3 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2298
AR256849/c
LOCUS       AR256849                  17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 3 from patent US 6485916.
ACCESSION   AR256849
VERSION     AR256849.1  GI:27306475
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Muramatsu,T., Fujita,T., Kiyama,M., Irie,T. and Okano,K.
  TITLE     Preparation method of nucleic acid sample for rare expressed genes
            and analyzing method using the prepared nucleic acid samples
            thereby
  JOURNAL   Patent: US 6485916-A 3 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2299
AR266626
LOCUS       AR266626                  17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 64 from patent US 6495319.
ACCESSION   AR266626
VERSION     AR266626.1  GI:29695690
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 64 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2300
AR266626/c
LOCUS       AR266626                  17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 64 from patent US 6495319.
ACCESSION   AR266626
VERSION     AR266626.1  GI:29695690
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 64 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2301
AR323328
LOCUS       AR323328                  17 bp    RNA     linear   PAT 17-AUG-2003
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  AUTHORS   Takamichi,M., Tsuyoshi,F., Masaharu,K., Takashi,I. and Kazunori,O.
  TITLE     Method for preparing nucleic acid sample for analyzing minor gene,
            nucleic acid sample thus prepared and method for analyzing nucleic
            acid sample by using the same, and reagent kit and analysis service
            for using the same
  JOURNAL   Patent: JP 2000037193-A 3 08-FEB-2000;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 2000037193-A/3
            PD   08-FEB-2000
            PF   19-MAY-1999 JP 1999138051
            PR
            PI   TAKAMICHI MATSUMURA,TSUYOSHI FUJITA,MASAHARU KIYAMA, PI
            TAKASHI IRIE,
            PI   KAZUNORI OKANO
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2293
E59657/c
LOCUS       E59657                   17 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for preparing nucleic acid sample for analyzing minor gene,
            nucleic acid sample thus prepared and method for analyzing nucleic
            acid sample by using the same, and reagent kit and analysis service
             for using the same.
ACCESSION   E59657
VERSION     E59657.1  GI:13019451
KEYWORDS    JP 2000037193-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Takamichi,M., Tsuyoshi,F., Masaharu,K., Takashi,I. and Kazunori,O.
  TITLE     Method for preparing nucleic acid sample for analyzing minor gene,
            nucleic acid sample thus prepared and method for analyzing nucleic
            acid sample by using the same, and reagent kit and analysis service
            for using the same
  JOURNAL   Patent: JP 2000037193-A 3 08-FEB-2000;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 2000037193-A/3
            PD   08-FEB-2000
            PF   19-MAY-1999 JP 1999138051
            PR
            PI   TAKAMICHI MATSUMURA,TSUYOSHI FUJITA,MASAHARU KIYAMA, PI
            TAKASHI IRIE,
            PI   KAZUNORI OKANO
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2294
AR186697
LOCUS       AR186697                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2185 from patent US 6346398.
ACCESSION   AR186697
VERSION     AR186697.1  GI:20232662
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2185 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
             |||||||||||||||
Db          3 GCTTTTTTTTTTTGA 17


RESULT 2295
AR186698
LOCUS       AR186698                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2186 from patent US 6346398.
ACCESSION   AR186698
VERSION     AR186698.1  GI:20232663
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2186 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
             |||||||||||||||
Db          2 GCTTTTTTTTTTTGA 16


RESULT 2296
AR186699
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KEYWORDS    JP 2002516564-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Umansky,S. and Melkonyan,H.
  TITLE     Gene family encoding apoptosis-associated peptides, peptides
            encoded thereby and method of using the same
  JOURNAL   Patent: JP 2002516564-A 6 04-JUN-2002;
            TANOX INC
COMMENT     OS   Unidentified
            PN   JP 2002516564-A/6
            PD   04-JUN-2002
            PF   24-SEP-1997 JP 1998515877
            PR   24-SEP-1996 US    60/026603,11-OCT-1996 US    60/028363 PI
            SAMUIL UMANSKY,HOVSEP MELKONYAN
            PC   C12N15/12,C12N15/62,C07K14/47,C07K16/18,C12Q1/68,G01N33/53, PC
              G01N33/68,
            PC   A61K38/17
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Gene family encoding apoptosis-associated peptides, peptides
            CC            encoded
            CC   thereby and method of using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2290
E34260
LOCUS       E34260                    17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34260
VERSION     E34260.1  GI:18624265
KEYWORDS    JP 2000106879-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 4 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/4
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2291
E34260/c
LOCUS       E34260                    17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34260
VERSION     E34260.1  GI:18624265
KEYWORDS    JP 2000106879-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 4 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/4
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .17
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FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2292
E59657
LOCUS       E59657                    17 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for preparing nucleic acid sample for analyzing minor gene,
            nucleic acid sample thus prepared and method for analyzing nucleic
            acid sample by using the same, and reagent kit and analysis service
             for using the same.
ACCESSION   E59657
VERSION     E59657.1  GI:13019451
KEYWORDS    JP 2000037193-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
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            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/19
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
            A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2287
BD171177/c
LOCUS       BD171177                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171177
VERSION     BD171177.1  GI:27876989
KEYWORDS    WO 0250269-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 2 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/2
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15A', an artificially
            CC           synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2288
BD171178
LOCUS       BD171178                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171178
VERSION     BD171178.1  GI:27876990
KEYWORDS    WO 0250269-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 3 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/3
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15C', an artificially
            CC           synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2289
BD217905
LOCUS       BD217905                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Gene family encoding apoptosis-associated peptides, peptides
            encoded thereby and method of using the same.
ACCESSION   BD217905
VERSION     BD217905.1  GI:33027675
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PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized

CC primer
CC sequence
FH Key Location/Qualifiers
FT source 1. .17
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 2284
BD167908
LOCUS BD167908 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD167908
VERSION BD167908.1 GI:27873720
KEYWORDS WO 0226962-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 7 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0226962-A/7
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC C12Q1/68,
PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized

CC primer
CC sequence
FH Key Location/Qualifiers
FT source 1. .17
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
|||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 2285
BD168111/c
LOCUS BD168111 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION BD168111
VERSION BD168111.1 GI:27873923
KEYWORDS WO 0233069-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0233069-A 18 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0233069-A/18
PD 25-APR-2002
PF 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC A61K39/395,
PC C07K14/47,C07K16/18//C12P21/02,C12P21/08
CC Description of Artificial Sequence:an artificially synthesized

CC anchor
CC primer sequence
FH Key Location/Qualifiers
FT source 1. .17
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 2286
BD168112
LOCUS BD168112 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION BD168112
VERSION BD168112.1 GI:27873924
KEYWORDS WO 0233069-A/19.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0233069-A 19 25-APR-2002;

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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2281
BD167835/c
LOCUS       BD167835                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167835
VERSION     BD167835.1  GI:27873647
KEYWORDS    WO 0233122-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 2 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/2
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2282
BD167836
LOCUS       BD167836                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167836
VERSION     BD167836.1  GI:27873648
KEYWORDS    WO 0233122-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 3 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/3
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2283
BD167907/c
LOCUS       BD167907                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167907
VERSION     BD167907.1  GI:27873719
KEYWORDS    WO 0226962-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 6 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/6
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
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RESULT 2278
BD142809
LOCUS       BD142809                 17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142809
VERSION     BD142809.1  GI:23237754
KEYWORDS    WO 0224903-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 3 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/3
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2279
BD143834/c
LOCUS       BD143834                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143834
VERSION     BD143834.1  GI:27849592
KEYWORDS    JP 2002095500-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 2 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/2
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
             C12N15/00
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2280
BD143835
LOCUS       BD143835                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143835
VERSION     BD143835.1  GI:27849593
KEYWORDS    JP 2002095500-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 3 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/3
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
             C12N15/00
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
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BD097334/c
LOCUS       BD097334                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097334
VERSION     BD097334.1  GI:22642908
KEYWORDS    WO 0165259-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 5 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/5
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2276
BD097335
LOCUS       BD097335                 17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097335
VERSION     BD097335.1  GI:22642909
KEYWORDS    WO 0165259-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 6 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/6
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
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FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2277
BD142808/c
LOCUS       BD142808                 17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142808
VERSION     BD142808.1  GI:23237753
KEYWORDS    WO 0224903-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 2 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/2
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2
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Db         16 AAAAAAAAAAAAAAA 2


RESULT 2272
BD091751
LOCUS       BD091751                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091751
VERSION     BD091751.1  GI:22637362
KEYWORDS    WO 0073439-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
            Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2273
BD091773/c
LOCUS       BD091773                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091773
VERSION     BD091773.1  GI:22637384
KEYWORDS    WO 0073440-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 2 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/2
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2274
BD091774
LOCUS       BD091774                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091774
VERSION     BD091774.1  GI:22637385
KEYWORDS    WO 0073440-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2275
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  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2269
BD091742/c
LOCUS       BD091742                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091742
VERSION     BD091742.1  GI:22637353
KEYWORDS    WO 0073435-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 2 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/2
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2270
BD091743
LOCUS       BD091743                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091743
VERSION     BD091743.1  GI:22637354
KEYWORDS    WO 0073435-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2271
BD091750/c
LOCUS       BD091750                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091750
VERSION     BD091750.1  GI:22637361
KEYWORDS    WO 0073439-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 2 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/2
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
            Sequence
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
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AR323671/c
LOCUS       AR323671                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1073 from patent US 6566127.
ACCESSION   AR323671
VERSION     AR323671.1  GI:33709479
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1073 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         17 AAAAAAAAAAAAAAA 3


RESULT 2266
AR323674
LOCUS       AR323674                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1076 from patent US 6566127.
ACCESSION   AR323674
VERSION     AR323674.1  GI:33709482
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1076 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2267
BD011730/c
LOCUS       BD011730                  17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011730
VERSION     BD011730.1  GI:22091919
KEYWORDS    WO 0065050-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 2 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/2
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2268
BD011731
LOCUS       BD011731                  17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011731
VERSION     BD011731.1  GI:22091920
KEYWORDS    WO 0065050-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 3 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/3
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
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  JOURNAL   Patent: JP 2000106879-A 3 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/3
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 2261
AR187061/c
LOCUS       AR187061                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2549 from patent US 6346398.
ACCESSION   AR187061
VERSION     AR187061.1  GI:20233026
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2549 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         17 AAAAAAAAAAAAAAA 3


RESULT 2262
AR187064
LOCUS       AR187064                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2552 from patent US 6346398.
ACCESSION   AR187064
VERSION     AR187064.1  GI:20233029
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2552 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2263
AR241830
LOCUS       AR241830                  17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 118 from patent US 6472154.
ACCESSION   AR241830
VERSION     AR241830.1  GI:27287642
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 118 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2264
AR266625/c
LOCUS       AR266625                  17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 63 from patent US 6495319.
ACCESSION   AR266625
VERSION     AR266625.1  GI:29695689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 63 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2265
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DEFINITION  Isolation of novel aging factor gene P23.
ACCESSION   BD073878
VERSION     BD073878.1  GI:22619481
KEYWORDS    JP 2001512698-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Suishelm,K., Hosier,S. and Kubbies,M.
  TITLE     Isolation of novel aging factor gene P23
  JOURNAL   Patent: JP 2001512698-A 3 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS   Unidentified
            PN   JP 2001512698-A/3
            PD   28-AUG-2001
            PF   05-AUG-1998 JP 2000506375
            PR   08-AUG-1997 US    08/908873
            PI   KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02,
            PC   C12P21/08,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Isolation of novel aging factor gene P23
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .16
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2258
BD073879
LOCUS       BD073879                 16 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Isolation of novel aging factor gene P23.
ACCESSION   BD073879
VERSION     BD073879.1  GI:22619482
KEYWORDS    JP 2001512698-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Suishelm,K., Hosier,S. and Kubbies,M.
  TITLE     Isolation of novel aging factor gene P23
  JOURNAL   Patent: JP 2001512698-A 4 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS   Unidentified
            PN   JP 2001512698-A/4
            PD   28-AUG-2001
            PF   05-AUG-1998 JP 2000506375
            PR   08-AUG-1997 US    08/908873
            PI   KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02,
            PC   C12P21/08,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Isolation of novel aging factor gene P23
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .16
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2259
E34258/c
LOCUS       E34258                   17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34258
VERSION     E34258.1  GI:18624263
KEYWORDS    JP 2000106879-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 2 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/2
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .17
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 2260
E34259
LOCUS       E34259                   17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34259
VERSION     E34259.1  GI:18624264
KEYWORDS    JP 2000106879-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="H-T11-A PRIMER"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2253
AX394753
LOCUS       AX394753                 16 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 4 from Patent WO0218568.
ACCESSION   AX394753
VERSION     AX394753.1  GI:21065832
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Molecules involved in the regulation of insulin resistance syndrome
            (irs)
  JOURNAL   Patent: WO 0218568-A 4 07-MAR-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="H-T11-C PRIMER"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2254
AX394783
LOCUS       AX394783                 16 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 7 from Patent WO0218421.
ACCESSION   AX394783
VERSION     AX394783.1  GI:21065857
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Human and mouse e2-protein, nucleic acids coding therefor and uses
            thereof
  JOURNAL   Patent: WO 0218421-A 7 07-MAR-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="H-T11-A"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2255
AX394784
LOCUS       AX394784                 16 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 8 from Patent WO0218421.
ACCESSION   AX394784
VERSION     AX394784.1  GI:21065858
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Human and mouse e2-protein, nucleic acids coding therefor and uses
            thereof
  JOURNAL   Patent: WO 0218421-A 8 07-MAR-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="H-T11-C"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2256
AX419608
LOCUS       AX419608                 16 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 13 from Patent WO0187935.
ACCESSION   AX419608
VERSION     AX419608.1  GI:21523980
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Heaney,A.P., Ishikawa,H., Yu,R., Horwitz,G.A., Zhang,X. and
            Melmed,S.
  TITLE     Methods of modulating angiogenesis by regulating the expression of
            pituitary tumor transforming gene (pttg)
  JOURNAL   Patent: WO 0187935-A 13 22-NOV-2001;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="n = a, g, or c; Anchored primer sequence."

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2257
BD073878
LOCUS       BD073878                 16 bp    DNA     linear   PAT 27-AUG-2002
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RESULT 2248
AX352388
LOCUS       AX352388                 16 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 13 from Patent WO0187934.
ACCESSION   AX352388
VERSION     AX352388.1  GI:18617659
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Horwitz,G.A., Zhang,X., Heaney,A. and Melmed,S.
  TITLE     Treatment of neoplasia / transformation using pituitary tumor
            transforming gene carboxy terminal peptides
  JOURNAL   Patent: WO 0187934-A 13 22-NOV-2001;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="n = a, g, or c; Anchored primer sequence."

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2249
AX359760/c
LOCUS       AX359760                 16 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 64 from Patent WO0200691.
ACCESSION   AX359760
VERSION     AX359760.1  GI:18675467
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Tchernev,V., Putturajan,M., Malyankar,U.M., Gusev,V.,
            Herrmann,J.L., Macdougall,J.R., Rastelli,L., Zhong,H., Spytek,K.A.,
            Shenoy,S., Gerlach,V.L., Gangolli,E.A., Stone,D.J. and Smithson,G.
  TITLE     Novel polynucleotides and polypeptides encoded thereby
  JOURNAL   Patent: WO 0200691-A 64 03-JAN-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTT 2179
              |||||||||||||||
Db         15 CTTTTTTTTTTTTTT 1


RESULT 2250
AX391465
LOCUS       AX391465                 16 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 1 from Patent WO0216632.
ACCESSION   AX391465
VERSION     AX391465.1  GI:19700075
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Pharmaceutical compositions comprising a modulator of adamts-1
  JOURNAL   Patent: WO 0216632-A 1 28-FEB-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2251
AX391466
LOCUS       AX391466                 16 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 2 from Patent WO0216632.
ACCESSION   AX391466
VERSION     AX391466.1  GI:19700076
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Pharmaceutical compositions comprising a modulator of adamts-1
  JOURNAL   Patent: WO 0216632-A 2 28-FEB-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2252
AX394752
LOCUS       AX394752                 16 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 3 from Patent WO0218568.
ACCESSION   AX394752
VERSION     AX394752.1  GI:21065831
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Molecules involved in the regulation of insulin resistance syndrome
            (irs)
  JOURNAL   Patent: WO 0218568-A 3 07-MAR-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
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REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 20 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2244
AX253410
LOCUS       AX253410                  16 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 22 from Patent WO0171013.
ACCESSION   AX253410
VERSION     AX253410.1  GI:16073944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Clendennen,S.K. and Kellogg,J.A.
  TITLE     Melon promoters for expression of transgenes in plants
  JOURNAL   Patent: WO 0171013-A 22 27-SEP-2001;
            Exelixis Plant Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2245
AX253411
LOCUS       AX253411                  16 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 23 from Patent WO0171013.
ACCESSION   AX253411
VERSION     AX253411.1  GI:16073945
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Clendennen,S.K. and Kellogg,J.A.
  TITLE     Melon promoters for expression of transgenes in plants
  JOURNAL   Patent: WO 0171013-A 23 27-SEP-2001;
            Exelixis Plant Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2246
AX306364
LOCUS       AX306364                  16 bp    DNA     linear   PAT 11-DEC-2001
DEFINITION  Sequence 13 from Patent WO0187039.
ACCESSION   AX306364
VERSION     AX306364.1  GI:17645596
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Prezant,T.R., Heaney,A.P. and Melmed,S.
  TITLE     Treatment of neoplasia / transformation using pituitary tumor
            transforming gene 2
  JOURNAL   Patent: WO 0187039-A 13 22-NOV-2001;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="n = a, g, or c; Anchored primer sequence."

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2247
AX320077
LOCUS       AX320077                  16 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 13 from Patent WO0188116.
ACCESSION   AX320077
VERSION     AX320077.1  GI:17901578
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stoika,R., Horwitz,G.A., Zhang,X. and Melmed,S.
  TITLE     Method of modulating activation of lymphocytes via modulation of
            pituitary tumor transforming gene, related screeining methods
  JOURNAL   Patent: WO 0188116-A 13 22-NOV-2001;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="n = a, g, or c; Anchored primer sequence."

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15
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  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2239
AX003112
LOCUS       AX003112                 16 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 14 from Patent WO9934217.
ACCESSION   AX003112
VERSION     AX003112.1  GI:9926974
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Xu,D. and Liew,F.Y.
  TITLE     Reagents specific for st21 and uses therefor
  JOURNAL   Patent: WO 9934217-A 14 08-JUL-1999;
            XU DAMO (GB); LIEW FOO YEW (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PRIMER"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2240
AX127438
LOCUS       AX127438                 16 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 81 from Patent WO0130999.
ACCESSION   AX127438
VERSION     AX127438.1  GI:14133903
KEYWORDS    .
SOURCE      Bruguiera gymnorrhiza
  ORGANISM  Bruguiera gymnorrhiza
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Malpighiales; Rhizophoraceae; Bruguiera.
REFERENCE   1
  AUTHORS   Karube,I. and Hanagata,N.
  TITLE     Salt tolerance genes
  JOURNAL   Patent: WO 0130999-A 81 03-MAY-2001;
            EBARA CORPORATION (JP)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Bruguiera gymnorrhiza"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:39984"
                     /note="Artificially Synthesized Primer Sequence"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2241
AX127439
LOCUS       AX127439                 16 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 82 from Patent WO0130999.
ACCESSION   AX127439
VERSION     AX127439.1  GI:14133906
KEYWORDS    .
SOURCE      Bruguiera gymnorrhiza
  ORGANISM  Bruguiera gymnorrhiza
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Malpighiales; Rhizophoraceae; Bruguiera.
REFERENCE   1
  AUTHORS   Karube,I. and Hanagata,N.
  TITLE     Salt tolerance genes
  JOURNAL   Patent: WO 0130999-A 82 03-MAY-2001;
            EBARA CORPORATION (JP)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Bruguiera gymnorrhiza"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:39984"
                     /note="Artificially Synthesized Primer Sequence"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2242
AX146677
LOCUS       AX146677                 16 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 19 from Patent WO0134834.
ACCESSION   AX146677
VERSION     AX146677.1  GI:14285070
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 19 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2243
AX146678
LOCUS       AX146678                 16 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 20 from Patent WO0134834.
ACCESSION   AX146678
VERSION     AX146678.1  GI:14285071
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
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                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2234
AR266620
LOCUS       AR266620                 16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 58 from patent US 6495319.
ACCESSION   AR266620
VERSION     AR266620.1  GI:29695684
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 58 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2235
AR266646
LOCUS       AR266646                 16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 84 from patent US 6495319.
ACCESSION   AR266646
VERSION     AR266646.1  GI:29695710
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 84 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2236
AR266647
LOCUS       AR266647                 16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 85 from patent US 6495319.
ACCESSION   AR266647
VERSION     AR266647.1  GI:29695711
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 85 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2237
AR429378
LOCUS       AR429378                 16 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 16 from patent US 6642438.
ACCESSION   AR429378
VERSION     AR429378.1  GI:40189571
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Clendennen,S.K., Kellogg,J.A., Phan,C.B., Mathews,H.V. and
            Webb,N.M.
  TITLE     Melon promoters for expression of transgenes in plants
  JOURNAL   Patent: US 6642438-A 16 04-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2238
AR429379
LOCUS       AR429379                 16 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 17 from patent US 6642438.
ACCESSION   AR429379
VERSION     AR429379.1  GI:40189572
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Clendennen,S.K., Kellogg,J.A., Phan,C.B., Mathews,H.V. and
            Webb,N.M.
  TITLE     Melon promoters for expression of transgenes in plants
  JOURNAL   Patent: US 6642438-A 17 04-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
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REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 6 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2229
AR257442
LOCUS       AR257442                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6486308.
ACCESSION   AR257442
VERSION     AR257442.1  GI:27307453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 7 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2230
AR257442/c
LOCUS       AR257442                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6486308.
ACCESSION   AR257442
VERSION     AR257442.1  GI:27307453
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 7 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2231
AR257443
LOCUS       AR257443                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6486308.
ACCESSION   AR257443
VERSION     AR257443.1  GI:27307454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 8 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2232
AR257443/c
LOCUS       AR257443                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 8 from patent US 6486308.
ACCESSION   AR257443
VERSION     AR257443.1  GI:27307454
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 8 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2233
AR266619
LOCUS       AR266619                  16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 57 from patent US 6495319.
ACCESSION   AR266619
VERSION     AR266619.1  GI:29695683
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 57 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .16
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ACCESSION   AR257439
VERSION     AR257439.1  GI:27307450
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 4 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2224
AR257439/c
LOCUS       AR257439                 16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 4 from patent US 6486308.
ACCESSION   AR257439
VERSION     AR257439.1  GI:27307450
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 4 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2225
AR257440
LOCUS       AR257440                 16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6486308.
ACCESSION   AR257440
VERSION     AR257440.1  GI:27307451
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 5 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2226
AR257440/c
LOCUS       AR257440                 16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6486308.
ACCESSION   AR257440
VERSION     AR257440.1  GI:27307451
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 5 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2227
AR257441
LOCUS       AR257441                 16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 6 from patent US 6486308.
ACCESSION   AR257441
VERSION     AR257441.1  GI:27307452
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 6 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2228
AR257441/c
LOCUS       AR257441                 16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 6 from patent US 6486308.
ACCESSION   AR257441
VERSION     AR257441.1  GI:27307452
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
RESULT 2218
AR221698/c
LOCUS       AR221698                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 8 from patent US 6426408.
ACCESSION   AR221698
VERSION     AR221698.1  GI:23328770
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 8 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2219
AR221992
LOCUS       AR221992                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 1 from patent US 6428994.
ACCESSION   AR221992
VERSION     AR221992.1  GI:23329318
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Thompson,R.F., Gomi,H. and Sun,W.
  TITLE     cDNA, genomic, and predicted protein sequences of learning-induced
            kinases
  JOURNAL   Patent: US 6428994-A 1 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2220
AR232210
LOCUS       AR232210                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6455305.
ACCESSION   AR232210
VERSION     AR232210.1  GI:27274200
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Melmed,S. and Pei,L.
  TITLE     Pituitary-tumor-transforming-genes, and related products
  JOURNAL   Patent: US 6455305-A 7 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2221
AR257438
LOCUS       AR257438                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 3 from patent US 6486308.
ACCESSION   AR257438
VERSION     AR257438.1  GI:27307449
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 3 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2222
AR257438/c
LOCUS       AR257438                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 3 from patent US 6486308.
ACCESSION   AR257438
VERSION     AR257438.1  GI:27307449
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 3 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2223
AR257439
LOCUS       AR257439                  16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 4 from patent US 6486308.
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```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2213
AR221696
LOCUS       AR221696                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 6 from patent US 6426408.
ACCESSION   AR221696
VERSION     AR221696.1  GI:23328768
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 6 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2214
AR221696/c
LOCUS       AR221696                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 6 from patent US 6426408.
ACCESSION   AR221696
VERSION     AR221696.1  GI:23328768
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 6 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2215
AR221697
LOCUS       AR221697                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 7 from patent US 6426408.
ACCESSION   AR221697
VERSION     AR221697.1  GI:23328769
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 7 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2216
AR221697/c
LOCUS       AR221697                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 7 from patent US 6426408.
ACCESSION   AR221697
VERSION     AR221697.1  GI:23328769
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 7 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2217
AR221698
LOCUS       AR221698                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 8 from patent US 6426408.
ACCESSION   AR221698
VERSION     AR221698.1  GI:23328770
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 8 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15
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     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2208
AR221693/c
LOCUS       AR221693                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from patent US 6426408.
ACCESSION   AR221693
VERSION     AR221693.1  GI:23328765
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 3 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2209
AR221694
LOCUS       AR221694                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 4 from patent US 6426408.
ACCESSION   AR221694
VERSION     AR221694.1  GI:23328766
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 4 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2210
AR221694/c
LOCUS       AR221694                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 4 from patent US 6426408.
ACCESSION   AR221694
VERSION     AR221694.1  GI:23328766
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 4 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2211
AR221695
LOCUS       AR221695                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 5 from patent US 6426408.
ACCESSION   AR221695
VERSION     AR221695.1  GI:23328767
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 5 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2212
AR221695/c
LOCUS       AR221695                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 5 from patent US 6426408.
ACCESSION   AR221695
VERSION     AR221695.1  GI:23328767
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 5 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
```

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            Webb,N.M.
  TITLE     Banana promoter and melon promoter for expression of transgene in
  JOURNAL   Patent: JP 2002539779-A 17 26-NOV-2002;
            EXELIXIS PLANT SCIENCES INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002539779-A/17
            PD   26-NOV-2002
            PF   17-MAR-2000 JP 2000606722
            PR   19-MAR-1999 US    60/125310
            PI   STEPHANIE K CLENDENNEN,JILL A KELLOGG,CHAU B PHAN,HELENA V  PI
              MATHEWS,
            PI   NANCY M WEBB
            PC   C12N15/09,A01H1/00,C12N5/10,C12Q1/68//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC   oligonucleotide primer
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2204
BD274864
LOCUS       BD274864                 16 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Bioassay for Identifying Estrogen Receptor beta/alpha Selective
            Modulators.
ACCESSION   BD274864
VERSION     BD274864.1  GI:33084632
KEYWORDS    JP 2002533098-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Harris,H. and But,R.A.
  TITLE     Bioassay for Identifying Estrogen Receptor beta/alpha Selective
            Modulators
  JOURNAL   Patent: JP 2002533098-A 14 08-OCT-2002;
            WYETH HOLDINGS CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002533098-A/14
            PD   08-OCT-2002
            PF   17-DEC-1999 JP 2000589734
            PR   18-DEC-1998 US    60/112790
            PI   heather harris,ramesh a but
            CC   Description of Artificial Sequence:oligonucleotide FH   Key
                 Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2205
I16032
LOCUS       I16032                   16 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 6 from patent US 5473060.
ACCESSION   I16032
VERSION     I16032.1  GI:1250940
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic applications
  JOURNAL   Patent: US 5473060-A 6 05-DEC-1995;
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTT 2179
              |||||||||||||||
Db          2 CTTTTTTTTTTTTTT 16


RESULT 2206
I28367
LOCUS       I28367                   16 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 6 from patent US 5571677.
ACCESSION   I28367
VERSION     I28367.1  GI:1819143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromomolecular structures
  JOURNAL   Patent: US 5571677-A 6 05-NOV-1996;
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTT 2179
              |||||||||||||||
Db          2 CTTTTTTTTTTTTTT 16


RESULT 2207
AR221693
LOCUS       AR221693                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from patent US 6426408.
ACCESSION   AR221693
VERSION     AR221693.1  GI:23328765
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 3 30-JUL-2002;
FEATURES              Location/Qualifiers
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RESULT 2199
AR002257
LOCUS       AR002257                  16 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 6 from patent US 5741643.
ACCESSION   AR002257
VERSION     AR002257.1  GI:3963811
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps
  JOURNAL   Patent: US 5741643-A 6 21-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTT 2179
             |||||||||||||||
Db          2 CTTTTTTTTTTTTTT 16


RESULT 2200
AR045207
LOCUS       AR045207                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5817795.
ACCESSION   AR045207
VERSION     AR045207.1  GI:5966672
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M. and Lloyd,D.H.
  TITLE     Oligonucleotide clamps having diagnostic and therapeutic
            applications
  JOURNAL   Patent: US 5817795-A 6 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTT 2179
             |||||||||||||||
Db          2 CTTTTTTTTTTTTTT 16


RESULT 2201
AR051238
LOCUS       AR051238                  16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5830658.
ACCESSION   AR051238
VERSION     AR051238.1  GI:5974602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5830658-A 6 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTT 2179
             |||||||||||||||
Db          2 CTTTTTTTTTTTTTT 16


RESULT 2202
BD268990
LOCUS       BD268990                  16 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Banana promoter and melon promoter for expression of transgene in
            plant.
ACCESSION   BD268990
VERSION     BD268990.1  GI:33078758
KEYWORDS    JP 2002539779-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Clendennen,S.K., Kellogg,J.A., Phan,C.B., Mathews,H.V. and
            Webb,N.M.
  TITLE     Banana promoter and melon promoter for expression of transgene in
  JOURNAL   Patent: JP 2002539779-A 16 26-NOV-2002;
            EXELIXIS PLANT SCIENCES INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002539779-A/16
            PD   26-NOV-2002
            PF   17-MAR-2000 JP 2000606722
            PR   19-MAR-1999 US    60/125310
            PI   STEPHANIE K CLENDENNEN,JILL A KELLOGG,CHAU B PHAN,HELENA V  PI
              MATHEWS,
            PI   NANCY M WEBB
            PC   C12N15/09,A01H1/00,C12N5/10,C12Q1/68//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC   oligonucleotide primer
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 2203
BD268991
LOCUS       BD268991                  16 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Banana promoter and melon promoter for expression of transgene in
            plant.
ACCESSION   BD268991
VERSION     BD268991.1  GI:33078759
KEYWORDS    JP 2002539779-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Clendennen,S.K., Kellogg,J.A., Phan,C.B., Mathews,H.V. and
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KEYWORDS    JP 2002512791-A/22.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 22 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/22
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                              virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2197
BD209488
LOCUS       BD209488                 15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD209488
VERSION     BD209488.1  GI:33019258
KEYWORDS    JP 2002512791-A/3078.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 3078 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/3078
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                              virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2198
BD209488/c
LOCUS       BD209488                 15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD209488
VERSION     BD209488.1  GI:33019258
KEYWORDS    JP 2002512791-A/3078.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 3078 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/3078
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                              virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1
```

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  AUTHORS   Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
            Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
  TITLE     Method and detector for identifying subtypes of human papiloma
  JOURNAL   Patent: JP 2002360271-A 647 17-DEC-2002;
            KING CAR FOOD INDUSTRIAL CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002360271-A/647
            PD   17-DEC-2002
            PF   28-NOV-2001 JP 2001362595
            PR   04-MAY-2001 TW     90110785
            PI   CHING-YEE LING,RUEY-WEN LIN,ZHOU-MENG YOO,XIN-HSUAN HUANG,BOW-
            PI   HAENG LEE,
            PI   SHENG-HSIUNG LEE,YI-JU LIN,CI-CHUNG HUANG,HAN-CHANG HSU,CHA-
            PI   WEN SHI,
            PI   CHIH-XIN YEH,YI-FENG CAO,CHIH-LONG PAN
            PC   C12N15/09,C12N15/09,C12M1/34,C12Q1/04,C12Q1/42,C12Q1/68 PC
            ,C12Q1/70,G01N21/64,
            PC   G01N33/53,G01N33/574,G01N33/58,G01N37/00//(C12M1/34,C12R1:93),
            PC   (C12Q1/70,C12R1:93),C12N15/00,C12N15/00
            CC   Added sequence for 3' end labeling of oligonucleic acid. FH
            Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .15
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2194
BD184668/c
LOCUS       BD184668                 15 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Method and detector for identifying subtypes of human papiloma
            viruses.
ACCESSION   BD184668
VERSION     BD184668.1  GI:31876868
KEYWORDS    JP 2002360271-A/647.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
            Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
  TITLE     Method and detector for identifying subtypes of human papiloma
  JOURNAL   Patent: JP 2002360271-A 647 17-DEC-2002;
            KING CAR FOOD INDUSTRIAL CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002360271-A/647
            PD   17-DEC-2002
            PF   28-NOV-2001 JP 2001362595
            PR   04-MAY-2001 TW     90110785
            PI   CHING-YEE LING,RUEY-WEN LIN,ZHOU-MENG YOO,XIN-HSUAN HUANG,BOW-
            PI   HAENG LEE,
            PI   SHENG-HSIUNG LEE,YI-JU LIN,CI-CHUNG HUANG,HAN-CHANG HSU,CHA-
            PI   WEN SHI,
            PI   CHIH-XIN YEH,YI-FENG CAO,CHIH-LONG PAN
            PC   C12N15/09,C12N15/09,C12M1/34,C12Q1/04,C12Q1/42,C12Q1/68 PC
            ,C12Q1/70,G01N21/64,
            PC   G01N33/53,G01N33/574,G01N33/58,G01N37/00//(C12M1/34,C12R1:93),
            PC   (C12Q1/70,C12R1:93),C12N15/00,C12N15/00
            CC   Added sequence for 3' end labeling of oligonucleic acid. FH
            Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .15
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db          15 AAAAAAAAAAAAAAA 1


RESULT 2195
BD206432
LOCUS       BD206432                 15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD206432
VERSION     BD206432.1  GI:33016202
KEYWORDS    JP 2002512791-A/22.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 22 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/22
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                 virus)'.
FEATURES            Location/Qualifiers
     source         1. .15
                    /organism="unidentified"
                    /mol_type="genomic RNA"
                    /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2196
BD206432/c
LOCUS       BD206432                 15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD206432
VERSION     BD206432.1  GI:33016202
```

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ACCESSION   BD074424
VERSION     BD074424.1  GI:22620027
KEYWORDS    JP 2001514855-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pecker,I., Vlodavsky,I. and Elena,F.
  TITLE     Polynucleotide encoding polypeptide having heparanase activity and
            expression of the polypeptide in induced cell
  JOURNAL   Patent: JP 2001514855-A 5 18-SEP-2001;
            INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
            & DEVELOPMENT LTD
COMMENT     OS   Nucleic acid
            PN   JP 2001514855-A/5
            PD   18-SEP-2001
            PF   31-AUG-1998 JP 2000508806
            PR   02-SEP-1997 US    08/922170,02-JUL-1998 US    09/109386 PI
            IRIS PECKER,ISRAEL VLODAVSKY,FEINSTEIN ELENA
            PC   C12N15/09,A61K38/00,A61P9/10,A61P17/00,A61P29/00,A61P35/00, PC
              A61P37/00,
            PC   A61P43/00,C12N5/10,C12N9/24,C12Q1/68,G01N33/15,G01N33/50// PC
             A61K39/395,
            PC   A61K39/395,C12N15/00,A61K37/02,C12N5/00
            CC   Polynucleotide encoding polypeptide having
            heparanase activity
            CC            and
            CC   expression of the polypeptide in induced cell FH   Key
                Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Nucleic acid'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2191
BD084687
LOCUS       BD084687                 15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Releasable nonvolatile mass-label molecules.
ACCESSION   BD084687
VERSION     BD084687.1  GI:22630297
KEYWORDS    JP 2001524808-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Montforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
  TITLE     Releasable nonvolatile mass-label molecules
  JOURNAL   Patent: JP 2001524808-A 5 04-DEC-2001;
            GENETRACE SYSTEMS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001524808-A/5
            PD   04-DEC-2001
            PF   10-DEC-1997 JP 1998526924
            PR   10-DEC-1996 US    60/033037,16-MAY-1997 US    60/046719 PI
            JOSEPH A MONTFORTE,CHRISTOPHER H BECKER,DANIEL J POLLART, PI
            THOMAS A SHALER
            PC   C12Q1/68,G01N15/06,G01N33/53,G01N33/542,C12P19/34,C12M1/00, PC
              B01D59/44,
            PC   H01J49/00,C07H21/04,C07K15/26,C07K15/28
            CC   Description of Artificial Sequence: oligo dT15 primer FH   Key
                    Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2192
BD084687/c
LOCUS       BD084687                 15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Releasable nonvolatile mass-label molecules.
ACCESSION   BD084687
VERSION     BD084687.1  GI:22630297
KEYWORDS    JP 2001524808-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Montforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
  TITLE     Releasable nonvolatile mass-label molecules
  JOURNAL   Patent: JP 2001524808-A 5 04-DEC-2001;
            GENETRACE SYSTEMS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001524808-A/5
            PD   04-DEC-2001
            PF   10-DEC-1997 JP 1998526924
            PR   10-DEC-1996 US    60/033037,16-MAY-1997 US    60/046719 PI
            JOSEPH A MONTFORTE,CHRISTOPHER H BECKER,DANIEL J POLLART, PI
            THOMAS A SHALER
            PC   C12Q1/68,G01N15/06,G01N33/53,G01N33/542,C12P19/34,C12M1/00, PC
              B01D59/44,
            PC   H01J49/00,C07H21/04,C07K15/26,C07K15/28
            CC   Description of Artificial Sequence: oligo dT15 primer FH   Key
                    Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2193
BD184668
LOCUS       BD184668                 15 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Method and detector for identifying subtypes of human papiloma
            viruses.
ACCESSION   BD184668
VERSION     BD184668.1  GI:31876868
KEYWORDS    JP 2002360271-A/647.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
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KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hammonds,T.R.
  TITLE     Method and polynukleotides for assaying the activity of a dna
            modifying enzyme
  JOURNAL   Patent: WO 03008643-A 6 30-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide 6"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2187
AX711176
LOCUS       AX711176                  15 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 476 from Patent EP1288296.
ACCESSION   AX711176
VERSION     AX711176.1  GI:29787557
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 476 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Polyadenylation region"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2188
AX711176/c
LOCUS       AX711176                  15 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 476 from Patent EP1288296.
ACCESSION   AX711176
VERSION     AX711176.1  GI:29787557
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 476 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Polyadenylation region"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2189
BD074424
LOCUS       BD074424                  15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polynucleotide encoding polypeptide having heparanase activity and
            expression of the polypeptide in induced cell.
ACCESSION   BD074424
VERSION     BD074424.1  GI:22620027
KEYWORDS    JP 2001514855-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pecker,I., Vlodavsky,I. and Elena,F.
  TITLE     Polynucleotide encoding polypeptide having heparanase activity and
            expression of the polypeptide in induced cell
  JOURNAL   Patent: JP 2001514855-A 5 18-SEP-2001;
            INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
            & DEVELOPMENT LTD
COMMENT     OS   Nucleic acid
            PN   JP 2001514855-A/5
            PD   18-SEP-2001
            PF   31-AUG-1998 JP 2000508806
            PR   02-SEP-1997 US    08/922170,02-JUL-1998 US    09/109386 PI
            IRIS PECKER,ISRAEL VLODAVSKY,FEINSTEIN ELENA
            PC   C12N15/09,A61K38/00,A61P9/10,A61P17/00,A61P29/00,A61P35/00, PC
              A61P37/00,
            PC   A61P43/00,C12N5/10,C12N9/24,C12Q1/68,G01N33/15,G01N33/50// PC
             A61K39/395,
            PC   A61K39/395,C12N15/00,A61K37/02,C12N5/00
            CC   Polynucleotide encoding polypeptide having
            heparanase activity
            CC          and
            CC   expression of the polypeptide in induced cell FH   Key
                Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Nucleic acid'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2190
BD074424/c
LOCUS       BD074424                  15 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Polynucleotide encoding polypeptide having heparanase activity and
            expression of the polypeptide in induced cell.
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Db          1 TTTTTTTTTTTTTTT 15


RESULT 2182
AX633199/c
LOCUS       AX633199                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 338 from Patent EP1260586.
ACCESSION   AX633199
VERSION     AX633199.1  GI:28468813
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 338 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2183
AX633201/c
LOCUS       AX633201                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 340 from Patent EP1260586.
ACCESSION   AX633201
VERSION     AX633201.1  GI:28468815
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 340 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
             |||||||||||||||
Db         15 GAAAAAAAAAAAAAA 1


RESULT 2184
AX633203/c
LOCUS       AX633203                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 342 from Patent EP1260586.
ACCESSION   AX633203
VERSION     AX633203.1  GI:28468817
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 342 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAA 2798
             |||||||||||||||
Db         15 TGAAAAAAAAAAAAA 1


RESULT 2185
AX696087
LOCUS       AX696087                 15 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 6 from Patent WO03008643.
ACCESSION   AX696087
VERSION     AX696087.1  GI:29419249
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hammonds,T.R.
  TITLE     Method and polynukleotides for assaying the activity of a dna
            modifying enzyme
  JOURNAL   Patent: WO 03008643-A 6 30-JAN-2003;
            Cancer Research Technology Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Polynucleotide 6"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2186
AX696087/c
LOCUS       AX696087                 15 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 6 from Patent WO03008643.
ACCESSION   AX696087
VERSION     AX696087.1  GI:29419249
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="lys-Digoxigenin"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2178
AX525143/c
LOCUS       AX525143                 15 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 3 from Patent WO02066675.
ACCESSION   AX525143
VERSION     AX525143.1  GI:25170128
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kahmann,S. and Mueller,O.
  TITLE     Methods for detecting mutations
  JOURNAL   Patent: WO 02066675-A 3 29-AUG-2002;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="lys-Digoxigenin"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2179
AX633197
LOCUS       AX633197                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 336 from Patent EP1260586.
ACCESSION   AX633197
VERSION     AX633197.1  GI:28468811
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 336 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2180
AX633197/c
LOCUS       AX633197                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 336 from Patent EP1260586.
ACCESSION   AX633197
VERSION     AX633197.1  GI:28468811
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 336 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2181
AX633199
LOCUS       AX633199                 15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 338 from Patent EP1260586.
ACCESSION   AX633199
VERSION     AX633199.1  GI:28468813
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 338 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
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RESULT 2173
AX429224
LOCUS       AX429224                 15 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 1 from Patent EP1201765.
ACCESSION   AX429224
VERSION     AX429224.1  GI:21540537
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schubart,D., Habenberger,P., Stein-Gerlach,M. and Bevec,D.
  TITLE     Cellular kinases involved in cytomegalovirus infection and their
            inhibition
  JOURNAL   Patent: EP 1201765-A 1 02-MAY-2002;
            Axxima Pharmaceuticals Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="N/A"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2174
AX429224/c
LOCUS       AX429224                 15 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 1 from Patent EP1201765.
ACCESSION   AX429224
VERSION     AX429224.1  GI:21540537
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schubart,D., Habenberger,P., Stein-Gerlach,M. and Bevec,D.
  TITLE     Cellular kinases involved in cytomegalovirus infection and their
            inhibition
  JOURNAL   Patent: EP 1201765-A 1 02-MAY-2002;
            Axxima Pharmaceuticals Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="N/A"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2175
AX525141
LOCUS       AX525141                 15 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 1 from Patent WO02066675.
ACCESSION   AX525141
VERSION     AX525141.1  GI:25170126
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kahmann,S. and Mueller,O.
  TITLE     Methods for detecting mutations
  JOURNAL   Patent: WO 02066675-A 1 29-AUG-2002;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="lys-Biotin"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2176
AX525141/c
LOCUS       AX525141                 15 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 1 from Patent WO02066675.
ACCESSION   AX525141
VERSION     AX525141.1  GI:25170126
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kahmann,S. and Mueller,O.
  TITLE     Methods for detecting mutations
  JOURNAL   Patent: WO 02066675-A 1 29-AUG-2002;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="lys-Biotin"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2177
AX525143
LOCUS       AX525143                 15 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 3 from Patent WO02066675.
ACCESSION   AX525143
VERSION     AX525143.1  GI:25170128
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kahmann,S. and Mueller,O.
  TITLE     Methods for detecting mutations
  JOURNAL   Patent: WO 02066675-A 3 29-AUG-2002;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
     misc_structure  1
                     /note="(dt-COOH)2-branch-"
     misc_feature    15
                     /note="NH2
                     kunstliche"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2169
AX180140
LOCUS       AX180140                 15 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 3 from Patent WO0146464.
ACCESSION   AX180140
VERSION     AX180140.1  GI:15132181
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: WO 0146464-A 3 28-JUN-2001;
            LION Bioscience AG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="stem of branched oligonucleotide - base 1
                     modified~Modification is (NH2-C6-TTT)2-branch-"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2170
AX180140/c
LOCUS       AX180140                 15 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 3 from Patent WO0146464.
ACCESSION   AX180140
VERSION     AX180140.1  GI:15132181
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: WO 0146464-A 3 28-JUN-2001;
            LION Bioscience AG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="stem of branched oligonucleotide - base 1
                     modified~Modification is (NH2-C6-TTT)2-branch-"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2171
AX180141
LOCUS       AX180141                 15 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 4 from Patent WO0146464.
ACCESSION   AX180141
VERSION     AX180141.1  GI:15132182
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: WO 0146464-A 4 28-JUN-2001;
            LION Bioscience AG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="stem of branched oligonucleotide - base 1
                     modified~Modification is (dT-COOH)2-branch-"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2172
AX180141/c
LOCUS       AX180141                 15 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 4 from Patent WO0146464.
ACCESSION   AX180141
VERSION     AX180141.1  GI:15132182
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Huber,M., Schmidt,W., Mueller,M. and Hiller,R.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: WO 0146464-A 4 28-JUN-2001;
            LION Bioscience AG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="stem of branched oligonucleotide - base 1
                     modified~Modification is (dT-COOH)2-branch-"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1
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  JOURNAL    Patent: WO 0125442-A 26 12-APR-2001;
             CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES               Location/Qualifiers
     source            1. .15
                       /organism="synthetic construct"
                       /mol_type="unassigned DNA"
                       /db_xref="taxon:32630"
                       /note="oligo dA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2165
AX127272
LOCUS       AX127272                  15 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 3 from Patent EP1111068.
ACCESSION   AX127272
VERSION     AX127272.1  GI:14133346
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: EP 1111068-A 3 27-JUN-2001;
            LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES               Location/Qualifiers
     source            1. .15
                       /organism="synthetic construct"
                       /mol_type="unassigned DNA"
                       /db_xref="taxon:32630"
     misc_structure    1
                       /note="(NH2-C6-ttt)2-branch-"
     misc_feature      15
                       /note="NH2
                       kunstliche"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2166
AX127272/c
LOCUS       AX127272                  15 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 3 from Patent EP1111068.
ACCESSION   AX127272
VERSION     AX127272.1  GI:14133346
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: EP 1111068-A 3 27-JUN-2001;
            LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES               Location/Qualifiers
     source            1. .15
                       /organism="synthetic construct"
                       /mol_type="unassigned DNA"
                       /db_xref="taxon:32630"
     misc_structure    1
                       /note="(NH2-C6-ttt)2-branch-"
     misc_feature      15
                       /note="NH2
                       kunstliche"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2167
AX127273
LOCUS       AX127273                  15 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 4 from Patent EP1111068.
ACCESSION   AX127273
VERSION     AX127273.1  GI:14133347
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: EP 1111068-A 4 27-JUN-2001;
            LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES               Location/Qualifiers
     source            1. .15
                       /organism="synthetic construct"
                       /mol_type="unassigned DNA"
                       /db_xref="taxon:32630"
     misc_structure    1
                       /note="(dt-COOH)2-branch-"
     misc_feature      15
                       /note="NH2
                       kunstliche"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2168
AX127273/c
LOCUS       AX127273                  15 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 4 from Patent EP1111068.
ACCESSION   AX127273
VERSION     AX127273.1  GI:14133347
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
  TITLE     Branched compound for use in nucleic acid detection and analysis
            reactions
  JOURNAL   Patent: EP 1111068-A 4 27-JUN-2001;
            LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES               Location/Qualifiers
     source            1. .15
                       /organism="synthetic construct"
                       /mol_type="unassigned DNA"
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2160
AX026066/c
LOCUS       AX026066                 15 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 4 from Patent WO0028046.
ACCESSION   AX026066
VERSION     AX026066.1  GI:10187502
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Marraccini,P. and Rogers,J.
  TITLE     Coffea arabica mannanase
  JOURNAL   Patent: WO 0028046-A 4 18-MAY-2000;
            NESTLE SA (CH) ; MARRACCINI PIERRE (FR) ; ROGERS JOHN (FR)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="OLIGONUCLEOTIDE DE SYNTHESE"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2161
AX048407
LOCUS       AX048407                 15 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 6 from Patent WO0071747.
ACCESSION   AX048407
VERSION     AX048407.1  GI:12225571
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 6 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Region A"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2162
AX048407/c
LOCUS       AX048407                 15 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 6 from Patent WO0071747.
ACCESSION   AX048407
VERSION     AX048407.1  GI:12225571
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 6 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Region A"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2163
AX106973
LOCUS       AX106973                 15 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 26 from Patent WO0125442.
ACCESSION   AX106973
VERSION     AX106973.1  GI:13922522
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
  TITLE     Dna polymerase lambda and uses thereof
  JOURNAL   Patent: WO 0125442-A 26 12-APR-2001;
            CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligo dA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2164
AX106973/c
LOCUS       AX106973                 15 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 26 from Patent WO0125442.
ACCESSION   AX106973
VERSION     AX106973.1  GI:13922522
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
  TITLE     Dna polymerase lambda and uses thereof
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RESULT 2155
AR410213
LOCUS       AR410213                  15 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 9 from patent US 6635452.
ACCESSION   AR410213
VERSION     AR410213.1  GI:40161460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
  TITLE     Releasable nonvolatile mass label molecules
  JOURNAL   Patent: US 6635452-A 9 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2156
AR410213/c
LOCUS       AR410213                  15 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 9 from patent US 6635452.
ACCESSION   AR410213
VERSION     AR410213.1  GI:40161460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
  TITLE     Releasable nonvolatile mass label molecules
  JOURNAL   Patent: US 6635452-A 9 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2157
AX004877
LOCUS       AX004877                  15 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 6 from Patent WO9910527.
ACCESSION   AX004877
VERSION     AX004877.1  GI:9928277
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 6 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3' palmityl modified oligonucleotide"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2158
AX004877/c
LOCUS       AX004877                  15 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 6 from Patent WO9910527.
ACCESSION   AX004877
VERSION     AX004877.1  GI:9928277
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 6 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3' palmityl modified oligonucleotide"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2159
AX026066
LOCUS       AX026066                  15 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 4 from Patent WO0028046.
ACCESSION   AX026066
VERSION     AX026066.1  GI:10187502
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Marraccini,P. and Rogers,J.
  TITLE     Coffea arabica mannanase
  JOURNAL   Patent: WO 0028046-A 4 18-MAY-2000;
            NESTLE SA (CH) ; MARRACCINI PIERRE (FR) ; ROGERS JOHN (FR)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="OLIGONUCLEOTIDE DE SYNTHESE"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
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  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2150
AR266630/c
LOCUS       AR266630                 15 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 68 from patent US 6495319.
ACCESSION   AR266630
VERSION     AR266630.1  GI:29695694
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 68 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2151
AR371280
LOCUS       AR371280                 15 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 17 from patent US 6395474.
ACCESSION   AR371280
VERSION     AR371280.1  GI:34608212
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 17 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2152
AR371280/c
LOCUS       AR371280                 15 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 17 from patent US 6395474.
ACCESSION   AR371280
VERSION     AR371280.1  GI:34608212
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 17 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2153
AR371281
LOCUS       AR371281                 15 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 18 from patent US 6395474.
ACCESSION   AR371281
VERSION     AR371281.1  GI:34608213
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 18 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2154
AR371281/c
LOCUS       AR371281                 15 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 18 from patent US 6395474.
ACCESSION   AR371281
VERSION     AR371281.1  GI:34608213
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 18 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1
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                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2145
AR200477
LOCUS       AR200477                 15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 20 from patent US 6357163.
ACCESSION   AR200477
VERSION     AR200477.1  GI:20251365
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Use of nucleic acid analogues in diagnostics and analytical
            procedures
  JOURNAL   Patent: US 6357163-A 20 19-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2146
AR200477/c
LOCUS       AR200477                 15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 20 from patent US 6357163.
ACCESSION   AR200477
VERSION     AR200477.1  GI:20251365
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Use of nucleic acid analogues in diagnostics and analytical
            procedures
  JOURNAL   Patent: US 6357163-A 20 19-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2147
AR222461
LOCUS       AR222461                 15 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 21 from patent US 6429300.
ACCESSION   AR222461
VERSION     AR222461.1  GI:23329992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 21 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2148
AR222461/c
LOCUS       AR222461                 15 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 21 from patent US 6429300.
ACCESSION   AR222461
VERSION     AR222461.1  GI:23329992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 21 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2149
AR266630
LOCUS       AR266630                 15 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 68 from patent US 6495319.
ACCESSION   AR266630
VERSION     AR266630.1  GI:29695694
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 68 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
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     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2140
I29068/c
LOCUS       I29068                  15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 6 from patent US 5576427.
ACCESSION   I29068
VERSION     I29068.1  GI:1819859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 6 19-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2141
I38641
LOCUS       I38641                  15 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5614617.
ACCESSION   I38641
VERSION     I38641.1  GI:2084695
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 1 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2142
I38641/c
LOCUS       I38641                  15 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5614617.
ACCESSION   I38641
VERSION     I38641.1  GI:2084695
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 1 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2143
AR200476
LOCUS       AR200476                15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 19 from patent US 6357163.
ACCESSION   AR200476
VERSION     AR200476.1  GI:20251364
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Use of nucleic acid analogues in diagnostics and analytical
            procedures
  JOURNAL   Patent: US 6357163-A 19 19-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2144
AR200476/c
LOCUS       AR200476                15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 19 from patent US 6357163.
ACCESSION   AR200476
VERSION     AR200476.1  GI:20251364
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Use of nucleic acid analogues in diagnostics and analytical
            procedures
  JOURNAL   Patent: US 6357163-A 19 19-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .15
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            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,
            Tsubura,H., Tanaka,H. and Ishiguro,Y.
  TITLE     S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
  JOURNAL   Patent: JP 1994335389-A 7 06-DEC-1994;
            KAGOME CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994335389-A/7
            PD   06-DEC-1994
            PF   27-MAY-1993 JP 1993126286
            PI   TEI ITSUIRU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI
            OTA AKINORI,
            PI   TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI
            ISHIGURO YUKIO
            PC   C12N9/22,C12N15/52;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .15
            FT                   /organism='Artificial sequences'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2137
E12591
LOCUS       E12591                    15 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  pRIMER.
ACCESSION   E12591
VERSION     E12591.1  GI:3251423
KEYWORDS    JP 1997028381-A/8.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Tei,I., Minami,K. and Takagi,M.
  TITLE     S- RIBONUCLEASE GENE AND PROMOTER SEQUENCE
  JOURNAL   Patent: JP 1997028381-A 8 04-FEB-1997;
            TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997028381-A/8
            PD   04-FEB-1997
            PF   24-JUL-1995 JP 1995187557
            PI   TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI PC
            C12N15/09,C07H21/04,C12N1/21//A01H1/00,C12N5/10,C12N9/22, PC
            (C12N1/21,
            PC   C12R1:19);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .15
            FT                   /organism='Artificial sequences'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2138
E12591/c
LOCUS       E12591                    15 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  pRIMER.
ACCESSION   E12591
VERSION     E12591.1  GI:3251423
KEYWORDS    JP 1997028381-A/8.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Tei,I., Minami,K. and Takagi,M.
  TITLE     S- RIBONUCLEASE GENE AND PROMOTER SEQUENCE
  JOURNAL   Patent: JP 1997028381-A 8 04-FEB-1997;
            TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997028381-A/8
            PD   04-FEB-1997
            PF   24-JUL-1995 JP 1995187557
            PI   TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI PC
            C12N15/09,C07H21/04,C12N1/21//A01H1/00,C12N5/10,C12N9/22, PC
            (C12N1/21,
            PC   C12R1:19);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .15
            FT                   /organism='Artificial sequences'.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2139
I29068
LOCUS       I29068                    15 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 6 from patent US 5576427.
ACCESSION   I29068
VERSION     I29068.1  GI:1819859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Cook,P.D., Delecki,D.J. and Guinosso,C.
  TITLE     Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
  JOURNAL   Patent: US 5576427-A 6 19-NOV-1996;
FEATURES              Location/Qualifiers
```

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RESULT 2132
AR113918/c
LOCUS       AR113918                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 364 from patent US 6132967.
ACCESSION   AR113918
VERSION     AR113918.1  GI:14094240
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 364 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAA 2798
              |||||||||||||||
Db         15 TGAAAAAAAAAAAAA 1


RESULT 2133
AR170375
LOCUS       AR170375                  15 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 1 from patent US 6291438.
ACCESSION   AR170375
VERSION     AR170375.1  GI:17908334
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Wang,J.H.
  TITLE     Antiviral anticancer poly-substituted phenyl derivatized
            oligoribonucleotides and methods for their use
  JOURNAL   Patent: US 6291438-A 1 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2134
AR170375/c
LOCUS       AR170375                  15 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 1 from patent US 6291438.
ACCESSION   AR170375
VERSION     AR170375.1  GI:17908334
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Wang,J.H.
  TITLE     Antiviral anticancer poly-substituted phenyl derivatized
            oligoribonucleotides and methods for their use
  JOURNAL   Patent: US 6291438-A 1 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2135
E08522
LOCUS       E08522                    15 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer.
ACCESSION   E08522
VERSION     E08522.1  GI:2176637
KEYWORDS    JP 1994335389-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,
            Tsubura,H., Tanaka,H. and Ishiguro,Y.
  TITLE     S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
  JOURNAL   Patent: JP 1994335389-A 7 06-DEC-1994;
            KAGOME CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994335389-A/7
            PD   06-DEC-1994
            PF   27-MAY-1993 JP 1993126286
            PI   TEI ITSUIRU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI
            OTA AKINORI,
            PI   TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI
            ISHIGURO YUKIO
            PC   C12N9/22,C12N15/52;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .15
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2136
E08522/c
LOCUS       E08522                    15 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer.
ACCESSION   E08522
VERSION     E08522.1  GI:2176637
KEYWORDS    JP 1994335389-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
```

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LOCUS       AR113915                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 361 from patent US 6132967.
ACCESSION   AR113915
VERSION     AR113915.1  GI:14094237
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 361 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2128
AR113915/c
LOCUS       AR113915                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 361 from patent US 6132967.
ACCESSION   AR113915
VERSION     AR113915.1  GI:14094237
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 361 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2129
AR113916
LOCUS       AR113916                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 362 from patent US 6132967.
ACCESSION   AR113916
VERSION     AR113916.1  GI:14094238
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 362 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2130
AR113916/c
LOCUS       AR113916                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 362 from patent US 6132967.
ACCESSION   AR113916
VERSION     AR113916.1  GI:14094238
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 362 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2131
AR113917/c
LOCUS       AR113917                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 363 from patent US 6132967.
ACCESSION   AR113917
VERSION     AR113917.1  GI:14094239
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Ribozyme treatment of diseases or conditions related to levels of
            intercellular adhesion molecule-1 (ICAM-1)
  JOURNAL   Patent: US 6132967-A 363 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
             |||||||||||||||
Db         15 GAAAAAAAAAAAAAA 1
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              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2122
AR084516/c
LOCUS       AR084516                  15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 5 from patent US 5981185.
ACCESSION   AR084516
VERSION     AR084516.1  GI:10011287
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 5 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2123
AR084520
LOCUS       AR084520                  15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 9 from patent US 5981185.
ACCESSION   AR084520
VERSION     AR084520.1  GI:10011291
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 9 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2124
AR084520/c
LOCUS       AR084520                  15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 9 from patent US 5981185.
ACCESSION   AR084520
VERSION     AR084520.1  GI:10011291
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 9 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2125
AR105981
LOCUS       AR105981                  15 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6103474.
ACCESSION   AR105981
VERSION     AR105981.1  GI:12820046
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
  TITLE     Hybridization assay signal enhancement
  JOURNAL   Patent: US 6103474-A 4 15-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2126
AR105981/c
LOCUS       AR105981                  15 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6103474.
ACCESSION   AR105981
VERSION     AR105981.1  GI:12820046
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
  TITLE     Hybridization assay signal enhancement
  JOURNAL   Patent: US 6103474-A 4 15-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2127
AR113915
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Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2117
AR056159/c
LOCUS       AR056159                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 363 from patent US 5837542.
ACCESSION   AR056159
VERSION     AR056159.1  GI:5981736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 363 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              |||||||||||||||
Db         15 GAAAAAAAAAAAAAA 1


RESULT 2118
AR056160/c
LOCUS       AR056160                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 364 from patent US 5837542.
ACCESSION   AR056160
VERSION     AR056160.1  GI:5981737
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 364 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAA 2798
              |||||||||||||||
Db         15 TGAAAAAAAAAAAAA 1


RESULT 2119
AR080676
LOCUS       AR080676                 15 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 5 from patent US 5968822.
ACCESSION   AR080676
VERSION     AR080676.1  GI:10007406
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     Polynucleotide encoding a polypeptide having heparanase activity
            and expression of same in transduced cells
  JOURNAL   Patent: US 5968822-A 5 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2120
AR080676/c
LOCUS       AR080676                 15 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 5 from patent US 5968822.
ACCESSION   AR080676
VERSION     AR080676.1  GI:10007406
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Pecker,I., Vlodavsky,I. and Feinstein,E.
  TITLE     Polynucleotide encoding a polypeptide having heparanase activity
            and expression of same in transduced cells
  JOURNAL   Patent: US 5968822-A 5 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2121
AR084516
LOCUS       AR084516                 15 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 5 from patent US 5981185.
ACCESSION   AR084516
VERSION     AR084516.1  GI:10011287
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 5 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2112
AR049971/c
LOCUS       AR049971                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5824793.
ACCESSION   AR049971
VERSION     AR049971.1  GI:5971963
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
  JOURNAL   Patent: US 5824793-A 4 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2113
AR056157
LOCUS       AR056157                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 361 from patent US 5837542.
ACCESSION   AR056157
VERSION     AR056157.1  GI:5981734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 361 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2114
AR056157/c
LOCUS       AR056157                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 361 from patent US 5837542.
ACCESSION   AR056157
VERSION     AR056157.1  GI:5981734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 361 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2115
AR056158
LOCUS       AR056158                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 362 from patent US 5837542.
ACCESSION   AR056158
VERSION     AR056158.1  GI:5981735
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 362 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2116
AR056158/c
LOCUS       AR056158                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 362 from patent US 5837542.
ACCESSION   AR056158
VERSION     AR056158.1  GI:5981735
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
  TITLE     Intercellular adhesion molecule-1 (ICAM-1) ribozymes
  JOURNAL   Patent: US 5837542-A 362 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2107
AR048768
LOCUS       AR048768                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5821354.
ACCESSION   AR048768
VERSION     AR048768.1  GI:5971111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Leclerc,G. and Martel,R.
  TITLE     Radiolabeled DNA oligonucleotide and method of preparation
  JOURNAL   Patent: US 5821354-A 2 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2108
AR048768/c
LOCUS       AR048768                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5821354.
ACCESSION   AR048768
VERSION     AR048768.1  GI:5971111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Leclerc,G. and Martel,R.
  TITLE     Radiolabeled DNA oligonucleotide and method of preparation
  JOURNAL   Patent: US 5821354-A 2 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2109
AR049970
LOCUS       AR049970                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5824793.
ACCESSION   AR049970
VERSION     AR049970.1  GI:5971962
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
  JOURNAL   Patent: US 5824793-A 3 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2110
AR049970/c
LOCUS       AR049970                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5824793.
ACCESSION   AR049970
VERSION     AR049970.1  GI:5971962
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
  JOURNAL   Patent: US 5824793-A 3 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2111
AR049971
LOCUS       AR049971                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5824793.
ACCESSION   AR049971
VERSION     AR049971.1  GI:5971963
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
  JOURNAL   Patent: US 5824793-A 4 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
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                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2102
AR029403/c
LOCUS       AR029403                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5859233.
ACCESSION   AR029403
VERSION     AR029403.1  GI:5941376
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates
  JOURNAL   Patent: US 5859233-A 4 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 2103
AR034895
LOCUS       AR034895                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 10 from patent US 5869643.
ACCESSION   AR034895
VERSION     AR034895.1  GI:5950500
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 10 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2104
AR034895/c
LOCUS       AR034895                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 10 from patent US 5869643.
ACCESSION   AR034895
VERSION     AR034895.1  GI:5950500
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 10 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2105
AR034898
LOCUS       AR034898                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5869643.
ACCESSION   AR034898
VERSION     AR034898.1  GI:5950503
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 16 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 2106
AR034898/c
LOCUS       AR034898                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 16 from patent US 5869643.
ACCESSION   AR034898
VERSION     AR034898.1  GI:5950503
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 16 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:32630"
                     /note="DQB1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              || || | ||||||||||||
Db         20 TGCAAGATAAAAAAAAAAAA 1


RESULT 2097
AR172578/c
LOCUS       AR172578                 26 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 10 from patent US 6303328.
ACCESSION   AR172578
VERSION     AR172578.1  GI:17912069
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Re,R. and Cook,J.
  TITLE     Inhibition of cellular proliferation in vitro by oligonucleotide
            binding to a chromosomal binding site for p53 protein
  JOURNAL   Patent: US 6303328-A 10 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 26;
  Best Local Similarity   85.0%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||||| |||||||  ||||
Db         25 GAAAAAGAAAAAAAGGAAAA 6


RESULT 2098
AR430169/c
LOCUS       AR430169                 26 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 10 from patent US 6645944.
ACCESSION   AR430169
VERSION     AR430169.1  GI:40190841
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Re,R. and Cook,J.
  TITLE     Inhibition of cellular proliferation by oligonucleotide binding to
            a chromosomal binding site for p53 protein
  JOURNAL   Patent: US 6645944-A 10 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 26;
  Best Local Similarity   85.0%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||||| |||||||  ||||
Db         25 GAAAAAGAAAAAAAGGAAAA 6


RESULT 2099
AR029402
LOCUS       AR029402                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5859233.
ACCESSION   AR029402
VERSION     AR029402.1  GI:5941375
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates
  JOURNAL   Patent: US 5859233-A 3 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 2100
AR029402/c
LOCUS       AR029402                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5859233.
ACCESSION   AR029402
VERSION     AR029402.1  GI:5941375
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates
  JOURNAL   Patent: US 5859233-A 3 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 2101
AR029403
LOCUS       AR029403                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5859233.
ACCESSION   AR029403
VERSION     AR029403.1  GI:5941376
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
            Nelson,J.S. and Schultz,R.G.
  TITLE     Synthons for synthesis of oligonucleotide N3-P5 phosphoramidates
  JOURNAL   Patent: US 5859233-A 4 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
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Db          1 TTTTTTTTTTTTCACTGCGA 20


RESULT 2092
AX043297/c
LOCUS       AX043297                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 863 from Patent WO0065088.
ACCESSION   AX043297
VERSION     AX043297.1  GI:11341905
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 863 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAA 2798
              ||| ||  ||||||||||||
Db         20 AGAGTTATAAAAAAAAAAAA 1


RESULT 2093
AX043310/c
LOCUS       AX043310                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 876 from Patent WO0065088.
ACCESSION   AX043310
VERSION     AX043310.1  GI:11341918
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 876 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAA 2797
              ||  | ||||||||||||
Db         20 TAAGACTGAAAAAAAAAAAA 1


RESULT 2094
AX043311/c
LOCUS       AX043311                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 877 from Patent WO0065088.
ACCESSION   AX043311
VERSION     AX043311.1  GI:11341919
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 877 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAA 2797
              ||  | ||||||||||||
Db         20 TAAGACTGAAAAAAAAAAAA 1


RESULT 2095
AX042593/c
LOCUS       AX042593                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 159 from Patent WO0065088.
ACCESSION   AX042593
VERSION     AX042593.1  GI:11341201
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 159 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Homozygote Primer Sequence"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              || || | ||||||||||||
Db         20 TGCAAGATAAAAAAAAAAAA 1


RESULT 2096
AX043312/c
LOCUS       AX043312                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 878 from Patent WO0065088.
ACCESSION   AX043312
VERSION     AX043312.1  GI:11341920
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 878 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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ACCESSION   AX698793
VERSION     AX698793.1  GI:29499581
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tchilian,E. and Beverley,P.
  TITLE     Screens for susceptibility to immunodeficiency and viral disease
  JOURNAL   Patent: WO 02103049-A 1 27-DEC-2002;
            The Edward Jenner Institute for Vaccine Research (GB)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1407 ACTACATCAAAGAAGCCCTG 1426
              |||||| |||||| |||| |
Db          2 ACTACAGCAAAGATGCCCAG 21


RESULT 2088
AX771993
LOCUS       AX771993                 23 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 8 from Patent WO03006065.
ACCESSION   AX771993
VERSION     AX771993.1  GI:32438641
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Braun,K., Waldeck,W., Pipkorn,R., Braun,I. and Debus,J.
  TITLE     PNA conjugate for the treatment of diseases associated with HIV
  JOURNAL   Patent: WO 03006065-A 8 23-JAN-2003;
            Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts
            (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PNA I"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTT 2181
              | |||||| ||||||||  ||
Db          4 CCCCTTTTCTTTTTTTCTT 23


RESULT 2089
I20186/c
LOCUS       I20186                   25 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5514546.
ACCESSION   I20186
VERSION     I20186.1  GI:1600541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kool,E.T.
  TITLE     Stem-loop oligonucleotides containing parallel and antiparallel
            binding domains
  JOURNAL   Patent: US 5514546-A 1 07-MAY-1996;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||| | | ||||||
Db         24 GAAAAAAAAGAGAGAAAAAA 5


RESULT 2090
AX042938/c
LOCUS       AX042938                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 504 from Patent WO0065088.
ACCESSION   AX042938
VERSION     AX042938.1  GI:11341546
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 504 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2803
              |||||   ||||||||||||
Db         20 TGAAAGCCAAAAAAAAAAAA 1


RESULT 2091
AX043680
LOCUS       AX043680                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1246 from Patent WO0065088.
ACCESSION   AX043680
VERSION     AX043680.1  GI:11342295
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1246 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGA 2194
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FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2119 TTTAGGAAACTTGTAGAAAC 2138
                || |||||||||| ||| |||
Db          1 TTGAGGAAACTTCTAGGAAC 20


RESULT 2084
BD191561/c
LOCUS       BD191561                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Diagnosis and treatment of tyrosine phosphatase-related disorders
            and related methods.
ACCESSION   BD191561
VERSION     BD191561.1  GI:33001300
KEYWORDS    JP 2002513289-A/42.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Plowman,G.D., Clary,D., Jallal,B., Peles,E., Onrust,S., Markby,D.,
            Courtneidge,S.A., App,H. and Hui,T.H.
  TITLE     Diagnosis and treatment of tyrosine phosphatase-related disorders
            and related methods
  JOURNAL   Patent: JP 2002513289-A 42 08-MAY-2002;
            SUGEN INC
COMMENT     PN   JP 2002513289-A/42
            PD   08-MAY-2002
            PF   27-APR-1998 JP 1998547244
            PR   28-APR-1997 US    60/044428,20-MAY-1997 US    60/047222 PR
            11-JUN-1997 US    60/049756,11-JUN-1997 US    60/049477 PR
            18-JUN-1997 US    60/049914,23-OCT-1997 US    60/063595 PI   GREG D
            PLOWMAN,DOUGLAS CLARY,BAHIJA JALLAL,ELIOR PELES,SUSAN  PI   ONRUST,
            PI   DAVE MARKBY,SARA A COURTNEIDGE,HARALD APP,TERANCE H HUI PC
            C12N15/54,C12N15/55,C12N9/12,C12N9/16,C07K14/705,C12N15/11, PC
            C07K16/40,
            PC   C07K16/28,C12N5/12,C12N15/62,C12Q1/42,C12Q1/48 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        885 ACAAAGTGACAGTGGCTGAA 904
                ||| |||||| ||||||| |
Db         21 ACATAGTGACCGTGGCTGGA 2


RESULT 2085
AB067984
LOCUS       AB067984                 22 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, forward primer for human STS sts-R377E14F
            at 1p36.
ACCESSION   AB067984
VERSION     AB067984.1  GI:15128788
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 22)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .22
                     /note="forward primer for human STS sts-R377E14F at 1p36
                     sts-R377E14F obtained from clones B133G8, B258F15, B267G5,
                     B375E7, B260J14, B377E14, Human BAC library RPCI-11"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2119 TTTAGGAAACTTGTAGAAAC 2138
                || |||||||||| ||| |||
Db          1 TTGAGGAAACTTCTAGGAAC 20


RESULT 2086
AX164418
LOCUS       AX164418                 23 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 248 from Patent WO0138564.
ACCESSION   AX164418
VERSION     AX164418.1  GI:14545352
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 248 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 2.8e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1111 GGACTTTGCCTATGTCTGTG 1130
                || |||||||||| ||| ||
Db          1 GGTCTTTGCCTATTTCTATG 20


RESULT 2087
AX698793
LOCUS       AX698793                 23 bp    DNA     linear   PAT 02-APR-2003
DEFINITION  Sequence 1 from Patent WO02103049.
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```
  TITLE     Nucleic acid molecule encoding abscisic acid responsive
            element-binding factor 2
  JOURNAL   Patent: US 6245905-A 16 12-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2084 CTCTAAACCCCGTGTTCAAA 2103
              | ||||| ||| ||||||||
Db         21 CCCTAAAACCCTTGTTCAAA 2


RESULT 2080
AX593265/c
LOCUS       AX593265                 22 bp    DNA     linear   PAT 13-FEB-2003
DEFINITION  Sequence 56 from Patent WO02088367.
ACCESSION   AX593265
VERSION     AX593265.1  GI:28374685
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bibb,M.J.
  TITLE     Production of the lantibiotic cinnamycin with genes isolated from
            streptomyces cinnamoneus
  JOURNAL   Patent: WO 02088367-A 56 07-NOV-2002;
            Plant Bioscience Limited (GB) ; Bibb, Mervyn James (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        591 CCTACCGCCGCTCCGACCTG 610
              |||||| ||||| | |||||
Db         22 CCTACCACCGCTTCTACCTG 3


RESULT 2081
AX751620/c
LOCUS       AX751620                 22 bp    DNA     linear   PAT 20-JUN-2003
DEFINITION  Sequence 41 from Patent WO03034072.
ACCESSION   AX751620
VERSION     AX751620.1  GI:32133899
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wilson,D.I., Hearn,T. and Walker,M.
  TITLE     Diagnosis and therapy of conditions involving ALMS1
  JOURNAL   Patent: WO 03034072-A 41 24-APR-2003;
            UNIVERSITY OF SOUTHAMPTON (GB)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        734 CAGACAGTCATTCGCAAAGG 753
              ||||||| ||||| || |||
Db         21 CAGACAGCCATTCACAGAGG 2


RESULT 2082
AX817759
LOCUS       AX817759                 22 bp    DNA     linear   PAT 10-DEC-2003
DEFINITION  Sequence 507 from Patent WO02081517.
ACCESSION   AX817759
VERSION     AX817759.1  GI:39722956
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Decristofaro,M.F., Padigaru,M., Miller,C., Tchernev,V., Zhong,H.,
            Zhong,M., Anderson,D., Ballinger,R., Gerlach,V., Spytek,K.A.,
            Rastelli,L., Kekuda,R., Guo,X., Zerhusen,B., Andrew,D., Mezes,P.,
            Patturajan,M., Burgess,C.E., Eisen,A., Wolenc,A., Baumgartner,J.,
            Shimkets,R.A., Gusev,V., Vernet,C.A., Taupier,R.J., Pena,C.,
            Shenoy,S., Li,L., Casman,S., Bolgog,F., Fernandes,E., Smithson,G.,
            Malyankar,U., Taillon,B. and Liu,X.
  TITLE     Novel polypeptides and nucleic acids encoded thereby
  JOURNAL   Patent: WO 02081517-A 507 17-OCT-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: PCR Primer
                     sequence"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1606 GGCCTGGGGGAAGAGTTTGT 1625
              ||||||  ||| ||||||||
Db          2 GGCCTGATGGAGGAGTTTGT 21


RESULT 2083
BD089101
LOCUS       BD089101                 22 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089101
VERSION     BD089101.1  GI:22634711
KEYWORDS    JP 2001321190-A/1345.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 1345 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/1345
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
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BD196252/c
LOCUS       BD196252                 21 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Endogenetic retroviral sequences, associated with autoimmune
            diseases and/or with pregnancy disorders.
ACCESSION   BD196252
VERSION     BD196252.1  GI:33006022
KEYWORDS    JP 2002512530-A/18.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Beseme,F., Blond,J.L., Bouton,O., Mandrand,B. and Mallet,F.
  TITLE     Endogenetic retroviral sequences, associated with autoimmune
            diseases and/or with pregnancy disorders
  JOURNAL   Patent: JP 2002512530-A 18 23-APR-2002;
            BIO MERIEUX
COMMENT     OS   Unidentified
            PN   JP 2002512530-A/18
            PD   23-APR-2002
            PF   06-JUL-1998 JP 1999508244
            PR   07-JUL-1997 FR     97/08815
            PI   FREDERIC BESEME,JEAN LUC BLOND,OLIVIER BOUTON,BERNARD
            MANDRAND,
            PI   FRANCOIS MALLET
            PC   C12N15/48,C07K14/15,C12Q1/68,C07K16/10,G01N33/569 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Endogenetic retroviral sequences, associated with autoimmune
            CC            diseases
            CC   and/or with pregnancy disorders
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2673 AGTGTGTGTGGGTGAAATGG 2692
              ||||| || |||| ||||||
Db         21 AGTGTCTGAGGGTCAAATGG 2


RESULT 2076
AR135198/c
LOCUS       AR135198                 22 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 16 from patent US 6194559.
ACCESSION   AR135198
VERSION     AR135198.1  GI:14124103
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kim,S.Young.
  TITLE     Abscisic acid responsive element-binding transcription factors
  JOURNAL   Patent: US 6194559-A 16 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2084 CTCTAAACCCCGTGTTCAAA 2103
              | ||||| ||| ||||||||
Db         21 CCCTAAAACCCTTGTTCAAA 2


RESULT 2077
AR146694/c
LOCUS       AR146694                 22 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 16 from patent US 6218527.
ACCESSION   AR146694
VERSION     AR146694.1  GI:15109883
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kim,S.Young.
  TITLE     Nucleic acid molecule encoding abscisic acid responsive
            element-binding factor 3
  JOURNAL   Patent: US 6218527-A 16 17-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2084 CTCTAAACCCCGTGTTCAAA 2103
              | ||||| ||| ||||||||
Db         21 CCCTAAAACCCTTGTTCAAA 2


RESULT 2078
AR152265/c
LOCUS       AR152265                 22 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 16 from patent US 6232461.
ACCESSION   AR152265
VERSION     AR152265.1  GI:15118315
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kim,S.Young.
  TITLE     Nucleic acid molecule encoding abscisic acid responsive
            element-binding ractor 4
  JOURNAL   Patent: US 6232461-A 16 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 2.6e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2084 CTCTAAACCCCGTGTTCAAA 2103
              | ||||| ||| ||||||||
Db         21 CCCTAAAACCCTTGTTCAAA 2


RESULT 2079
AR157803/c
LOCUS       AR157803                 22 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 16 from patent US 6245905.
ACCESSION   AR157803
VERSION     AR157803.1  GI:16218815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Kim,S.Young.
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Qy       2673 AGTGTGTGTGGGTGAAATGG 2692
              ||||| || |||| ||||||
Db         21 AGTGTCTGAGGGTCAAATGG 2

RESULT 2071
AX146093/c
LOCUS       AX146093                 21 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 284 from Patent WO0134840.
ACCESSION   AX146093
VERSION     AX146093.1  GI:14284611
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Au,K.G., Chen,J.G., Patil,N. and Thomas,D.
  TITLE     Genetic compositions and methods
  JOURNAL   Patent: WO 0134840-A 284 17-MAY-2001;
            GLAXO GROUP LIMITED (GB) ; Affymetrix, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     variation       1. .21
                     /note="'n' represents a polymorphic base"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        573 TGAGCGCCCGCAGGGATGCCT 593
              ||||| || | ||||| ||||
Db         21 TGAGCTCCTGNAGGGAAGCCT 1

RESULT 2072
AX268236
LOCUS       AX268236                 21 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 30 from Patent WO0175135.
ACCESSION   AX268236
VERSION     AX268236.1  GI:16541493
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kingsman,A.J., Maden,M.B. and Corcoran,J.B.
  TITLE     Retinoic acid receptor beta-2, its antagonists, and gene therapy
            vectors for the treatment of neurological disorders
  JOURNAL   Patent: WO 0175135-A 30 11-OCT-2001;
            Oxford Biomedica (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2209 AATGGGAGACTCTTTGAAAT 2228
              | |||||||| |||||| ||
Db          1 ATTGGGAGACCCTTTGACAT 20

RESULT 2073
AX463864
LOCUS       AX463864                 21 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 3 from Patent EP1219705.
ACCESSION   AX463864
VERSION     AX463864.1  GI:21898947
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hunt,N.
  TITLE     Virus like particles, their preparation and their use preferably in
            pharmaceutical screening and functional genomics
  JOURNAL   Patent: EP 1219705-A 3 03-JUL-2002;
            Evotec OAI AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Peptide capable of forming coiled-coil structures"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1388 GCGGTGTCTGCCCTGCAGAA 1407
              | |||||| |||||| ||||
Db          1 GAGGTGTCCGCCCTGGAGAA 20

RESULT 2074
BD089734
LOCUS       BD089734                 21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089734
VERSION     BD089734.1  GI:22635344
KEYWORDS    JP 2001321190-A/1978.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 1978 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/1978
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1939 GGTAATGGTTGGTTTTTGTG 1958
              ||||||| | |||| |||||
Db          2 GGTAATGATGGGTTGTTGTG 21

RESULT 2075
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              :|||||||||||||||
Db         21 BAAAAAAAAAAAAAAA 6


RESULT 2066
AR029929
LOCUS       AR029929                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 118 from patent US 5861244.
ACCESSION   AR029929
VERSION     AR029929.1  GI:5943143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 118 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTT 2183
              ||| || |||||||||| |||
Db          1 CCTCTTCTTTTTTTTTCTTT 20


RESULT 2067
I49863/c
LOCUS       I49863                   21 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 48 from patent US 5641663.
ACCESSION   I49863
VERSION     I49863.1  GI:2472083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     Expression system for the secretion of bioactive human granulocyte
            macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from steptomyces
  JOURNAL   Patent: US 5641663-A 48 24-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        553 CGGGCTGGAGGCGGGCGCGG 572
              |||||||| || | ||||||
Db         21 CGGGCTGGGGGAGCGCGCGG 2


RESULT 2068
AR297993
LOCUS       AR297993                 21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 9728 from patent US 6537751.
ACCESSION   AR297993
VERSION     AR297993.1  GI:31685277
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 9728 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTT 2180
              || ||||||||||||||  ||
Db          1 TCCCCTTTTTTTTTTCCTT 20


RESULT 2069
AR298358/c
LOCUS       AR298358                 21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 10093 from patent US 6537751.
ACCESSION   AR298358
VERSION     AR298358.1  GI:31685642
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 10093 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1112 GACTTTGCCTATGTCTGTGA 1131
              || |||| |||| |||||||
Db         21 GATTTTGACTATTTCTGTGA 2


RESULT 2070
AX000973/c
LOCUS       AX000973                 21 bp    DNA     linear   PAT 10-MAR-2000
DEFINITION  Sequence 18 from Patent WO9902696.
ACCESSION   AX000973
VERSION     AX000973.1  GI:7241215
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Beseme,F. and Blond,J.
  TITLE     ENDOGENETIC RETROVIRAL SEQUENCES, ASSOCIATED WITH AUTOIMMUNE
            DISEASES OR WITH PREGNANCY DISORDERS
  JOURNAL   Patent: WO 9902696-A 18 21-JAN-1999;
            BIO MERIEUX (FR); BESEME FREDERIC (FR)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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  JOURNAL    Patent: JP 2001321190-A 2666 20-NOV-2001;
             THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
             GENOTECHS
COMMENT      OS   Artificial Sequence
             PN   JP 2001321190-A/2666
             PD   20-NOV-2001
             PF   12-MAR-2001 JP 2001068285
             PI   EIICHI SOEDA
             PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
               C12N15/00,
             PC   C12N15/00
             CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                    Location/Qualifiers
             FT   source          1. .20
             FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1178 CATCTTGGAGGACGAAATGA 1197
              | || ||||||| |||||||
Db         20 CCTCATGGAGGAAGAAATGA 1


RESULT 2063
BD138163
LOCUS       BD138163                 20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Antisense modulation of human MDM2 expression.
ACCESSION   BD138163
VERSION     BD138163.1  GI:23233108
KEYWORDS    JP 2002508944-A/89.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of human MDM2 expression
  JOURNAL   Patent: JP 2002508944-A 89 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002508944-A/89
            PD   26-MAR-2002
            PF   26-MAR-1999 JP 2000538025
            PR   26-MAR-1998 US    09/048810
            PI   LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

            PI   COWSERT
            PC   C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
            PC   C12Q1/68,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense modulation of human MDM2 expression FH   Key
                   Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2313 CAATTTGTTGCTGCTTGTCA 2332
              |||| ||||| ||||| |||
Db          1 CAATATGTTGTTGCTTCTCA 20


RESULT 2064
BD176500/c
LOCUS       BD176500                 20 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  A method of arraying genome clone.
ACCESSION   BD176500
VERSION     BD176500.1  GI:29122208
KEYWORDS    WO 02072815-A/300.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: WO 02072815-A 300 19-SEP-2002;
            EIICHI SOEDA,TAKESHI KUKITA
COMMENT     OS   Artificial Sequence
            PN   WO 02072815-A/300
            PD   19-SEP-2002
            PF   17-MAY-2001 WO 2001JP004139
            PR   12-MAR-2001 JP 01P    68285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12Q1/68
            CC   Description of Artificial Sequence: Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1178 CATCTTGGAGGACGAAATGA 1197
              | || ||||||| |||||||
Db         20 CCTCATGGAGGAAGAAATGA 1


RESULT 2065
AX356851/c
LOCUS       AX356851                 21 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 9 from Patent WO0206490.
ACCESSION   AX356851
VERSION     AX356851.1  GI:18674099
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dudler,R., Schaffrath,U. and Lawton,K.A.
  TITLE     Lipoxygenase genes, promoters, transit peptides and proteins
            thereof
  JOURNAL   Patent: WO 0206490-A 9 24-JAN-2002;
            Syngenta Participations AG (CH) ; Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2800
```

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  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||   |||||||||
Db         20 TTTTTTTCAAATTTTTTTTT 1


RESULT 2058
AX441511/c
LOCUS       AX441511                  20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 15 from Patent WO0206531.
ACCESSION   AX441511
VERSION     AX441511.1  GI:21690472
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 15 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02022"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||   |||||||||
Db         20 TTTTTTTCCAATTTTTTTTT 1


RESULT 2059
AX441514/c
LOCUS       AX441514                  20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 18 from Patent WO0206531.
ACCESSION   AX441514
VERSION     AX441514.1  GI:21690475
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 18 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02025"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||  |  |||||||||
Db         20 TTTTTTTATAATTTTTTTTT 1


RESULT 2060
AX594032
LOCUS       AX594032                  20 bp    DNA     linear   PAT 13-FEB-2003
DEFINITION  Sequence 110 from Patent WO0246477.
ACCESSION   AX594032
VERSION     AX594032.1  GI:28375269
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Garcia,P., Hardy,S.F., Williams,L.T. and Escobedo,J.
  TITLE     Endogenous retroviruses up-regulated in prostate cancer
  JOURNAL   Patent: WO 0246477-A 110 13-JUN-2002;
            CHIRON CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||  ||||||| ||
Db          1 GAAAAAAATCAAAAAAAGAA 20


RESULT 2061
AX786006/c
LOCUS       AX786006                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sequence 2 from Patent WO03050272.
ACCESSION   AX786006
VERSION     AX786006.1  GI:32953626
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bandelier,M.A., Denys,P., Denormandie,P., Sapena,R.,
            Lepailleur-Enouf,D. and Youssefian,T.
  TITLE     Bone development model
  JOURNAL   Patent: WO 03050272-A 2 19-JUN-2003;
            Sympathos (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Amorce PCR antisens pour l'amplification specifique
                     du gene de l'osteocalcine"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        336 CACCCTACTTTCCCCCTCCC 355
              |||||| |||||| | ||||
Db         20 CACCCTTCTTTCCTCTTCCC 1


RESULT 2062
BD090422/c
LOCUS       BD090422                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD090422
VERSION     BD090422.1  GI:22636032
KEYWORDS    JP 2001321190-A/2666.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
```

```
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 31 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||| | |
Db          1 TTTTTTTTTTTTTAAGGTGG 20


RESULT 2054
AX048433/c
LOCUS       AX048433                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 32 from Patent WO0071747.
ACCESSION   AX048433
VERSION     AX048433.1  GI:12225597
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 32 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1971 TTACCTTGAAAAAAAGAAAA 1990
              | ||||| ||||||| ||||
Db         20 TCACCTTAAAAAAAAAAAAA 1


RESULT 2055
AX048437
LOCUS       AX048437                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 36 from Patent WO0071747.
ACCESSION   AX048437
VERSION     AX048437.1  GI:12225601
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 36 30-NOV-2000,
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTT 2192
              |||||||||||||| | || |
Db          1 TTTTTTTTTTTTTAAGCTGT 20


RESULT 2056
AX057494/c
LOCUS       AX057494                 20 bp    DNA     linear   PAT 17-JAN-2001
DEFINITION  Sequence 30 from Patent WO0077204.
ACCESSION   AX057494
VERSION     AX057494.1  GI:12310228
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lorenz,E., Schwartz,D.A. and Schutte,B.C.
  TITLE     Variant tlr4 nucleic acid and uses thereof
  JOURNAL   Patent: WO 0077204-A 30 21-DEC-2000;
            University of Iowa Research Foundation (US) ; Lorenz, Eva (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1166 TTAACCAGACCTCATCTTGG 1185
              ||| |||| ||||||| |||
Db         20 TTACCCAGTCCTCATCCTGG 1


RESULT 2057
AX441509/c
LOCUS       AX441509                 20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 13 from Patent WO0206531.
ACCESSION   AX441509
VERSION     AX441509.1  GI:21690470
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 13 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02020"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
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```
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 13 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||   |||||||||
Db         20 TTTTTTTCAAATTTTTTTTT 1


RESULT 2049
AR360427/c
LOCUS       AR360427                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 15 from patent US 6596490.
ACCESSION   AR360427
VERSION     AR360427.1  GI:33767457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 15 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||   |||||||||
Db         20 TTTTTTTCCAATTTTTTTTT 1


RESULT 2050
AR360430/c
LOCUS       AR360430                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 18 from patent US 6596490.
ACCESSION   AR360430
VERSION     AR360430.1  GI:33767460
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 18 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||| |  |||||||||
Db         20 TTTTTTTATAATTTTTTTTT 1


RESULT 2051
AR429749
LOCUS       AR429749                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 29 from patent US 6645745.
ACCESSION   AR429749
VERSION     AR429749.1  GI:40190087
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wojnowski,L., Gellner,K. and Eiselt,R.
  TITLE     Identification of a new member of the cytochrome P450 3A (CYP3A)
            gene family: CYP3AX
  JOURNAL   Patent: US 6645745-A 29 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1863 CACACTTAGCCATTGAAATG 1882
              ||  ||||  |||||  ||||||
Db          1 CAAACTTTGCCATGGAAATG 20


RESULT 2052
AX004425
LOCUS       AX004425                 20 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 7 from Patent WO9916899.
ACCESSION   AX004425
VERSION     AX004425.1  GI:9927884
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Anctil,J.L. and Cote,G.
  TITLE     Molecular diagnostic of glaucomas associated with chromosomes 2 and
            6
  JOURNAL   Patent: WO 9916899-A 7 08-APR-1999;
            ANCTIL JEAN LOUIS (CA); COTE GILLES (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="OLIGONUCLEOTIDE"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1332 GCTTGTCTCATTTCAGCCTG 1351
              ||||||  |||| ||| ||||
Db          1 GCTTGTTTCATCTCACCCTG 20


RESULT 2053
AX048432
LOCUS       AX048432                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 31 from Patent WO0071747.
ACCESSION   AX048432
VERSION     AX048432.1  GI:12225596
KEYWORDS    .
SOURCE      synthetic construct
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Brown,S.Joel., Dattagupta,N. and Naidu,Y.M.
  TITLE     Method for inhibiting cellular proliferation using antisense
            oligonucleotides to interleukin-6 receptor mRNA
  JOURNAL   Patent: US 5716846-A 14 10-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAGCAGG 470
              | |||| |||| ||||||||
Db         20 CTCAGGAAGCCGGCAGCAGG 1


RESULT 2044
AR315615/c
LOCUS       AR315615                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6152 from patent US 6559294.
ACCESSION   AR315615
VERSION     AR315615.1  GI:31709041
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 6152 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1525 GAACGAAGAAAGGTTAGGAG 1544
              || |||||||||  || ||||
Db         20 GACCGAAGAAAGATTGGGAG 1


RESULT 2045
AR360398/c
LOCUS       AR360398                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 13 from patent US 6596489.
ACCESSION   AR360398
VERSION     AR360398.1  GI:33767428
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 13 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||   |||||||||
Db         20 TTTTTTTCAAATTTTTTTTT 1


RESULT 2046
AR360400/c
LOCUS       AR360400                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 15 from patent US 6596489.
ACCESSION   AR360400
VERSION     AR360400.1  GI:33767430
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 15 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||||   |||||||||
Db         20 TTTTTTTCCAATTTTTTTTT 1


RESULT 2047
AR360403/c
LOCUS       AR360403                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 18 from patent US 6596489.
ACCESSION   AR360403
VERSION     AR360403.1  GI:33767433
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 18 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||| |  |||||||||
Db         20 TTTTTTTATAATTTTTTTTT 1


RESULT 2048
AR360425/c
LOCUS       AR360425                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 13 from patent US 6596490.
ACCESSION   AR360425
VERSION     AR360425.1  GI:33767455
KEYWORDS    .
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     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        266 TCCGCCGGGCAGCACCTCTA 285
              ||| ||||||||||| | |
Db         20 TCCTCCGGGCAGCACCACGA 1


RESULT 2039
AR174362/c
LOCUS       AR174362                 20 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 22 from patent US 6306655.
ACCESSION   AR174362
VERSION     AR174362.1  GI:17914682
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP alpha expression
  JOURNAL   Patent: US 6306655-A 22 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        212 GAGGATCGCCACGACGGGAG 231
              |||| |||||| | ||||||
Db         20 GAGGCTCGCCATGCCGGGAG 1


RESULT 2040
AR178788/c
LOCUS       AR178788                 20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 34 from patent US 6319906.
ACCESSION   AR178788
VERSION     AR178788.1  GI:20219926
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Vickers,T.A.
  TITLE     Oligonucleotide compositions and methods for the modulation of the
            expression of B7 protein
  JOURNAL   Patent: US 6319906-A 34 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        541 GCCCCACCTCTCCGGGCTGG 560
              ||| |||||||||| || |||
Db         20 GCCTCACCTCTCCTGGTTGG 1


RESULT 2041
AR178895/c
LOCUS       AR178895                 20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 141 from patent US 6319906.
ACCESSION   AR178895
VERSION     AR178895.1  GI:20220033
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Vickers,T.A.
  TITLE     Oligonucleotide compositions and methods for the modulation of the
            expression of B7 protein
  JOURNAL   Patent: US 6319906-A 141 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        541 GCCCCACCTCTCCGGGCTGG 560
              ||| |||||||||| || |||
Db         20 GCCTCACCTCTCCTGGTTGG 1


RESULT 2042
E59334
LOCUS       E59334                   20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for purifying oligonucleotide.
ACCESSION   E59334
VERSION     E59334.1  GI:18622511
KEYWORDS    JP 2000342265-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hirose,K. and Yoshida,T.
  TITLE     Method for purifying oligonucleotide
  JOURNAL   Patent: JP 2000342265-A 15 12-DEC-2000;
            TOAGOSEI CHEM IND CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000342265-A/15
            PD   12-DEC-2000
            PF   02-JUN-1999 JP 1999154974
            PR
            PI   KUNIHIKO HIROSE,TADAO YOSHIDA
            PC   C12N15/09,B01D15/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||| |||| |||| ||||
Db          1 TTTTTCTTTTGTTTTATTTT 20


RESULT 2043
I88036/c
LOCUS       I88036                   20 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 14 from patent US 5716846.
ACCESSION   I88036
VERSION     I88036.1  GI:3407976
```

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                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
                     /tissue_type="spleen"
                     /dev_stage="adult"
                     /tissue_lib="E. Ostrander, in pBluescript+"
     primer_bind     1. .20

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2219 TCTTTGAAATGACATGTTCC 2238
              ||||||||||| ||| ||
Db          1 TCTTTGAAATGAAATGGGCC 20


RESULT 2034
AR099507/c
LOCUS       AR099507                 20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 34 from patent US 6077833.
ACCESSION   AR099507
VERSION     AR099507.1  GI:12809273
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Vickers,T.A.
  TITLE     Oligonucleotide compositions and methods for the modulation of the
            expression of B7 protein
  JOURNAL   Patent: US 6077833-A 34 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        541 GCCCCACCTCTCCGGGCTGG 560
              ||| |||||||||| || |||
Db         20 GCCTCACCTCTCCTGGTTGG 1


RESULT 2035
AR118884/c
LOCUS       AR118884                 20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 10 from patent US 6150092.
ACCESSION   AR118884
VERSION     AR118884.1  GI:14100794
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
  TITLE     Antisense nucleic acid compound targeted to VEGF
  JOURNAL   Patent: US 6150092-A 10 21-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||| || ||||| |||||||
Db         20 TTTGTTGTTTTTGTTTTTT 1


RESULT 2036
AR137400
LOCUS       AR137400                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 15 from patent US 6197507.
ACCESSION   AR137400
VERSION     AR137400.1  GI:14478909
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Berg,T., Tollersrud,O.Kristien. and Nilssen,O.
  TITLE     Genetic test for .alpha.-mannosidosis
  JOURNAL   Patent: US 6197507-A 15 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAGA 70
              | ||||| |||||| |||||
Db          1 GTGGCGGCGGCGGCTGCAGA 20


RESULT 2037
AR158936
LOCUS       AR158936                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 558 from patent US 6251588.
ACCESSION   AR158936
VERSION     AR158936.1  GI:16221351
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and
            Kincaid,R.H.
  TITLE     Method for evaluating oligonucleotide probe sequences
  JOURNAL   Patent: US 6251588-A 558 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTG 2193
              |||||| |||||||||  ||
Db          1 TTTTTTCTTTTTTAACCCTG 20


RESULT 2038
AR163830/c
LOCUS       AR163830                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 28 from patent US 6271030.
ACCESSION   AR163830
VERSION     AR163830.1  GI:16234602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP beta expression
  JOURNAL   Patent: US 6271030-A 28 07-AUG-2001;
FEATURES             Location/Qualifiers
```

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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
            genes
  JOURNAL   Patent: US 6342376-A 2 29-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2800
              :|||||||||||||||
Db         16 BAAAAAAAAAAAAAA 1


RESULT 2030
AR429726
LOCUS       AR429726                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2 from patent US 6645741.
ACCESSION   AR429726
VERSION     AR429726.1  GI:40190064
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
            genes
  JOURNAL   Patent: US 6645741-A 2 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTV 16


RESULT 2031
AR429726/c
LOCUS       AR429726                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2 from patent US 6645741.
ACCESSION   AR429726
VERSION     AR429726.1  GI:40190064
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
            genes
  JOURNAL   Patent: US 6645741-A 2 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2800
              :|||||||||||||||
Db         16 BAAAAAAAAAAAAAA 1


RESULT 2032
AX048436/c
LOCUS       AX048436                  20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 35 from Patent WO0071747.
ACCESSION   AX048436
VERSION     AX048436.1  GI:12225600
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 35 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAA 2798
              | || | ||||||||||||||
Db         20 ACAACTTAAAAAAAAAAAAA 1


RESULT 2033
DOGP34201
LOCUS       DOGP34201                 20 bp    DNA     linear   MAM 11-OCT-1994
DEFINITION  Dog (Clone: CXX.342) primer for STS 342, 5' end.
ACCESSION   L24226
VERSION     L24226.1  GI:401882
KEYWORDS    PCR identification; PCR primer; STS.
SEGMENT     1 of 2
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
  TITLE     85 new simple sequence repeat markers for the canine genome
  JOURNAL   Unpublished
COMMENT     Original source text: Canis familiaris (library: E. Ostrander, in
            pBluescript+) adult spleen DNA.
            Submitted by:
            Fred Hutchinson Cancer Research Center
            Transplantation Biology Dept
            1124 Columbia; Mailstop M318
            Seattle, WA 98104, USA
            e-mail: EAOstrander@lbl.gov
            PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
            PCR Profile:  Denaturation:    94 degrees C for 1.00 minute
            Annealing:       55 or 59 degrees C for 0.45 minutes
            Polymerization:  74 degrees C for 1.00 minutes
            PCR Cycles:      33
            Final Extension:  74 degrees C for 5.00 minutes.
FEATURES             Location/Qualifiers
     source          1. .20
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          FT   source          1. .16
          FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2799
              |:||||||||||||||
Db         16 TDAAAAAAAAAAAAAA 1


RESULT 2026
E53842
LOCUS       E53842                    16 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LUNX gene and method for detecting micrometastasis of cancer.
ACCESSION   E53842
VERSION     E53842.1  GI:18633612
KEYWORDS    JP 2001078772-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kadota,M., Fujiwara,Y., Watanabe,R. and Ozaki,K.
  TITLE     LUNX gene and method for detecting micrometastasis of cancer
  JOURNAL   Patent: JP 2001078772-A 3 27-MAR-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   Unidentified
            PN   JP 2001078772-A/3
            PD   27-MAR-2001
            PF   07-SEP-1999 JP 1999253186
            PR
            PI   MORITO KADOTA,YOSHIYUKI FUJIWARA,RYUJI WATANABE,KOICHI OZAKI
            PC   C12N15/09,C07K14/82,C07K16/32,C12N1/15,C12N1/19,C12N1/21, PC
            C12N5/10,C12Q1/68,
            PC   G01N33/15,G01N33/50,G01N33/566,G01N33/574//A61K31/713, PC
            A61K35/12,A61K35/76,
            PC   A61K39/395,A61K39/395,A61K48/00,A61P35/00,A61P35/04,C12P21/08,
            PC   C12N15/00,
            PC   C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAA 2188
              ||||||||||||||:|
Db          1 TTTTTTTTTTTTTTVA 16


RESULT 2027
E53842/c
LOCUS       E53842                    16 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LUNX gene and method for detecting micrometastasis of cancer.
ACCESSION   E53842
VERSION     E53842.1  GI:18633612
KEYWORDS    JP 2001078772-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kadota,M., Fujiwara,Y., Watanabe,R. and Ozaki,K.
  TITLE     LUNX gene and method for detecting micrometastasis of cancer
  JOURNAL   Patent: JP 2001078772-A 3 27-MAR-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   Unidentified
            PN   JP 2001078772-A/3
            PD   27-MAR-2001
            PF   07-SEP-1999 JP 1999253186
            PR
            PI   MORITO KADOTA,YOSHIYUKI FUJIWARA,RYUJI WATANABE,KOICHI OZAKI
            PC   C12N15/09,C07K14/82,C07K16/32,C12N1/15,C12N1/19,C12N1/21, PC
            C12N5/10,C12Q1/68,
            PC   G01N33/15,G01N33/50,G01N33/566,G01N33/574//A61K31/713, PC
            A61K35/12,A61K35/76,
            PC   A61K39/395,A61K39/395,A61K48/00,A61P35/00,A61P35/04,C12P21/08,
            PC   C12N15/00,
            PC   C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2799
              |:||||||||||||||
Db         16 TBAAAAAAAAAAAAAA 1


RESULT 2028
AR183909
LOCUS       AR183909                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2 from patent US 6342376.
ACCESSION   AR183909
VERSION     AR183909.1  GI:20227878
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
            genes
  JOURNAL   Patent: US 6342376-A 2 29-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.4e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTV 16


RESULT 2029
AR183909/c
LOCUS       AR183909                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2 from patent US 6342376.
ACCESSION   AR183909
VERSION     AR183909.1  GI:20227878
```

```
  JOURNAL    Patent: WO 0065088-A 853 02-NOV-2000;
             Amersham Pharmacia Biotech AB (SE)
FEATURES               Location/Qualifiers
     source            1. .25
                       /organism="synthetic construct"
                       /mol_type="unassigned DNA"
                       /db_xref="taxon:32630"
                       /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTT 2191
              ||||||||||||||| ||
Db          1 TTTTTTTTTTTTAAATT 17


RESULT 2022
AX498245
LOCUS       AX498245                 25 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 1 from Patent WO0218951.
ACCESSION   AX498245
VERSION     AX498245.1  GI:23343164
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 1 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES               Location/Qualifiers
     source            1. .25
                       /organism="synthetic construct"
                       /mol_type="unassigned DNA"
                       /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||||||||||||||  |
Db          6 TTTTTTTTTTTTTTCT 22


RESULT 2023
AR409905/c
LOCUS       AR409905                 29 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 18 from patent US 6635422.
ACCESSION   AR409905
VERSION     AR409905.1  GI:40161040
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 18 21-OCT-2003;
FEATURES               Location/Qualifiers
     source            1. .29
                       /organism="unknown"
                       /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 29;
  Best Local Similarity   76.0%;  Pred. No. 3.6e+03;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
                  ||||   |||||||   ||||||||
Db         25 AGAAAATAAAAAAATTTAAAAAAAA 1


RESULT 2024
E52143
LOCUS       E52143                   16 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  TSA7005 gene.
ACCESSION   E52143
VERSION     E52143.1  GI:18629626
KEYWORDS    JP 2001025389-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Ogawara,T., Suzuki,M. and Ozaki,K.
  TITLE     TSA7005 gene
  JOURNAL   Patent: JP 2001025389-A 3 30-JAN-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   Unknown
            PN   JP 2001025389-A/3
            PD   30-JAN-2001
            PF   15-JUL-1999 JP 1999201279
            PR
            PI   TSUYOSHI OGAWARA,MIKIO SUZUKI,KOICHI OZAKI
            PC   C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21, PC
            C12N5/10//A61K31/00,
            PC   A61K38/00,A61K48/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Unknown'.
FEATURES               Location/Qualifiers
     source            1. .16
                       /organism="unidentified"
                       /mol_type="genomic DNA"
                       /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              |||||||||||||||:|
Db          1 TTTTTTTTTTTTTTHA 16


RESULT 2025
E52143/c
LOCUS       E52143                   16 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  TSA7005 gene.
ACCESSION   E52143
VERSION     E52143.1  GI:18629626
KEYWORDS    JP 2001025389-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Ogawara,T., Suzuki,M. and Ozaki,K.
  TITLE     TSA7005 gene
  JOURNAL   Patent: JP 2001025389-A 3 30-JAN-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT     OS   Unknown
            PN   JP 2001025389-A/3
            PD   30-JAN-2001
            PF   15-JUL-1999 JP 1999201279
            PR
            PI   TSUYOSHI OGAWARA,MIKIO SUZUKI,KOICHI OZAKI
            PC   C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21, PC
            C12N5/10//A61K31/00,
            PC   A61K38/00,A61K48/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC

            FH   Key             Location/Qualifiers
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  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   76.0%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              ||||||||||||  |  | ||| |
Db          1 TTTTTTTTTTTTTGCAAGTAGAACG 25


RESULT 2017
AX043038/c
LOCUS       AX043038                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 604 from Patent WO0065088.
ACCESSION   AX043038
VERSION     AX043038.1  GI:11341646
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 604 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              ||| ||||||||||||||
Db         17 TTGGAAAAAAAAAAAAA 1


RESULT 2018
AX042684/c
LOCUS       AX042684                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 250 from Patent WO0065088.
ACCESSION   AX042684
VERSION     AX042684.1  GI:11341292
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 250 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-A Homozygote Primer Sequence"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2798
              | ||||||||||||||||
Db         17 ACTGAAAAAAAAAAAAA 1


RESULT 2019
AX043487/c
LOCUS       AX043487                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1053 from Patent WO0065088.
ACCESSION   AX043487
VERSION     AX043487.1  GI:11342095
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1053 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2798
              | ||||||||||||||||
Db         17 ACTGAAAAAAAAAAAAA 1


RESULT 2020
AX042585
LOCUS       AX042585                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 151 from Patent WO0065088.
ACCESSION   AX042585
VERSION     AX042585.1  GI:11341193
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 151 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTT 2191
              |||||||||||||| ||
Db          1 TTTTTTTTTTTTAAATT 17


RESULT 2021
AX043287
LOCUS       AX043287                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 853 from Patent WO0065088.
ACCESSION   AX043287
VERSION     AX043287.1  GI:11341895
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
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  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 6 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 24;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||||||||||||||  |
Db          6 TTTTTTTTTTTTTTCT 22


RESULT 2013
BD229208
LOCUS       BD229208                  24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Genotype determination of human UDP-glucuronosyl transferase 2B4
            (UGT2B4), 2B7 (UGT2B7) and 2B15 (UGT2B15) genes.
ACCESSION   BD229208
VERSION     BD229208.1  GI:33038978
KEYWORDS    JP 2002521067-A/80.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Galvin,M., Miller,A., Penny,L. and Riedy,M.
  TITLE     Genotype determination of human UDP-glucuronosyl transferase 2B4
            (UGT2B4), 2B7 (UGT2B7) and 2B15 (UGT2B15) genes
  JOURNAL   Patent: JP 2002521067-A 80 16-JUL-2002;
            AXYS PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002521067-A/80
            PD   16-JUL-2002
            PF   22-JUL-1999 JP 2000562558
            PR   28-JUL-1998 US    60/094391
            PI   MARGARET GALVIN,ANDREW MILLER,LAURA PENNY,MICHAEL RIEDY PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,C12N15/00,C12N15/00 CC
            Genotype determination of human UDP-glucuronosyl transferase  CC
                  2B4 (UGT2B4),
            CC   2B7 (UGT2B7) and 2B15 (UGT2B15) genes
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 24;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||  |||||||||
Db          1 AAAAAAAGAAAAAAAAA 17


RESULT 2014
AR349460
LOCUS       AR349460                  24 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 82 from patent US 6586175.
ACCESSION   AR349460
VERSION     AR349460.1  GI:33750253
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Galvin,M., Miller,A., Penny,L. and Riedy,M.
  TITLE     Genotyping the human UDP-glucuronosyltransferase 2B7 (UGT2B7) gene
  JOURNAL   Patent: US 6586175-A 82 01-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 24;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||  |||||||||
Db          1 AAAAAAAGAAAAAAAAA 17


RESULT 2015
AX043281/c
LOCUS       AX043281                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 847 from Patent WO0065088.
ACCESSION   AX043281
VERSION     AX043281.1  GI:11341889
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 847 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   76.0%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAA 2800
              | |  |||  || ||||||||||||
Db         25 GGTCAAATCTAAGAAAAAAAAAAAA 1


RESULT 2016
AX043100
LOCUS       AX043100                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 666 from Patent WO0065088.
ACCESSION   AX043100
VERSION     AX043100.1  GI:11341708
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 666 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"
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Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2008
AX052993/c
LOCUS       AX052993                 23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 9 from Patent WO0071749.
ACCESSION   AX052993
VERSION     AX052993.1  GI:12227095
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 9 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Komponente (b)-2"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 23;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         17 ACAAAAAAAAAAAAAAA 1


RESULT 2009
AX053002/c
LOCUS       AX053002                 23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 18 from Patent WO0071749.
ACCESSION   AX053002
VERSION     AX053002.1  GI:12227104
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 18 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Komponente (b)-5"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 23;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         17 ACAAAAAAAAAAAAAAA 1


RESULT 2010
AX038544/c
LOCUS       AX038544                 23 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 301 from Patent WO0061795.
ACCESSION   AX038544
VERSION     AX038544.1  GI:11227892
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   De Canck,I.D., Rossau,R. and Rombout,A.
  TITLE     Method for the amplification of hla class i alleles
  JOURNAL   Patent: WO 0061795-A 301 19-OCT-2000;
            CANCK ILSE DE (BE) ; ROSSAU RUDI (BE) ; INNOGENETICS NV (BE) ;
            ROMBOUT ANNELIES (BE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 23;
  Best Local Similarity   76.2%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1055 GCTCATGTGACTCTCCTGACA 1075
              |: ||||||||: |||||| |
Db         23 GSCCATGTGACYATCCTGAGA 3


RESULT 2011
AX468432
LOCUS       AX468432                 23 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 5 from Patent WO0220759.
ACCESSION   AX468432
VERSION     AX468432.1  GI:21901268
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Eling,T.E. and Baek,S.J.
  TITLE     A non-steroidal anti-inflammatory drug activated gene with
            anti-tumorigenic properties
  JOURNAL   Patent: WO 0220759-A 5 14-MAR-2002;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 23;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1550 GGAAGGAACAGGACTGC 1566
              ||||||| |||||||||
Db         5 GGAAGGACCAGGACTGC 21


RESULT 2012
AX498250
LOCUS       AX498250                 24 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 6 from Patent WO0218951.
ACCESSION   AX498250
VERSION     AX498250.1  GI:23343169
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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          ROMBOUT ANNELIES (BE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   76.2%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1055 GCTCATGTGACTCTCCTGACA 1075
              |: ||||||||: |||||| |
Db         22 GSCCATGTGACYATCCTGAGA 2


RESULT 2005
BD206198
LOCUS       BD206198                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206198
VERSION     BD206198.1  GI:33015968
KEYWORDS    JP 2002515252-A/11.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 11 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/11
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2006
BD206199
LOCUS       BD206199                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206199
VERSION     BD206199.1  GI:33015969
KEYWORDS    JP 2002515252-A/12.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 12 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/12
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2007
BD206200
LOCUS       BD206200                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206200
VERSION     BD206200.1  GI:33015970
KEYWORDS    JP 2002515252-A/13.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 13 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/13
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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                    |||||| ||||||||||
Db          18 CAGAAGGGCCAAATCGA 2


RESULT 2000
E40160/c
LOCUS       E40160                    22 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Genetic diagnosis method of bovine Chediak-Higashi syndrome.
ACCESSION   E40160
VERSION     E40160.1  GI:18627234
KEYWORDS    JP 2000189176-A/25.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Yamaguchi,H., Kashiguwa,A., Sugimoto,Y. and Tahara,N.
  TITLE     Genetic diagnosis method of bovine Chediak-Higashi syndrome
  JOURNAL   Patent: JP 2000189176-A 25 11-JUL-2000;
            KAGOSHIMA PREF,LIVESTOCK TECHNOLOGY ASSOCIATION
COMMENT     OS   Artificial Sequence
            PN   JP 2000189176-A/25
            PD   11-JUL-2000
            PF   15-OCT-1999 JP 1999294619
            PR
            PI   HIROSHI YAMAGUCHI,AGABA KASHIGUWA,YOSHINORI SUGIMOTO, PI
            NORIO TAHARA
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        964 CAGAAGAGCCAAATCGA 980
              |||||| ||||||||||
Db         18 CAGAAGGGCCAAATCGA 2


RESULT 2001
I30196
LOCUS       I30196                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 25 from patent US 5580726.
ACCESSION   I30196
VERSION     I30196.1  GI:1820987
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 25 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              |||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2002
I30197
LOCUS       I30197                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 26 from patent US 5580726.
ACCESSION   I30197
VERSION     I30197.1  GI:1820988
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 26 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              |||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2003
I30198
LOCUS       I30198                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 27 from patent US 5580726.
ACCESSION   I30198
VERSION     I30198.1  GI:1820989
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 27 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              |||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2004
AX038543/c
LOCUS       AX038543                  22 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 300 from Patent WO0061795.
ACCESSION   AX038543
VERSION     AX038543.1  GI:11227891
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   De Canck,I.D., Rossau,R. and Rombout,A.
  TITLE     Method for the amplification of hla class i alleles
  JOURNAL   Patent: WO 0061795-A 300 19-OCT-2000;
            CANCK ILSE DE (BE) ; ROSSAU RUDI (BE) ; INNOGENETICS NV (BE) ;
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            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        932 TGCTTAAATGCCTCGTT 948
              ||||| ||||||||||
Db          4 TGCTTCAATGCCTCGTT 20


RESULT 1996
AR003285
LOCUS       AR003285                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 7 from patent US 5744300.
ACCESSION   AR003285
VERSION     AR003285.1  GI:3964544
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 7 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 1997
AR003286
LOCUS       AR003286                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 8 from patent US 5744300.
ACCESSION   AR003286
VERSION     AR003286.1  GI:3964545
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 8 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 1998
AR003287
LOCUS       AR003287                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 9 from patent US 5744300.
ACCESSION   AR003287
VERSION     AR003287.1  GI:3964546
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 9 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 1999
E36538/c
LOCUS       E36538                    22 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method of gene diagnosis of bovine Chediak-Higashi syndrome.
ACCESSION   E36538
VERSION     E36538.1  GI:18626475
KEYWORDS    JP 2000189165-A/25.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Yamaguchi,H., Kashiguwa,A., Sugimoto,Y. and Tahara,N.
  TITLE     Method of gene diagnosis of bovine Chediak-Higashi syndrome
  JOURNAL   Patent: JP 2000189165-A 25 11-JUL-2000;
            KAGOSHIMA PREF,LIVESTOCK TECHNOLOGY ASSOCIATION
COMMENT     OS   Artificial Sequence
            PN   JP 2000189165-A/25
            PD   11-JUL-2000
            PF   25-DEC-1998 JP 1998368649
            PR
            PI   HIROSHI YAMAGUCHI,AGABA KASHIGUWA,YOSHINORI SUGIMOTO, PI
            NORIO TAHARA
            PC   C12N15/09,C12Q1/68//(C12N15/09,C12R1:91),C12N15/00,(C12N15/00,
            PC   C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        964 CAGAAGAGCCAAATCGA 980
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1055 GCTCATGTGACTCTCCTGACA 1075
              |: ||||||||: |||||| |
Db         21 GSCCATGTGACYATCCTGAGA 1


RESULT 1992
AX094961
LOCUS       AX094961                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 139 from Patent WO0118250.
ACCESSION   AX094961
VERSION     AX094961.1  GI:13511164
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 139 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAACCTG 661
              | |||||||:|| ||||||
Db          2 GAGCCTGGCYGACAACCTG 20


RESULT 1993
AX095913
LOCUS       AX095913                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 1091 from Patent WO0118250.
ACCESSION   AX095913
VERSION     AX095913.1  GI:13512140
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1091 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2004 TTCTTCAGAGATCAAGTCC 2022
              | || |||||:||||||||
Db          1 TACTCCAGAGRTCAAGTCC 19


RESULT 1994
AX810934
LOCUS       AX810934                 21 bp    DNA     linear   PAT 02-DEC-2003
DEFINITION  Sequence 61 from Patent EP1333100.
ACCESSION   AX810934
VERSION     AX810934.1  GI:38635531
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Park,J.G., Kim,I.J., Kang,H.C. and Park,J.H.
  TITLE     Ret oligonucleotide microchip and method for detecting hereditary
            cancer employing same
  JOURNAL   Patent: EP 1333100-A 61 06-AUG-2003;
            National Cancer Center (KR)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="804M-(L)"

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1175 CCTCATCTTGGAGGACG 1191
              ||||||||||||| |||
Db          4 CCTCATCTTGGAGTACG 20


RESULT 1995
BD185851
LOCUS       BD185851                 21 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  A stabilization method and a preservation method for a reagent for
            nucleic acid amplification or detection reaction.
ACCESSION   BD185851
VERSION     BD185851.1  GI:31878051
KEYWORDS    WO 02101042-A/47.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Sagawa,H., Uemori,T., Mukai,H., Yamamoto,J., Tomono,J.,
            Kobayashi,E., Enoki,T., Asada,K. and Kato,I.
  TITLE     A stabilization method and a preservation method for a reagent for
            nucleic acid amplification or detection reaction
  JOURNAL   Patent: WO 02101042-A 47 19-DEC-2002;
            TAKARA BIO INC,HIROAKI SAGAWA,TAKASHI UEMORI,HIROYUKI MUKAI,JUNKO
            YAMAMOTO, JUN TOMONO,EIJI KOBAYASHI,TATSUJI ENOKI,KIYOZO
            ASADA,IKUNOSHIN KATO
COMMENT     OS   Artificial Sequence
            PN   WO 02101042-A/47
            PD   19-DEC-2002
            PF   12-JUN-2002 WO 2002JP005832
            PR   12-JUN-2001 JP 01P   177737,20-AUG-2001 JP 01P   249689 PI
            HIROAKI SAGAWA,TAKASHI UEMORI,HIROYUKI MUKAI,JUNKO YAMAMOTO, PI
            JUN TOMONO,
            PI   EIJI KOBAYASHI,TATSUJI ENOKI,KIYOZO ASADA,IKUNOSHIN KATO PC
            C12N15/09,C12Q1/68
            CC   Designed chimeric oligonucleotide primer designated as pJDB F-
            CC           2 to amplify
            CC   a portion of CppB gene from Neisseria gonorrhoeae. CC
            'Nucleotides 19 to 21 are ribonucleotides-other nucleotides  CC
                  are
            CC   deoxyribonucleotides.'
            FH   Key             Location/Qualifiers
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                    /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        150 GGGGGACGCCGGACGCC 166
              ||||||||||||| |||
Db         19 GGGGGACGCCGGAGGCC 3


RESULT 1987
AR045091/c
LOCUS       AR045091                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5817788.
ACCESSION   AR045091
VERSION     AR045091.1  GI:5966556
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Berkner,K.L., Petersen,L.Christian., Hart,C.E., Hedner,U. and
            Bregengaard,C.
  TITLE     Modified factor VII
  JOURNAL   Patent: US 5817788-A 3 06-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        150 GGGGGACGCCGGACGCC 166
              ||||||||||||| |||
Db         19 GGGGGACGCCGGAGGCC 3


RESULT 1988
AR052947/c
LOCUS       AR052947                 21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5833982.
ACCESSION   AR052947
VERSION     AR052947.1  GI:5977809
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Berkner,K.L., Petersen,L.Christian., Hart,C.E., Hedner,U. and
            Bregengaard,C.
  TITLE     Modified factor VII
  JOURNAL   Patent: US 5833982-A 3 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        150 GGGGGACGCCGGACGCC 166
              ||||||||||||| |||
Db         19 GGGGGACGCCGGAGGCC 3


RESULT 1989
AR122900/c
LOCUS       AR122900                 21 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 3 from patent US 6168789.
ACCESSION   AR122900
VERSION     AR122900.1  GI:14107866
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Berkner,K.L., Petersen,L.Christian., Hart,C.E., Hedner,U. and
            Bregengaard,C.
  TITLE     Modified factor VII
  JOURNAL   Patent: US 6168789-A 3 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        150 GGGGGACGCCGGACGCC 166
              ||||||||||||| |||
Db         19 GGGGGACGCCGGAGGCC 3


RESULT 1990
AR127822/c
LOCUS       AR127822                 21 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 3 from patent US 6183743.
ACCESSION   AR127822
VERSION     AR127822.1  GI:14115484
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hart,C.E., Petersen,L.C., Hedner,U. and Rasmussen,M.E.
  TITLE     Modified factor VII
  JOURNAL   Patent: US 6183743-A 3 06-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        150 GGGGGACGCCGGACGCC 166
              ||||||||||||| |||
Db         19 GGGGGACGCCGGAGGCC 3


RESULT 1991
AX038542/c
LOCUS       AX038542                 21 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 299 from Patent WO0061795.
ACCESSION   AX038542
VERSION     AX038542.1  GI:11227890
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   De Canck,I.D., Rossau,R. and Rombout,A.
  TITLE     Method for the amplification of hla class i alleles
  JOURNAL   Patent: WO 0061795-A 299 19-OCT-2000;
            CANCK ILSE DE (BE) ; ROSSAU RUDI (BE) ; INNOGENETICS NV (BE) ;
            ROMBOUT ANNELIES (BE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
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DEFINITION  Sequence 4601 from Patent WO02072882.
ACCESSION   AX613576
VERSION     AX613576.1  GI:28409005
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cullen,P. and Seedorf,U.
  TITLE     Coronary chip
  JOURNAL   Patent: WO 02072882-A 4601 19-SEP-2002;
            OGHAM GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1312 GGAGACGAACATACAGA 1328
              |||||| ||||||||||
Db          4 GGAGACAAACATACAGA 20


RESULT 1984
BD171234
LOCUS       BD171234                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of detecting pathogenic microorganism.
ACCESSION   BD171234
VERSION     BD171234.1  GI:27877046
KEYWORDS    WO 02052043-A/26.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Shimada,M., Hino,F. and Kato,I.
  TITLE     Method of detecting pathogenic microorganism
  JOURNAL   Patent: WO 02052043-A 26 04-JUL-2002;
            TAKARA SHUZO CO LTD,MASAMITSU SHIMADA,FUMITSUGU HINO,IKUNOSHIN KATO
COMMENT     OS   Artificial Sequence
            PN   WO 02052043-A/26
            PD   04-JUL-2002
            PF   26-DEC-2001 WO 2001JP011422
            PR   26-DEC-2000 JP 00P   396222,26-DEC-2000 JP 00P   396321 PR
            29-JUN-2001 JP 01P   199552,13-SEP-2001 JP 01P   278920 PI
            MASAMITSU SHIMADA,FUMITSUGU HINO,IKUNOSHIN KATO PC
            C12Q1/68,C12N15/09
            CC   Chimeric oligonucleotide primer to amplify
            the DNA fragment of
            CC            Neisseria
            CC   gonorrhoeae cppB gene.
            CC   'nucleotides 18 to 20 are ribonucleotides-other nucleotides
            CC            are
            CC   deoxyribonucleotides'
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        932 TGCTTAAATGCCTCGTT 948
              ||||| ||||||||||
Db          4 TGCTTCAATGCCTCGTT 20


RESULT 1985
BD185850
LOCUS       BD185850                  20 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  A stabilization method and a preservation method for a reagent for
            nucleic acid amplification or detection reaction.
ACCESSION   BD185850
VERSION     BD185850.1  GI:31878050
KEYWORDS    WO 02101042-A/46.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sagawa,H., Uemori,T., Mukai,H., Yamamoto,J., Tomono,J.,
            Kobayashi,E., Enoki,T., Asada,K. and Kato,I.
  TITLE     A stabilization method and a preservation method for a reagent for
            nucleic acid amplification or detection reaction
  JOURNAL   Patent: WO 02101042-A 46 19-DEC-2002;
            TAKARA BIO INC,HIROAKI SAGAWA,TAKASHI UEMORI,HIROYUKI MUKAI,JUNKO
            YAMAMOTO, JUN TOMONO,EIJI KOBAYASHI,TATSUJI ENOKI,KIYOZO
            ASADA,IKUNOSHIN KATO
COMMENT     OS   Artificial Sequence
            PN   WO 02101042-A/46
            PD   19-DEC-2002
            PF   12-JUN-2002 WO 2002JP005832
            PR   12-JUN-2001 JP 01P   177737,20-AUG-2001 JP 01P   249689 PI
            HIROAKI SAGAWA,TAKASHI UEMORI,HIROYUKI MUKAI,JUNKO YAMAMOTO, PI
            JUN TOMONO,
            PI   EIJI KOBAYASHI,TATSUJI ENOKI,KIYOZO ASADA,IKUNOSHIN KATO PC
            C12N15/09,C12Q1/68
            CC   Designed chimeric oligonucleotide primer designated as pJDB F-
            CC            1 to amplify
            CC   a portion of CppB gene from Neisseria gonorrhoeae. CC
            'Nucleotides 18 to 20 are ribonucleotides-other nucleotides  CC
                  are
            CC   deoxyribonucleotides.'
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        932 TGCTTAAATGCCTCGTT 948
              ||||| ||||||||||
Db          4 TGCTTCAATGCCTCGTT 20


RESULT 1986
AR030787/c
LOCUS       AR030787                  21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5861374.
ACCESSION   AR030787
VERSION     AR030787.1  GI:5944001
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Berkner,K.L., Petersen,L.Christian. and Hart,C.E.
  TITLE     Modified Factor VII
  JOURNAL   Patent: US 5861374-A 3 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
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            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2800
              || |||||||||||||||
Db         17 TGCAAAAAAAAAAAAAA 1


RESULT 1979
AX104239
LOCUS       AX104239                 20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 431 from Patent WO0122972.
ACCESSION   AX104239
VERSION     AX104239.1  GI:13920436
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 431 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2179
              || |||||||||||||||
Db          4 TCGTTTTTTTTTTTTTT 20


RESULT 1980
AX294137/c
LOCUS       AX294137                 20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 5899 from Patent WO0179548.
ACCESSION   AX294137
VERSION     AX294137.1  GI:17055820
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 5899 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2642 TGGGCTGAACCCTAAGG 2658
              |||||||||| ||||||
Db         19 TGGGCTGAACGCTAAGG 3


RESULT 1981
AX355709
LOCUS       AX355709                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 737 from Patent WO0197843.
ACCESSION   AX355709
VERSION     AX355709.1  GI:18620377
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 737 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide~phosphorothioate
                     backbone"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2179
              || |||||||||||||||
Db          4 TCGTTTTTTTTTTTTTT 20


RESULT 1982
AX547292
LOCUS       AX547292                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 431 from Patent WO02053141.
ACCESSION   AX547292
VERSION     AX547292.1  GI:25812436
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 431 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2179
              || |||||||||||||||
Db          4 TCGTTTTTTTTTTTTTT 20


RESULT 1983
AX613576
LOCUS       AX613576                 20 bp    DNA     linear   PAT 17-FEB-2003
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  AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6451968-A 49 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||| |||| ||||||
Db         19 AAAAAANAAAAGAAAAAA 2


RESULT 1975
AR086109/c
LOCUS       AR086109                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 3 from patent US 5985556.
ACCESSION   AR086109
VERSION     AR086109.1  GI:10012875
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Okano,K.
  TITLE     DNA sequencing method and DNA sample preparation method
  JOURNAL   Patent: US 5985556-A 3 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              || |||||||||||||||
Db         17 TGCAAAAAAAAAAAAAA 1


RESULT 1976
AR086110/c
LOCUS       AR086110                 20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from patent US 5985556.
ACCESSION   AR086110
VERSION     AR086110.1  GI:10012876
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Okano,K.
  TITLE     DNA sequencing method and DNA sample preparation method
  JOURNAL   Patent: US 5985556-A 4 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              || |||||||||||||||
Db         17 TGCAAAAAAAAAAAAAA 1


RESULT 1977
E13187/c
LOCUS       E13187                   20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide.
ACCESSION   E13187
VERSION     E13187.1  GI:3251992
KEYWORDS    JP 1997140400-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okano,K. and Kanbara,H.
  TITLE     DETERMINATION OF BASE SEQUENCE
  JOURNAL   Patent: JP 1997140400-A 1 03-JUN-1997;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997140400-A/1
            PD   03-JUN-1997
            PF   13-SEP-1996 JP 1996242929
            PR   18-SEP-1995 JP 95P   238141
            PI   OKANO KAZUNOBU, KANBARA HIDEKI
            PC   C12Q1/68,G01N27/447,G01N33/58//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              || |||||||||||||||
Db         17 TGCAAAAAAAAAAAAAA 1


RESULT 1978
E13188/c
LOCUS       E13188                   20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide.
ACCESSION   E13188
VERSION     E13188.1  GI:3251993
KEYWORDS    JP 1997140400-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okano,K. and Kanbara,H.
  TITLE     DETERMINATION OF BASE SEQUENCE
  JOURNAL   Patent: JP 1997140400-A 2 03-JUN-1997;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997140400-A/2
            PD   03-JUN-1997
            PF   13-SEP-1996 JP 1996242929
            PR   18-SEP-1995 JP 95P   238141
            PI   OKANO KAZUNOBU, KANBARA HIDEKI
            PC   C12Q1/68,G01N27/447,G01N33/58//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
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            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              | ||||||||||||||||
Db         18 TCAAAAAAAAAAAAAAA 2


RESULT 1971
E32460/c
LOCUS       E32460                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32460
VERSION     E32460.1  GI:13018696
KEYWORDS    JP 2000037190-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 20 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/20
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
Db         18 GCAAAAAAAAAAAAAAA 2


RESULT 1972
AX078832/c
LOCUS       AX078832                  18 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 6 from Patent WO0105963.
ACCESSION   AX078832
VERSION     AX078832.1  GI:13158449
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Fundytus,M.E., Coderre,T.J., Cohen,S.R., Henry,J.L. and Vainio,A.
  TITLE     Antisense oligonucleotides for metabotropic glutamate receptor type
            1 (mglur1)
  JOURNAL   Patent: WO 0105963-A 6 25-JAN-2001;
            McGill University (CA)
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTT 2178
              |||||||| ||||||||
Db         18 CTCCTTTGTTTTTTTT 2


RESULT 1973
AX804555/c
LOCUS       AX804555                  18 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 723 from Patent WO03060160.
ACCESSION   AX804555
VERSION     AX804555.1  GI:38521696
KEYWORDS    .
SOURCE      Oreochromis niloticus (Nile tilapia)
  ORGANISM  Oreochromis niloticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Labroidei; Cichlidae; Oreochromis.
REFERENCE   1
  AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
  TITLE     Verification of food origin based on nucleic acid pattern
            recognition
  JOURNAL   Patent: WO 03060160-A 723 24-JUL-2003;
            Genomar ASA (NO)
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Oreochromis niloticus"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:8128"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        815 GTAATGAACCCCACTGA 831
              | ||||||||||||||||
Db         18 GAAATGAACCCCACTGA 2


RESULT 1974
AR231312/c
LOCUS       AR231312                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 49 from patent US 6451968.
ACCESSION   AR231312
VERSION     AR231312.1  GI:27272243
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
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VERSION     E32454.1  GI:13018690
KEYWORDS    JP 2000037190-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 14 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/14
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTGT 18


RESULT 1968
E32454/c
LOCUS       E32454                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32454
VERSION     E32454.1  GI:13018690
KEYWORDS    JP 2000037190-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 14 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/14
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              | |||||||||||||||
Db         18 ACAAAAAAAAAAAAAA 2


RESULT 1969
E32457
LOCUS       E32457                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32457
VERSION     E32457.1  GI:13018693
KEYWORDS    JP 2000037190-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 17 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/17
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTGA 18


RESULT 1970
E32457/c
LOCUS       E32457                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32457
VERSION     E32457.1  GI:13018693
KEYWORDS    JP 2000037190-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 17 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/17
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
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KEYWORDS    JP 2000037190-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 15 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/15
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
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                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTCT 18


RESULT 1964
E32459/c
LOCUS       E32459                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32459
VERSION     E32459.1  GI:13018695
KEYWORDS    JP 2000037190-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 19 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/19
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
Db         18 GTAAAAAAAAAAAAAA 2


RESULT 1965
A67594
LOCUS       A67594                    18 bp    DNA     linear   PAT 05-MAY-1999
DEFINITION  Sequence 14 from Patent WO9744485.
ACCESSION   A67594
VERSION     A67594.1  GI:4756457
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Goodfellow,P.N.
  TITLE     METHODS FOR IDENTIFYING A MUTATION IN A GENE OF INTEREST
  JOURNAL   Patent: WO 9744485-A 14 27-NOV-1997;
            HEXAGEN TECHNOLOGY LIMITED (GB)
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32644"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              ||||||| |||||||||
Db          1 GCGGCGGCGGCGGCGGC 17


RESULT 1966
AR089732
LOCUS       AR089732                  18 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 14 from patent US 5994075.
ACCESSION   AR089732
VERSION     AR089732.1  GI:10016487
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Goodfellow,P.N.
  TITLE     Methods for identifying a mutation in a gene of interest without a
            phenotypic guide
  JOURNAL   Patent: US 5994075-A 14 30-NOV-1999;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              ||||||| |||||||||
Db          1 GCGGCGGCGGCGGCGGC 17


RESULT 1967
E32454
LOCUS       E32454                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32454
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  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATATT 2476
              ||||| ||||||||||
Db          1 GATCCCATTTTAATATT 17


RESULT 1960
E32456/c
LOCUS       E32456                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32456
VERSION     E32456.1  GI:13018692
KEYWORDS    JP 2000037190-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 16 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/16
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              || ||||||||||||||
Db         18 TTAAAAAAAAAAAAAAA 2


RESULT 1961
E32458
LOCUS       E32458                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32458
VERSION     E32458.1  GI:13018694
KEYWORDS    JP 2000037190-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 18 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/18
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
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  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTCA 18


RESULT 1962
E32453/c
LOCUS       E32453                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32453
VERSION     E32453.1  GI:13018689
KEYWORDS    JP 2000037190-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 13 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/13
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         18 ATAAAAAAAAAAAAAAA 2


RESULT 1963
E32455
LOCUS       E32455                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32455
VERSION     E32455.1  GI:13018691
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```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5259 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||| |
Db          1 TTTTTTTTTTTTTTGA 17


RESULT 1956
AX692527/c
LOCUS       AX692527                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5259 from Patent EP1281758.
ACCESSION   AX692527
VERSION     AX692527.1  GI:29415485
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5259 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              | ||||||||||||||||
Db         17 TCAAAAAAAAAAAAAAA 1


RESULT 1957
AX728891
LOCUS       AX728891                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 525 from Patent WO03025175.
ACCESSION   AX728891
VERSION     AX728891.1  GI:30508234
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 525 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2013 GATCAAGTCCTCTGGTA 2029
              ||||||||| |||||||
Db          1 GATCAAGTCTTCTGGTA 17


RESULT 1958
AX732819
LOCUS       AX732819                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 4453 from Patent WO03025175.
ACCESSION   AX732819
VERSION     AX732819.1  GI:30512162
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 4453 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTT 2169
              ||| |||||||||||||
Db          1 GATCTTTTTCTCCTTTT 17


RESULT 1959
AX760024
LOCUS       AX760024                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 3345 from Patent WO03040369.
ACCESSION   AX760024
VERSION     AX760024.1  GI:32254640
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 3345 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
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  JOURNAL   Patent: US 6566127-A 1072 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTT 2179
              | ||||||||||||||||
Db          1 TACTTTTTTTTTTTTT 17


RESULT 1951
AR323675/c
LOCUS       AR323675                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1077 from patent US 6566127.
ACCESSION   AR323675
VERSION     AR323675.1  GI:33709483
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1077 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              | ||||||||||||||||
Db         17 TGGAAAAAAAAAAAAAA 1


RESULT 1952
AR323676/c
LOCUS       AR323676                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1078 from patent US 6566127.
ACCESSION   AR323676
VERSION     AR323676.1  GI:33709484
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1078 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              ||| ||||||||||||||
Db         17 TTGGAAAAAAAAAAAAA 1
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RESULT 1953
AX692523
LOCUS       AX692523                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5255 from Patent EP1281758.
ACCESSION   AX692523
VERSION     AX692523.1  GI:29415481
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5255 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTT 2179
              | ||||||||||||||||
Db          1 TTCTTTTTTTTTTTTT 17


RESULT 1954
AX692523/c
LOCUS       AX692523                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5255 from Patent EP1281758.
ACCESSION   AX692523
VERSION     AX692523.1  GI:29415481
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5255 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||||||||| ||
Db         17 AAAAAAAAAAAAAAGAA 1


RESULT 1955
AX692527
LOCUS       AX692527                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5259 from Patent EP1281758.
ACCESSION   AX692527
VERSION     AX692527.1  GI:29415485
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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          related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2548 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTT 2179
              | ||||||||||||||||
Db          1 TACTTTTTTTTTTTTT 17


RESULT 1946
AR187065/c
LOCUS       AR187065                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2553 from patent US 6346398.
ACCESSION   AR187065
VERSION     AR187065.1  GI:20233030
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2553 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2799
              | ||||||||||||||||
Db         17 TGGAAAAAAAAAAAAA 1


RESULT 1947
AR187066/c
LOCUS       AR187066                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2554 from patent US 6346398.
ACCESSION   AR187066
VERSION     AR187066.1  GI:20233031
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2554 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2799
              ||| ||||||||||||
Db         17 TTGGAAAAAAAAAAAA 1


RESULT 1948
AR323668
LOCUS       AR323668                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1070 from patent US 6566127.
ACCESSION   AR323668
VERSION     AR323668.1  GI:33709476
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1070 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTT 2177
              ||| ||||||||||||
Db          1 TCTACTTTTTTTTTTT 17


RESULT 1949
AR323669
LOCUS       AR323669                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1071 from patent US 6566127.
ACCESSION   AR323669
VERSION     AR323669.1  GI:33709477
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1071 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTT 2178
              || ||||||||||||||
Db          1 CTACTTTTTTTTTTTT 17


RESULT 1950
AR323670
LOCUS       AR323670                 17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1072 from patent US 6566127.
ACCESSION   AR323670
VERSION     AR323670.1  GI:33709478
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 26;
  Best Local Similarity   81.8%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              | |  |||||||||||||||| |
Db          1 TGTGGTTTTTTTTTTTTTTCA 22


RESULT 1941
AX118414
LOCUS       AX118414                  26 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 3537 from Patent WO0129262.
ACCESSION   AX118414
VERSION     AX118414.1  GI:14035365
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 3537 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 26;
  Best Local Similarity   81.8%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAAA 2804
              |||||| |||  |||| |||||
Db          3 TTGAAACAAATCAAAACAAAAA 24


RESULT 1942
AX692524/c
LOCUS       AX692524                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5256 from Patent EP1281758.
ACCESSION   AX692524
VERSION     AX692524.1  GI:29415482
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5256 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||||||||||  |
Db         17 AAAAAAAAAAAAAAGA 1


RESULT 1943
AR187058
LOCUS       AR187058                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2546 from patent US 6346398.
ACCESSION   AR187058
VERSION     AR187058.1  GI:20233023
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2546 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTT 2177
              ||| ||||||||||||
Db          1 TCTACTTTTTTTTTTT 17


RESULT 1944
AR187059
LOCUS       AR187059                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2547 from patent US 6346398.
ACCESSION   AR187059
VERSION     AR187059.1  GI:20233024
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2547 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTT 2178
              || ||||||||||||||
Db          1 CTACTTTTTTTTTTTT 17


RESULT 1945
AR187060
LOCUS       AR187060                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2548 from patent US 6346398.
ACCESSION   AR187060
VERSION     AR187060.1  GI:20233025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
```

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  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 155 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||   |  |||
Db          1 TTTTTTTTTTTTTTCCTCCCTT 22


RESULT 1937
AX043290
LOCUS       AX043290                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 856 from Patent WO0065088.
ACCESSION   AX043290
VERSION     AX043290.1  GI:11341898
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 856 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||   |  |||
Db          1 TTTTTTTTTTTTTTCCTCCCTT 22


RESULT 1938
AX042902/c
LOCUS       AX042902                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 468 from Patent WO0065088.
ACCESSION   AX042902
VERSION     AX042902.1  GI:11341510
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 468 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAA 2800
              ||   || ||||||||||||||
Db         22 AGGGGTGCAAAAAAAAAAAAAA 1


RESULT 1939
AX043108
LOCUS       AX043108                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 674 from Patent WO0065088.
ACCESSION   AX043108
VERSION     AX043108.1  GI:11341716
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 674 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||| | || || ||
Db          2 TTTTTTTTTTCTGTTGTTCTA 23


RESULT 1940
E31574
LOCUS       E31574                    26 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for preparing DNA sample and reagent.
ACCESSION   E31574
VERSION     E31574.1  GI:13018517
KEYWORDS    JP 1999341986-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kazunori,O., Hideki,K., Tim,C.R. and Michal,A.L.
  TITLE     Method for preparing DNA sample and reagent
  JOURNAL   Patent: JP 1999341986-A 10 14-DEC-1999;
            HITACHI LTD,NYCOMED AMERSHAM PLC
COMMENT     OS   Unidentified
            PN   JP 1999341986-A/10
            PD   14-DEC-1999
            PF   02-JUN-1998 JP 1998152598
            PR
            PI   KAZUNORI OKANO,HIDEKI KAMIBARA,TIM C RICHADSON,MICHAL A LIBU
            PC   C12N15/09,C12Q1/68,G01N33/50,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unidentified"
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  AUTHORS   Fieldhouse,D. and Kobler,D.
  TITLE     Polynucleotides for use as tags and tag complements, manufacture
            and use thereof
  JOURNAL   Patent: WO 02059355-A 929 01-AUG-2002;
            TM BIOSCIENCE CORP (CA)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificially Synthesized DNA Sequence"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2751 ATACGTGTATAATAAAAGTATT 2772
              ||| |||||||| | |||| ||
Db          1 ATAAGTGTATAAGAGAAGTGTT 22


RESULT 1933
AX554007
LOCUS       AX554007                  24 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 30 from Patent WO02074799.
ACCESSION   AX554007
VERSION     AX554007.1  GI:25897944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Freyssinet,G., Rang,C. and Frutos,R.
  TITLE     Pepsin-sensitive modified bacillus thuringiensis insecticidal toxin
  JOURNAL   Patent: WO 02074799-A 30 26-SEP-2002;
            AVENTIS CROPSCIENCE S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="mutant 18"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTT 2186
              |||||||| || || ||||| |
Db          1 CTTTTTTTATTATTATTTTTAT 22


RESULT 1934
BD082997
LOCUS       BD082997                  24 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for distinguishing cancer cell.
ACCESSION   BD082997
VERSION     BD082997.1  GI:22628607
KEYWORDS    JP 2001309791-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kaneuchi,H. and Kamimori,M.
  TITLE     Method for distinguishing cancer cell
  JOURNAL   Patent: JP 2001309791-A 13 06-NOV-2001;
            HAJIME KANEUCHI,MAKOTO KAMIMORI
COMMENT     OS   Artificial Sequence
            PN   JP 2001309791-A/13
            PD   06-NOV-2001
            PF   02-MAY-2000 JP 2000138250
            PI   HAJIME KANEUCHI,MAKOTO KAMIMORI
            PC   C12N15/09,C12Q1/02,C12Q1/68//G01N33/574,C12N15/00 CC
            Description of Artificial Sequence:Artificially Synthesized CC
            Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2566 CTCTGTTCTTGGCTTGGAAGAT 2587
              |||||| || ||| |||| |||
Db          2 CTCTGTGCTGGGCCTGGACGAT 23


RESULT 1935
BD091788
LOCUS       BD091788                  24 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091788
VERSION     BD091788.1  GI:22637399
KEYWORDS    WO 0073440-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 17 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/17
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        773 AACCCTCTGAACCTCCCCTGTC 794
              | |||||||||| |||| || ||
Db          1 AGCCCTCTGAATCTCCACTCTC 22


RESULT 1936
AX042589
LOCUS       AX042589                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 155 from Patent WO0065088.
ACCESSION   AX042589
VERSION     AX042589.1  GI:11341197
KEYWORDS    .
SOURCE      synthetic construct
```

```
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2519 TTTTATTCATATATATACAGGG 2540
              ||||||| || ||| || ||||
Db         24 TTTTATTTATTTATTTAGAGGG 3


RESULT 1928
AX207497/c
LOCUS       AX207497                  24 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 6 from Patent WO0157077.
ACCESSION   AX207497
VERSION     AX207497.1  GI:15422218
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gaulis,S.T., Larminie,C.G. and vinals y de Bassols,C.S.
  TITLE     Proteins that are specifically expressed or highly overexpressed in
            tumors and nucleic acids encoding them
  JOURNAL   Patent: WO 0157077-A 6 09-AUG-2001;
            SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE) ; SMITHKLINE BEECHAM PLC
            (GB)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1394 TCTGCCCTGCAGAACTACATCA 1415
              |||||| || | .| ||||||||
Db         22 TCTGCCTTGGACACCTACATCA 1


RESULT 1929
AX291683
LOCUS       AX291683                  24 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 3445 from Patent WO0179548.
ACCESSION   AX291683
VERSION     AX291683.1  GI:17053366
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 3445 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        717 ACCTGTTGCTGCACGATCAGAC 738
              ||| ||| ||||||| || |||
Db          2 ACCCGTTTCTGCACGGTCTGAC 23


RESULT 1930
AX451724
LOCUS       AX451724                  24 bp    DNA     linear   PAT 03-JUL-2002
DEFINITION  Sequence 13 from Patent WO0226944.
ACCESSION   AX451724
VERSION     AX451724.1  GI:21698628
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brownlie,A.
  TITLE     Methods and compositions employing a stearoyl-coa desaturase-hscd5
  JOURNAL   Patent: WO 0226944-A 13 04-APR-2002;
            Xenon Genetics, Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR Primer"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        464 CAGCAGGCCTGGCCCGGCCGCC 485
              || || ||| |||||||||| ||
Db          1 CACCATGCCAGGCCCGGCCACC 22


RESULT 1931
AX493123
LOCUS       AX493123                  24 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 97 from Patent WO02059355.
ACCESSION   AX493123
VERSION     AX493123.1  GI:23338755
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Fieldhouse,D. and Kobler,D.
  TITLE     Polynucleotides for use as tags and tag complements, manufacture
            and use thereof
  JOURNAL   Patent: WO 02059355-A 97 01-AUG-2002;
            TM BIOSCIENCE CORP (CA)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificially Synthesized DNA Sequence"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2685 TGAAATGGAGATTTGGAATTGA 2706
              ||||   |||||||| ||||||
Db          3 TGAAGAAGAGATTTGAAATTGA 24


RESULT 1932
AX493955
LOCUS       AX493955                  24 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 929 from Patent WO02059355.
ACCESSION   AX493955
VERSION     AX493955.1  GI:23339587
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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DEFINITION  Sequence 10 from patent US 6281344.
ACCESSION   AR166607
VERSION     AR166607.1  GI:16241999
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Nucleic acid-protein fusion molecules and libraries
  JOURNAL   Patent: US 6281344-A 10 28-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTT 2183
              | |  ||||| ||||||||||
Db          1 CGCGGTTTTTATTTTTTTTTT 22


RESULT 1924
BD238389
LOCUS       BD238389                 24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sorting of proteins using RNA-protein fused body.
ACCESSION   BD238389
VERSION     BD238389.1  GI:33048159
KEYWORDS    JP 2002536025-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Sorting of proteins using RNA-protein fused body
  JOURNAL   Patent: JP 2002536025-A 7 29-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002536025-A/7
            PD   29-OCT-2002
            PF   01-FEB-2000 JP 2000598669
            PR   09-FEB-1999 US    09/247190
            PI   JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
            PC   C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
            Translation template
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTT 2183
              | |  ||||| ||||||||||
Db          1 CGCGGTTTTTATTTTTTTTTT 22


RESULT 1925
AR279815
LOCUS       AR279815                 24 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 10 from patent US 6518018.
ACCESSION   AR279815
VERSION     AR279815.1  GI:29714960
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Szostak,J.W. and Roberts,R.W.
  TITLE     RNA-antibody fusions and their selection
  JOURNAL   Patent: US 6518018-A 10 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTT 2183
              | |  ||||| ||||||||||
Db          1 CGCGGTTTTTATTTTTTTTTT 22


RESULT 1926
A57515
LOCUS       A57515                   24 bp    DNA     linear   PAT 03-MAR-1998
DEFINITION  Sequence 7 from Patent WO9632483.
ACCESSION   A57515
VERSION     A57515.1  GI:3713373
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Masucci,M.G.
  TITLE     IMMUNE-EVADING PROTEINS
  JOURNAL   Patent: WO 9632483-A 7 17-OCT-1996;
            MASUCCI MARIA GRAZIA (SE)
COMMENT     Other publication AU 5284296 961030.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        795 AGAAGGAGCTGGTGGGGGCCGT 816
              ||||||||||||| || | | ||
Db          3 AGAAGGAGCTGGAGGTGCCGGT 24


RESULT 1927
I30522/c
LOCUS       I30522                   24 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 13 from patent US 5580967.
ACCESSION   I30522
VERSION     I30522.1  GI:1821313
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Joyce,G.F.
  TITLE     Optimized catalytic DNA-cleaving ribozymes
  JOURNAL   Patent: US 5580967-A 13 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
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     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2250 GAAGCTTTATTTGCATATTTAT 2271
              ||||||||||||  ||  ||| |
Db          2 GAAGCTTTATTTCCAACTTTGT 23


RESULT 1919
I36707
LOCUS       I36707                  23 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 16 from patent US 5608039.
ACCESSION   I36707
VERSION     I36707.1  GI:2086532
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pastan,I., Willingham,M., Fitzgerald,D., Brinkmann,U. and Pai,L.
  TITLE     Single chain B3 antibody fusion proteins and their uses
  JOURNAL   Patent: US 5608039-A 16 04-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2250 GAAGCTTTATTTGCATATTTAT 2271
              ||||||||||||  ||  ||| |
Db          2 GAAGCTTTATTTCCAACTTTGT 23


RESULT 1920
AX003445/c
LOCUS       AX003445                23 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 25 from Patent WO9928439.
ACCESSION   AX003445
VERSION     AX003445.1  GI:9927249
KEYWORDS    .
SOURCE      B19 virus
  ORGANISM  B19 virus
            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Erythrovirus.
REFERENCE   1
  AUTHORS   Auguste,V., Garbarg-Chenon,A. and Nguyen,Q.T.
  TITLE     Erythrovirus and its applications
  JOURNAL   Patent: WO 9928439-A 25 10-JUN-1999;
            ASSIST PUBL HOPITAUX DE PARIS (FR); AUGUSTE VERONIQUE (FR); GARBARG
            CHENON ANTOINE (FR); NGUYEN QUANG TRI (FR)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="B19 virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10798"

  Query Match              0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAA 2188
              |||  ||||||  | ||||||||
Db         22 TTTCATTTTTTATATTTTTTAA 1


RESULT 1921
BD087061/c
LOCUS       BD087061                23 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Erythrovirus and application thereof.
ACCESSION   BD087061
VERSION     BD087061.1  GI:22632671
KEYWORDS    JP 2001525163-A/25.
SOURCE      Erythrovirus
  ORGANISM  Erythrovirus
            Viruses; ssDNA viruses; Parvoviridae; Parvovirinae.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Nguyen,Q.T., Garbarg,C.A. and Auguste,V.
  TITLE     Erythrovirus and application thereof
  JOURNAL   Patent: JP 2001525163-A 25 11-DEC-2001;
            ASSISTANCE PUBLIQUE HOPITAUX DE PARIS
COMMENT     OS   Erythrovirus
            PN   JP 2001525163-A/25
            PD   11-DEC-2001
            PF   03-DEC-1998 JP 2000523317
            PR   03-DEC-1997 FR     97/15197
            PI   QUANG TRI NGUYEN,CHENON ANTOINE GARBARG,VERONIQUE AUGUSTE PC
            C12N15/09,A61K39/12,A61K48/00,C07K14/015,C07K16/08,C12Q1/68, PC
            G01N33/53,
            PC   C12N15/00
            CC   Erythrovirus and application thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Erythrovirus'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Erythrovirus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:40121"

  Query Match              0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAA 2188
              |||  ||||||  | ||||||||
Db         22 TTTCATTTTTTATATTTTTTAA 1


RESULT 1922
AR162082
LOCUS       AR162082                24 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 10 from patent US 6258558.
ACCESSION   AR162082
VERSION     AR162082.1  GI:16229146
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Method for selection of proteins using RNA-protein fusions
  JOURNAL   Patent: US 6258558-A 10 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTT 2183
              | |  ||||| ||||||||||
Db          1 CGCGGTTTTTATTTTTTTTTT 22


RESULT 1923
AR166607
LOCUS       AR166607                24 bp    DNA     linear   PAT 17-OCT-2001
```

```
Db         22 ACAGTGTGTGGGTGAGAAAGGG 1


RESULT 1914
AX922725
LOCUS       AX922725                 22 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1065 from Patent WO02068649.
ACCESSION   AX922725
VERSION     AX922725.1  GI:40215690
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   .
  JOURNAL   Patent: WO 02068649-A 1065 06-SEP-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Ag2964 Reverse"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        993 GGTCCTTGCGGGAGAAGTTGGA 1014
              ||||  || ||||||||||| |
Db          1 GGTCTGTGAGGGAGAAGTTGTA 22


RESULT 1915
BD073283
LOCUS       BD073283                 22 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Hop mosaic virus gene and method for detecting hop mosaic virus.
ACCESSION   BD073283
VERSION     BD073283.1  GI:22618886
KEYWORDS    JP 2001510689-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Suda,S. and Hataya,T.
  TITLE     Hop mosaic virus gene and method for detecting hop mosaic virus
  JOURNAL   Patent: JP 2001510689-A 6 07-AUG-2001;
            SAPPORO BREWERIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001510689-A/6
            PD   07-AUG-2001
            PF   22-JUL-1998 JP 2000504159
            PI   SEIJI SUDA,TATSUJI HATAYA
            PC   C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
            CC   Description of Artificial Sequence:Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1282 CCATGGGACCAGCAGGCTCGCC 1303
              | |||| ||| |||||| ||||
Db          1 CGATGGTACCTGCAGGCGCGCC 22


RESULT 1916
AR085444
LOCUS       AR085444                 23 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 16 from patent US 5981726.
ACCESSION   AR085444
VERSION     AR085444.1  GI:10012213
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pastan,I. and Benhar,I.
  TITLE     Chimeric and mutationally stabilized tumor-specific B1, B3 and B5
            antibody fragments; immunotoxic fusion proteins; and uses thereof
  JOURNAL   Patent: US 5981726-A 16 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2250 GAAGCTTTATTTGCATATTTAT 2271
              |||||||||||| ||  ||| |
Db          2 GAAGCTTTATTTCCAACTTTGT 23


RESULT 1917
AR088850
LOCUS       AR088850                 23 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 16 from patent US 5990296.
ACCESSION   AR088850
VERSION     AR088850.1  GI:10015613
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pastan,I., Willingham,M., Fitzgerald,D., Brinkmann,U. and Pai,L.
  TITLE     Single chain B3 antibody fusion proteins and their uses
  JOURNAL   Patent: US 5990296-A 16 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 2.5e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2250 GAAGCTTTATTTGCATATTTAT 2271
              |||||||||||| ||  ||| |
Db          2 GAAGCTTTATTTCCAACTTTGT 23


RESULT 1918
AR167324
LOCUS       AR167324                 23 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 16 from patent US 6287562.
ACCESSION   AR167324
VERSION     AR167324.1  GI:17903097
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pastan,I., Benhar,I., Padlan,E.A., Jung,S.-H. and Lee,B.
  TITLE     Methods of inhibiting the growth of cells bearing LewisY antigens
            using B1, B3, or B5 targeted immunoconjugates
  JOURNAL   Patent: US 6287562-A 16 11-SEP-2001;
FEATURES             Location/Qualifiers
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RESULT 1909
AR027635/c
LOCUS       AR027635                  22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 152 from patent US 5856301.
ACCESSION   AR027635
VERSION     AR027635.1  GI:5938455
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Craig,S., Hunter,M.George., Edwards,R.Mark., Czaplewski,L.George.
            and Gilbert,R.James.
  TITLE     Stem cell inhibiting proteins
  JOURNAL   Patent: US 5856301-A 152 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2576 GGCTTGGAAGATTCTATTTAAT 2597
              | ||||||||||||   ||||
Db         22 GACTTGGAAGATTCTGCCTAAT 1


RESULT 1910
AR106296
LOCUS       AR106296                  22 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 9 from patent US 6107022.
ACCESSION   AR106296
VERSION     AR106296.1  GI:12820826
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Suda,N. and Hataya,T.
  TITLE     Hop mosaic virus gene and method for detecting hop mosaic virus
  JOURNAL   Patent: US 6107022-A 9 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1282 CCATGGGACCAGCAGGCTCGCC 1303
              | |||| ||| |||||| ||||
Db          1 CGATGGTACCTGCAGGCGCGCC 22


RESULT 1911
AR178618
LOCUS       AR178618                  22 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 15 from patent US 6319710.
ACCESSION   AR178618
VERSION     AR178618.1  GI:20219756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Olafsdottir,B.Ran. and Gulcher,J.
  TITLE     Human narcolepsy gene
  JOURNAL   Patent: US 6319710-A 15 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1006 GAAGTTGGACAAGATCGGGTTG 1027
              ||||||| | | ||| ||||||
Db          1 GAAGTTGTAGATGATGGGGTTG 22


RESULT 1912
AX088188
LOCUS       AX088188                  22 bp    DNA     linear   PAT 17-MAR-2001
DEFINITION  Sequence 15 from Patent WO0114555.
ACCESSION   AX088188
VERSION     AX088188.1  GI:13397099
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Olafsdottir,B.R. and Gulcher,J.
  TITLE     Human narcolepsy gene
  JOURNAL   Patent: WO 0114555-A 15 01-MAR-2001;
            Decode Genetics EHF. (IS)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="nucleic acid primers based on human mRNA sequence"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1006 GAAGTTGGACAAGATCGGGTTG 1027
              ||||||| | | ||| ||||||
Db          1 GAAGTTGTAGATGATGGGGTTG 22


RESULT 1913
AX283017/c
LOCUS       AX283017                  22 bp    DNA     linear   PAT 02-NOV-2001
DEFINITION  Sequence 66 from Patent WO0175171.
ACCESSION   AX283017
VERSION     AX283017.1  GI:16609944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Houghton,R.L., Dillon,D.C., Molesh,D.A., Xu,J., Zehentner,B. and
            Persing,D.H.
  TITLE     Methods, compositions and kits for the detection and monitoring of
            breast cancer
  JOURNAL   Patent: WO 0175171-A 66 11-OCT-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR Primer"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2671 ACAGTGTGTGTGGGTGAAATGG 2692
              |||||||||| | | |||| ||
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            PR   07-SEP-1998 DE 198 40 731.9
            PI   DETLEF KOZIAN,BIRGIT REUNER
            PC   C12Q1/68,G01N33/58//A61K45/00,C12N15/09,C12N15/09,C12N15/00,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   /note= 'M = A, C, G; N = A, C, G, T'
            FH   Key             Location/Qualifiers
            FT   exon            1. .17.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTM 16


RESULT 1906
BD233654/c
LOCUS       BD233654                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Two-color differential display as a method for detecting regulated
            genes.
ACCESSION   BD233654
VERSION     BD233654.1  GI:33043424
KEYWORDS    JP 2002524088-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
  JOURNAL   Patent: JP 2002524088-A 2 06-AUG-2002;
            AVENTIS PHARMA DEUTSCHLAND GMBH
COMMENT     OS   Unidentified
            PN   JP 2002524088-A/2
            PD   06-AUG-2002
            PF   26-AUG-1999 JP 2000569015
            PR   07-SEP-1998 DE 198 40 731.9
            PI   DETLEF KOZIAN,BIRGIT REUNER
            PC   C12Q1/68,G01N33/58//A61K45/00,C12N15/09,C12N15/09,C12N15/00,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   /note= 'M = A, C, G; N = A, C, G, T'
            FH   Key             Location/Qualifiers
            FT   exon            1. .17.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2800
              :|||||||||||||||
Db         16 KAAAAAAAAAAAAAA 1


RESULT 1907
BD217905/c
LOCUS       BD217905                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Gene family encoding apoptosis-associated peptides, peptides
            encoded thereby and method of using the same.
ACCESSION   BD217905
VERSION     BD217905.1  GI:33027675
KEYWORDS    JP 2002516564-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Umansky,S. and Melkonyan,H.
  TITLE     Gene family encoding apoptosis-associated peptides, peptides
            encoded thereby and method of using the same
  JOURNAL   Patent: JP 2002516564-A 6 04-JUN-2002;
            TANOX INC
COMMENT     OS   Unidentified
            PN   JP 2002516564-A/6
            PD   04-JUN-2002
            PF   24-SEP-1997 JP 1998515877
            PR   24-SEP-1996 US    60/026603,11-OCT-1996 US    60/028363 PI
            SAMUIL UMANSKY,HOVSEP MELKONYAN
            PC   C12N15/12,C12N15/62,C07K14/47,C07K16/18,C12Q1/68,G01N33/53, PC
              G01N33/68,
            PC   A61K38/17
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Gene family encoding apoptosis-associated peptides, peptides
            CC          encoded
            CC   thereby and method of using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              : ||||||||||||||||
Db         17 SNAAAAAAAAAAAAAAA 1


RESULT 1908
A17252/c
LOCUS       A17252                   22 bp    DNA     linear   PAT 31-MAR-1994
DEFINITION  Oligonucleotide 22-mer BB10380 (SEQ ID NO: 152).
ACCESSION   A17252
VERSION     A17252.1  GI:513021
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   .
  TITLE     STEM CELL INHIBITING PROTEINS
  JOURNAL   Patent: WO 9313206-A 152 08-JUL-1993;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2576 GGCTTGGAAGATTCTATTTAAT 2597
              | ||||||||||||   ||||
Db         22 GACTTGGAAGATTCTGCCTAAT 1
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  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2799
              | |||| ||||||||||||
Db         19 AGTTGACAAAAAAAAAAAA 1


RESULT 1901
AX043284
LOCUS       AX043284                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 850 from Patent WO0065088.
ACCESSION   AX043284
VERSION     AX043284.1  GI:11341892
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 850 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCA 1789
              |||||||||||  || ||||
Db          2 TTTTTTTTTTCAATCCCA 20


RESULT 1902
AX043413
LOCUS       AX043413                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 979 from Patent WO0065088.
ACCESSION   AX043413
VERSION     AX043413.1  GI:11342021
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 979 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DRB345 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              |||||||||||||| | ||
Db          1 TTTTTTTTTTTTTCTCTT 19


RESULT 1903
AR098680/c
LOCUS       AR098680                  34 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 38 from patent US 6077668.
ACCESSION   AR098680
VERSION     AR098680.1  GI:12808446
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Kool,E.T.
  TITLE     Highly sensitive multimeric nucleic acid probes
  JOURNAL   Patent: US 6077668-A 38 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 34;
  Best Local Similarity   89.5%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||| ||| ||||
Db         34 GAAAAAAAAAGAAAGAAAA 16


RESULT 1904
AR204754/c
LOCUS       AR204754                  34 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 38 from patent US 6368802.
ACCESSION   AR204754
VERSION     AR204754.1  GI:21502161
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Kool,E.T.
  TITLE     Circular DNA vectors for synthesis of RNA and DNA
  JOURNAL   Patent: US 6368802-A 38 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 34;
  Best Local Similarity   89.5%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||| ||| ||||
Db         34 GAAAAAAAAAGAAAGAAAA 16


RESULT 1905
BD233654
LOCUS       BD233654                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Two-color differential display as a method for detecting regulated
            genes.
ACCESSION   BD233654
VERSION     BD233654.1  GI:33043424
KEYWORDS    JP 2002524088-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kozian,D. and Reuner,B.
  TITLE     Two-color differential display as a method for detecting regulated
  JOURNAL   Patent: JP 2002524088-A 2 06-AUG-2002;
            AVENTIS PHARMA DEUTSCHLAND GMBH
COMMENT     OS   Unidentified
            PN   JP 2002524088-A/2
            PD   06-AUG-2002
            PF   26-AUG-1999 JP 2000569015
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RESULT 1896
AX042992/c
LOCUS       AX042992                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 558 from Patent WO0065088.
ACCESSION   AX042992
VERSION     AX042992.1  GI:11341600
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 558 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2799
              | ||| ||||||||||||||
Db         19 AGTTGGAAAAAAAAAAAAA 1


RESULT 1897
I45922/c
LOCUS       I45922                    25 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 10 from patent US 5639595.
ACCESSION   I45922
VERSION     I45922.1  GI:2469887
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Mirabelli,C.K., Ecker,D.J., Vickers,T.A. and Robertson,D.L.
  TITLE     Identification of novel drugs and reagents
  JOURNAL   Patent: US 5639595-A 10 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||  ||
Db         25 AAAAAAAAAAAAAAACCAA 7


RESULT 1898
AX042527/c
LOCUS       AX042527                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 93 from Patent WO0065088.
ACCESSION   AX042527
VERSION     AX042527.1  GI:11341135
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 93 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Homozygote primer sequence"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2799
              | |||| ||||||||||||
Db         19 AGTTGACAAAAAAAAAAAA 1


RESULT 1899
AX042569
LOCUS       AX042569                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 135 from Patent WO0065088.
ACCESSION   AX042569
VERSION     AX042569.1  GI:11341177
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 135 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTT 2192
              |||||||||||| || |||
Db          1 TTTTTTTTTTTCAAGTTT 19


RESULT 1900
AX043112/c
LOCUS       AX043112                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 678 from Patent WO0065088.
ACCESSION   AX043112
VERSION     AX043112.1  GI:11341720
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 678 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
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     gene            1. .24
                     /gene="T cell antigen receptor-beta chain"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2243 AGGTACTGAAGCTTTATTT 2261
              ||| |||||||||| |||
Db          6 AGGAACTGAAGCTTTCTTT 24


RESULT 1892
BD090045
LOCUS       BD090045                  25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD090045
VERSION     BD090045.1  GI:22635655
KEYWORDS    JP 2001321190-A/2289.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 2289 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/2289
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                 Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| || ||||||||||||
Db          2 AAAAGAAGAAAAAAAAAAA 20


RESULT 1893
AX043131/c
LOCUS       AX043131                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 697 from Patent WO0065088.
ACCESSION   AX043131
VERSION     AX043131.1  GI:11341739
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 697 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="DPA1 Heterozygote Primer Sequence"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2799
              || | |||||||||||||||
Db         19 AACTCAAAAAAAAAAAAAA 1


RESULT 1894
AX115872/c
LOCUS       AX115872                  25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 995 from Patent WO0129262.
ACCESSION   AX115872
VERSION     AX115872.1  GI:14032814
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 995 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Primer"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||| ||||| ||||
Db         25 AAAAAAAAGAAAAAGAAAA 7


RESULT 1895
AX042590/c
LOCUS       AX042590                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 156 from Patent WO0065088.
ACCESSION   AX042590
VERSION     AX042590.1  GI:11341198
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 156 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="DQA1 Homozygote primer sequence"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              ||| || ||||||||||||
Db         19 AGAGTTAAAAAAAAAAAAA 1
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```
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTT 2171
              ||||||||| || ||||||
Db         19 GATTTTTTTTTCTTTTTTT 1


RESULT 1888
AR349460/c
LOCUS       AR349460                  24 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 82 from patent US 6586175.
ACCESSION   AR349460
VERSION     AR349460.1  GI:33750253
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Galvin,M., Miller,A., Penny,L. and Riedy,M.
  TITLE     Genotyping the human UDP-glucuronosyltransferase 2B7 (UGT2B7) gene
  JOURNAL   Patent: US 6586175-A 82 01-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTT 2171
              ||||||||| || ||||||
Db         19 GATTTTTTTTTCTTTTTTT 1


RESULT 1889
AX043137
LOCUS       AX043137                  24 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 703 from Patent WO0065088.
ACCESSION   AX043137
VERSION     AX043137.1  GI:11341745
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 703 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTGA 2194
              ||||||||||||||  ||
Db          1 TTTTTTTTTTTAACTACGA 19


RESULT 1890
BD085850/c
LOCUS       BD085850                  24 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Methods of diagnosing and treating chronic obstructive airway
            diseases.
ACCESSION   BD085850
VERSION     BD085850.1  GI:22631460
KEYWORDS    JP 2001522586-A/14.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Duff,G.W., Giovain,M., Barnes,P.J. and Rim,S.
  TITLE     Methods of diagnosing and treating chronic obstructive airway
  JOURNAL   Patent: JP 2001522586-A 14 20-NOV-2001;
            INTERLEUKIN GENETICS INC
COMMENT     OS   Unidentified
            PN   JP 2001522586-A/14
            PD   20-NOV-2001
            PF   09-NOV-1998 JP 2000519607
            PR   07-NOV-1997 GB    9723553.5,12-JAN-1998 US    09/005923 PI
            GORDON W DUFF,MARKO GIOVAIN,PETER J BARNES,SIMON RIM PC
            C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Methods of diagnosing and treating chronic obstructive airway
            CC           diseases
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2444 CTTTTTTGAGACATGGGAT 2462
              ||| ||||| |||||||||
Db         19 CTTCTTTGACACATGGGAT 1


RESULT 1891
S81366
LOCUS       S81366                    24 bp    mRNA    linear   PRI 07-MAY-1993
DEFINITION  T cell antigen receptor-beta chain {rearranged DJ region} [human,
            8-wk fetal thymus, sample 2, mRNA, 24 nt].
ACCESSION   S81366
VERSION     S81366.1  GI:245124
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   George,J.F. Jr. and Schroeder,H.W. Jr.
  TITLE     Developmental regulation of D beta reading frame and junctional
            diversity in T cell receptor-beta transcripts from human thymus
  JOURNAL   J. Immunol. 148 (4), 1230-1239 (1992)
  MEDLINE   92148146
   PUBMED   1310710
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 81366] from the original journal article.
            This sequence comes from Figure 2.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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```
RESULT 1883
A33476/c
LOCUS       A33476                    24 bp    DNA     linear   PAT 23-JUL-1996
DEFINITION  Synthetic pCAS7 poliovirus coding sequence 3' end.
ACCESSION   A33476
VERSION     A33476.1  GI:1567921
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   .
  TITLE     POLIOVIRUS CHIMAERAS
  JOURNAL   Patent: WO 9015145-A 33 13-DEC-1990;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTT 2180
              | | ||||||||||||||||
Db         19 CGCGTTTTTTTTTTTTTTT 1


RESULT 1884
AR078306/c
LOCUS       AR078306                  24 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 16 from patent US 5962332.
ACCESSION   AR078306
VERSION     AR078306.1  GI:10005052
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Singer,R.H. and Taneja,K.L.
  TITLE     Detection of trinucleotide repeats by in situ hybridization
  JOURNAL   Patent: US 5962332-A 16 05-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db         21 GCGGCGGCGGCGGCGGCGG 3


RESULT 1885
AR078307
LOCUS       AR078307                  24 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 17 from patent US 5962332.
ACCESSION   AR078307
VERSION     AR078307.1  GI:10005053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Singer,R.H. and Taneja,K.L.
  TITLE     Detection of trinucleotide repeats by in situ hybridization
  JOURNAL   Patent: US 5962332-A 17 05-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          4 GCGGCGGCGGCGGCGGCGG 22


RESULT 1886
AR116903/c
LOCUS       AR116903                  24 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 8 from patent US 6140047.
ACCESSION   AR116903
VERSION     AR116903.1  GI:14097809
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Duff,G.W., di Giovine,F., Barnes,P. and Lim,S.
  TITLE     Method and kit for predicting susceptibility to asthma
  JOURNAL   Patent: US 6140047-A 8 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2444 CTTTTTTGAGACATGGGAT 2462
              ||| ||||| |||||||||
Db         19 CTTCTTTGACACATGGGAT 1


RESULT 1887
BD229208/c
LOCUS       BD229208                  24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Genotype determination of human UDP-glucuronosyl transferase 2B4
            (UGT2B4), 2B7 (UGT2B7) and 2B15 (UGT2B15) genes.
ACCESSION   BD229208
VERSION     BD229208.1  GI:33038978
KEYWORDS    JP 2002521067-A/80.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Galvin,M., Miller,A., Penny,L. and Riedy,M.
  TITLE     Genotype determination of human UDP-glucuronosyl transferase 2B4
            (UGT2B4), 2B7 (UGT2B7) and 2B15 (UGT2B15) genes
  JOURNAL   Patent: JP 2002521067-A 80 16-JUL-2002;
            AXYS PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002521067-A/80
            PD   16-JUL-2002
            PF   22-JUL-1999 JP 2000562558
            PR   28-JUL-1998 US    60/094391
            PI   MARGARET GALVIN,ANDREW MILLER,LAURA PENNY,MICHAEL RIEDY PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,C12N15/00,C12N15/00 CC
            Genotype determination of human UDP-glucuronosyl transferase  CC
                  2B4 (UGT2B4),
            CC   2B7 (UGT2B7) and 2B15 (UGT2B15) genes
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Homo sapiens (human)'.
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DEFINITION  Sequence 3 from patent US 5834193.
ACCESSION   AR053253
VERSION     AR053253.1  GI:5978115
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kozlowski,M.R., Prowse,K.R., Wang,S.-S., Wong,S., Kim,N.Woo. and
            Allsopp,R.
  TITLE     Methods for measuring telomere length
  JOURNAL   Patent: US 5834193-A 3 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1800 CTCTGAAAGTGGTGCTATAAG 1820
              ||||||||||||  |:|| ||
Db          3 CTCTGAAAGTGGACCWATCAG 23


RESULT 1879
AR053257/c
LOCUS       AR053257                 23 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 7 from patent US 5834193.
ACCESSION   AR053257
VERSION     AR053257.1  GI:5978119
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kozlowski,M.R., Prowse,K.R., Wang,S.-S., Wong,S., Kim,N.Woo. and
            Allsopp,R.
  TITLE     Methods for measuring telomere length
  JOURNAL   Patent: US 5834193-A 7 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1800 CTCTGAAAGTGGTGCTATAAG 1820
              ||||||||||||  |:|| ||
Db         21 CTCTGAAAGTGGACCWATCAG 1


RESULT 1880
AX084400
LOCUS       AX084400                 23 bp    DNA     linear   PAT 28-FEB-2001
DEFINITION  Sequence 6 from Patent WO0112830.
ACCESSION   AX084400
VERSION     AX084400.1  GI:13185851
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hallenbeck,P.L. and Chen,C.T.
  TITLE     Adenoviral vectors including dna sequences encoding angiogenic
            inhibitors
  JOURNAL   Patent: WO 0112830-A 6 22-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1922 TTTTTTTTCAGTGTTAAGG 1940
              |||||||||||||| || |
Db          2 TTTTTTTTCAGTGTAAAAG 20


RESULT 1881
AX103868/c
LOCUS       AX103868                 24 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 60 from Patent WO0122972.
ACCESSION   AX103868
VERSION     AX103868.1  GI:13920065
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 60 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||| |||||
Db         24 AAAAACAAAAAAACAAAAA 6


RESULT 1882
AX546921/c
LOCUS       AX546921                 24 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 60 from Patent WO02053141.
ACCESSION   AX546921
VERSION     AX546921.1  GI:25812065
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 60 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||| |||||
Db         24 AAAAACAAAAAAACAAAAA 6
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            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
COMMENT     OS   Canis familiaris (dog)
            PN   JP 2002530091-A/794
            PD   17-SEP-2002
            PF   15-NOV-1999 JP 2000582596
            PR   13-NOV-1998 US    60/108193
            PI   FRANCIS GALIBERT,CATHERINE ANDRE
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   FH2335
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Canis familiaris (dog)'.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Canis familiaris"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9615"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        777 CTCTGAACCTCCCCTGTCA 795
              ||||||| ||| |||||||
Db          4 CTCTGAAACTCTCCTGTCA 22


RESULT 1875
AX011524/c
LOCUS       AX011524                 22 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 21 from Patent WO9955892.
ACCESSION   AX011524
VERSION     AX011524.1  GI:9998074
KEYWORDS    .
SOURCE      Caprine arthritis-encephalitis virus
  ORGANISM  Caprine arthritis-encephalitis virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Ovine/caprine
            lentivirus.
REFERENCE   1
  AUTHORS   Charneau,P., Firat,H. and Zennou,V.
  TITLE     Use of triplex structure dna sequences for transferring nucleotide
            sequences
  JOURNAL   Patent: WO 9955892-A 21 04-NOV-1999;
            CHARNEAU PIERRE (FR); FIRAT HUESEYIN (FR); PASTEUR INSTITUT (FR);
            ZENNOU VERONIQUE (FR)
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Caprine arthritis-encephalitis virus"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:11660"
     misc_feature     complement(1. .22)
                      /note="Sequence a double brin"
     misc_feature     4
                      /note="A peut etre T"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTT 2182
              ||||| ||||||| |||||
Db         19 CCTTTCTTTTTTTATTTTT 1


RESULT 1876
AX352320
LOCUS       AX352320                 22 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 616 from Patent WO0193902.
ACCESSION   AX352320
VERSION     AX352320.1  GI:18617603
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 616 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Synthetic HDR"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTT 2174
              ||| ||||| |||||||||
Db          4 TTTGTTCTCTTTTTTTTTT 22


RESULT 1877
BD226411/c
LOCUS       BD226411                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Use of triplex structure DNA sequences for transferring nucleotide
            sequences.
ACCESSION   BD226411
VERSION     BD226411.1  GI:33036181
KEYWORDS    JP 2002512804-A/21.
SOURCE      Caprine arthritis-encephalitis virus
  ORGANISM  Caprine arthritis-encephalitis virus
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Ovine/caprine
            lentivirus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Charneau,P., Zennou,V. and Firat,H.
  TITLE     Use of triplex structure DNA sequences for transferring nucleotide
            sequences
  JOURNAL   Patent: JP 2002512804-A 21 08-MAY-2002;
            INSTITUT PASTEUR
COMMENT     OS   Caprine arthritis-encephalitis virus
            PN   JP 2002512804-A/21
            PD   08-MAY-2002
            PF   23-APR-1999 JP 2000546035
            PR   24-APR-1998 FR     98/05197
            PI   PIERRE CHARNEAU,VERONIQUE ZENNOU,HUESEYIN FIRAT PC
            C12N15/09,A61K48/00,C12N5/10,C12N7/00//A61K35/12,C07K14/16, PC
            C12N15/00,
            PC   C12N5/00
            CC   Strandedness: Double;
            CC   A can be T
            CC   Sequence of double strand
            FH   Key             Location/Qualifiers
            FT   misc_feature    (4)
            FT   misc_feature    complement(1. .22).
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Caprine arthritis-encephalitis virus"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:11660"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTT 2182
              ||||| ||||||| |||||
Db         19 CCTTTCTTTTTTTATTTTT 1


RESULT 1878
AR053253
LOCUS       AR053253                 23 bp    DNA     linear   PAT 29-SEP-1999
```

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  AUTHORS   Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
  TITLE     Polymorphisms in the human gene for the multidrug
            resistance-associated protein 1 (mrp-1) and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 02059142-A 336 01-AUG-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="y = c or t"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        289 CCCCGCGCCACCCCTCTCCCA 309
              ||||||||||:|||   ||||
Db          1 CCCCGCGCCAYCCCCACCCCA 21


RESULT 1871
BD129806/c
LOCUS       BD129806                  21 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Asthma-associated gene.
ACCESSION   BD129806
VERSION     BD129806.1  GI:23224751
KEYWORDS    JP 2002500895-A/96.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Wilson,A.R.B., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
            Miller,A. and North,M.
  TITLE     Asthma-associated gene
  JOURNAL   Patent: JP 2002500895-A 96 15-JAN-2002;
            AXYS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002500895-A/96
            PD   15-JAN-2002
            PF   21-JAN-1998 JP 2000528715
            PI   ANGELA R BROOKS WILSON,ALAN BUCKLER,LON
            CARDON,ALISOUN H CAREY,
            PI   MARGARET GALVIN,ANDREW MILLER,MICHAEL NORTH
            PC   C12Q1/68,A01K67/027,C07K14/47,C12N15/09,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Asthma-associated gene
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1968 TATTTACCTTGAAAAAAAGA 1987
              ||||| |||| ||||||| |
Db         21 TATTTTCCTTNAAAAAAAAA 2


RESULT 1872
AX103869/c
LOCUS       AX103869                  22 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 61 from Patent WO0122972.
ACCESSION   AX103869
VERSION     AX103869.1  GI:13920066
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 61 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||| |||||
Db         22 AAAAACAAAAAAACAAAAA 4


RESULT 1873
AX546922/c
LOCUS       AX546922                  22 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 61 from Patent WO02053141.
ACCESSION   AX546922
VERSION     AX546922.1  GI:25812066
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 61 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||| |||||
Db         22 AAAAACAAAAAAACAAAAA 4


RESULT 1874
BD230925
LOCUS       BD230925                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Total genome radiation hybrid map of canine genome and its use for
            identification of interesting genes.
ACCESSION   BD230925
VERSION     BD230925.1  GI:33040695
KEYWORDS    JP 2002530091-A/794.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Galibert,F. and Andre,C.
  TITLE     Total genome radiation hybrid map of canine genome and its use for
            identification of interesting genes
  JOURNAL   Patent: JP 2002530091-A 794 17-SEP-2002;
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     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 1866
AR093142
LOCUS       AR093142                 21 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 11 from patent US 5998596.
ACCESSION   AR093142
VERSION     AR093142.1  GI:10019894
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Bergan,R. and Neckers,L.
  TITLE     Inhibition of protein kinase activity by aptameric action of
            oligonucleotides
  JOURNAL   Patent: US 5998596-A 11 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 1867
AR103576/c
LOCUS       AR103576                 21 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 100 from patent US 6087485.
ACCESSION   AR103576
VERSION     AR103576.1  GI:12815164
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Brooks-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
            Miller,A. and North,M.
  TITLE     Asthma related genes
  JOURNAL   Patent: US 6087485-A 100 11-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1968 TATTTACCTTGAAAAAAAGA 1987
              ||||| |||| ||||||| |
Db         21 TATTTTCCTTNAAAAAAAAA 2


RESULT 1868
AX154293/c
LOCUS       AX154293                 21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 391 from Patent WO0138576.
ACCESSION   AX154293
VERSION     AX154293.1  GI:14535907
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0138576-A 391 31-MAY-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        718 CCTGTTGCTGCACGATCAGAC 738
              ||||||||||:  ||| ||||
Db         21 CCTGTTGCTGYCGGATTAGAC 1


RESULT 1869
AX539548/c
LOCUS       AX539548                 21 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 335 from Patent WO02059142.
ACCESSION   AX539548
VERSION     AX539548.1  GI:25273065
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
  TITLE     Polymorphisms in the human gene for the multidrug
            resistance-associated protein 1 (mrp-1) and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 02059142-A 335 01-AUG-2002;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="r = g or a"

  Query Match              0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        289 CCCCGCGCCACCCCTCTCCCA 309
              ||||||||||:|||   ||||
Db         21 CCCCGCGCCAYCCCCACCCCA 1


RESULT 1870
AX539549
LOCUS       AX539549                 21 bp    DNA     linear   PAT 23-NOV-2002
DEFINITION  Sequence 336 from Patent WO02059142.
ACCESSION   AX539549
VERSION     AX539549.1  GI:25273067
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 52 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          51 GCGGCGGGGGCGGCGGCAG 69
               ||||||| ||||||||| |
Db          19 GCGGCGGCGGCGGCGGCGG 1


RESULT 1861
AR084566/c
LOCUS       AR084566                21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 55 from patent US 5981185.
ACCESSION   AR084566
VERSION     AR084566.1  GI:10011337
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 55 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          51 GCGGCGGGGGCGGCGGCAG 69
               ||||||| ||||||||| |
Db          21 GCGGCGGCGGCGGCGGCGG 3


RESULT 1862
AR084567
LOCUS       AR084567                21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 56 from patent US 5981185.
ACCESSION   AR084567
VERSION     AR084567.1  GI:10011338
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 56 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          51 GCGGCGGGGGCGGCGGCAG 69
               ||||||| ||||||||| |
Db           3 GCGGCGGCGGCGGCGGCGG 21


RESULT 1863
AR084578/c
LOCUS       AR084578                21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 67 from patent US 5981185.
ACCESSION   AR084578
VERSION     AR084578.1  GI:10011349
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 67 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          51 GCGGCGGGGGCGGCGGCAG 69
               ||||||| ||||||||| |
Db          20 GCGGCGGCGGCGGCGGCGG 2


RESULT 1864
AR084579
LOCUS       AR084579                21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 68 from patent US 5981185.
ACCESSION   AR084579
VERSION     AR084579.1  GI:10011350
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 68 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          51 GCGGCGGGGGCGGCGGCAG 69
               ||||||| ||||||||| |
Db           1 GCGGCGGCGGCGGCGGCGG 19


RESULT 1865
AR084582
LOCUS       AR084582                21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 71 from patent US 5981185.
ACCESSION   AR084582
VERSION     AR084582.1  GI:10011353
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 71 09-NOV-1999;
FEATURES             Location/Qualifiers
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  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
            Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
            Koga,H.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002017375-A 3501 22-JAN-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2002017375-A/3501
            PD   22-JAN-2002
            PF   07-JUL-2000 JP 2000253172
            PI   TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
            PI   ISHII,
            PI   YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
            SHINICHI KOJIMA,
            PI   TETSUJI OTSUKI,HISASHI KOGA
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Description of Artificial Sequence: an artificially  CC
            synthesized primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2294 GAAAAGGGTAGGCACGAAG 2312
              ||||||||||||||  |||
Db          1 GAAAAGGGTAGGCAGCAAG 19


RESULT 1858
BD128107
LOCUS       BD128107                 20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD128107
VERSION     BD128107.1  GI:23223052
KEYWORDS    JP 2002017375-A/3538.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
            Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
            Koga,H.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002017375-A 3538 22-JAN-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Unidentified
            PN   JP 2002017375-A/3538
            PD   22-JAN-2002
            PF   07-JUL-2000 JP 2000253172
            PI   TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
            PI   ISHII,
            PI   YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
            SHINICHI KOJIMA,
            PI   TETSUJI OTSUKI,HISASHI KOGA
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Description of Artificial Sequence: an artificially  CC
            synthesized primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2294 GAAAAGGGTAGGCACGAAG 2312
              ||||||||||||||  |||
Db          1 GAAAAGGGTAGGCAGCAAG 19


RESULT 1859
BD168596/c
LOCUS       BD168596                 20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Farnesyl pyrophosphate synthase protein and nuclear and promoter
            domains thereof.
ACCESSION   BD168596
VERSION     BD168596.1  GI:27874408
KEYWORDS    WO 0231164-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okada,Y. and Ito,K.
  TITLE     Farnesyl pyrophosphate synthase protein and nuclear and promoter
            domains thereof
  JOURNAL   Patent: WO 0231164-A 14 18-APR-2002;
            SAPPORO BREWERIES LTD,YUKIO OKADA,KAZUTOSHI ITO
COMMENT     OS   Artificial Sequence
            PN   WO 0231164-A/14
            PD   18-APR-2002
            PF   05-OCT-2001 WO 2001JP008816
            PR   06-OCT-2000 JP 00P   308054
            PI   YUKIO OKADA,KAZUTOSHI ITO
            PC   C12N15/60,C12N9/88
            CC   Description of Artificial Sequence: synthetic oligo nucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1561 GACTGCAAAAATCCTTCTC 1579
              | ||||  ||||||||||||
Db         20 GGCTGCCAAAATCCTTCTC 2


RESULT 1860
AR084563/c
LOCUS       AR084563                 21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 52 from patent US 5981185.
ACCESSION   AR084563
VERSION     AR084563.1  GI:10011334
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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LOCUS       AX495922                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 1687 from Patent WO02059256.
ACCESSION   AX495922
VERSION     AX495922.1  GI:23341532
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 1687 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTT 2178
              ||| | |||||||||| ||||
Db         20 TTTNTTCTTTTTTTTGTTTT 1


RESULT 1854
AX547104
LOCUS       AX547104                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 243 from Patent WO02053141.
ACCESSION   AX547104
VERSION     AX547104.1  GI:25812248
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 243 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| |||||||||  |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 1855
AX645713/c
LOCUS       AX645713                 20 bp    DNA     linear   PAT 03-MAR-2003
DEFINITION  Sequence 4 from Patent EP1271146.
ACCESSION   AX645713
VERSION     AX645713.1  GI:28798089
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Smith,L.J.
  TITLE     Method and composition of cellular reprogramming
  JOURNAL   Patent: EP 1271146-A 4 02-JAN-2003;
            BOARD OF REGENTS OF THE UNIVERSITY OF NEBRASKA (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Phosphorothioate oligonucleotide~Antisense
                     oligonucleotide complementary to the human p53 gene
                     sequence"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              |||||||| |||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 1856
BD069976
LOCUS       BD069976                 20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Use of nucleic acids containing unmethylated CPG dinucleotide in
            the treatment of LPS-associated disorders.
ACCESSION   BD069976
VERSION     BD069976.1  GI:22615579
KEYWORDS    JP 2001513776-A/65.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Schwartz,D.A. and Krieg,A.M.
  TITLE     Use of nucleic acids containing unmethylated CPG dinucleotide in
            the treatment of LPS-associated disorders
  JOURNAL   Patent: JP 2001513776-A 65 04-SEP-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT     OS   Artificial Sequence
            PN   JP 2001513776-A/65
            PD   04-SEP-2001
            PF   25-FEB-1998 JP 1998537810
            PR   28-FEB-1997 US    60/039405
            PI   DAVID A SCHWARTZ,ARTHUR M KRIEG
            PC   A61K49/00,C07H21/02,C07H21/04,A01N43/04
            CC   synthetic oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| |||||||||  |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 1857
BD128070
LOCUS       BD128070                 20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD128070
VERSION     BD128070.1  GI:23223015
KEYWORDS    JP 2002017375-A/3501.
SOURCE      unidentified
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  AUTHORS   Wyatt,J.
  TITLE     Antisense modulation of protein phosphatase 2 catalytic subunit
            beta expression
  JOURNAL   Patent: US 6602713-A 104 05-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              |||||||||| |||||| |
Db         20 GCGGCGGGGGAGGCGGCGG 2


RESULT 1849
AX078047
LOCUS       AX078047                 20 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 61 from Patent WO0105435.
ACCESSION   AX078047
VERSION     AX078047.1  GI:13157802
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gleave,M.
  TITLE     Antisense therapy for hormone-regulated tumors
  JOURNAL   Patent: WO 0105435-A 61 25-JAN-2001;
            THE UNIVERSITY OF BRITISH COLUMBIA (CA) ; Miyake, Hideaki (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAGCAG 469
              || |||| ||||||||||
Db          2 CATAGGCGGCCAGCAGCAG 20


RESULT 1850
AX104051
LOCUS       AX104051                 20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 243 from Patent WO0122972.
ACCESSION   AX104051
VERSION     AX104051.1  GI:13920248
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 243 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 1851
AX184029/c
LOCUS       AX184029                 20 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 1782 from Patent WO0142511.
ACCESSION   AX184029
VERSION     AX184029.1  GI:15135365
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
  TITLE     Ibd-related polymorphisms
  JOURNAL   Patent: WO 0142511-A 1782 14-JUN-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
            Biotherapeutics Corporation (CA)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              |||| ||| ||||| |||||
Db         20 TTTTCTTTNTTTTTCTTTTT 1


RESULT 1852
AX355382
LOCUS       AX355382                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 410 from Patent WO0197843.
ACCESSION   AX355382
VERSION     AX355382.1  GI:18620050
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 410 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphodiester backbone"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 1853
AX495922/c
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           Unclassified.
REFERENCE  1  (bases 1 to 20)
  AUTHORS  Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
  TITLE    Vectors and methods for immunization or therapeutic protocols
  JOURNAL  Patent: US 6339068-A 57 15-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 1844
AR204058/c
LOCUS       AR204058                 20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 2 from patent US 6365577.
ACCESSION   AR204058
VERSION     AR204058.1  GI:21500607
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Iversen,P.L.
  TITLE     p53 antisense agent and method
  JOURNAL   Patent: US 6365577-A 2 02-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              |||||||| |||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 1845
AR264951/c
LOCUS       AR264951                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 35 from patent US 6492121.
ACCESSION   AR264951
VERSION     AR264951.1  GI:29693338
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 35 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2517 GGTTTTATTCATATATATA 2535
              |||||| || |||||||||
Db         20 GGTTTTTTTTATATATATA 2


RESULT 1846
AR300019/c
LOCUS       AR300019                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 11754 from patent US 6537751.
ACCESSION   AR300019
VERSION     AR300019.1  GI:31687303
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 11754 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1483 CAAAACCCTGGAGAAAATG 1501
              |||||||||||| ||| ||
Db         20 CAAAACCCTGGAAAAACTG 2


RESULT 1847
AR309119/c
LOCUS       AR309119                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2 from patent US 6555525.
ACCESSION   AR309119
VERSION     AR309119.1  GI:31700961
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Burke,P.A.
  TITLE     Microencapsulation and sustained release of oligonucleotides
  JOURNAL   Patent: US 6555525-A 2 29-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              |||||||| |||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 1848
AR373534/c
LOCUS       AR373534                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 104 from patent US 6602713.
ACCESSION   AR373534
VERSION     AR373534.1  GI:40075663
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
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  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||||  ||||||  |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 1839
BD243970/c
LOCUS       BD243970                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  P53 antisense agent and method.
ACCESSION   BD243970
VERSION     BD243970.1  GI:33053740
KEYWORDS    JP 2002528464-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Iversen,P.L.
  TITLE     P53 antisense agent and method
  JOURNAL   Patent: JP 2002528464-A 2 03-SEP-2002;
            AVI BIOPHARMA INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002528464-A/2
            PD   03-SEP-2002
            PF   22-OCT-1999 JP 2000578439
            PR   26-OCT-1998 US    60/105695
            PI   PATRICK L IVERSEN
            PC   A61K31/712,A61K31/17,A61K31/203,A61K31/216,A61K31/337,A61K31/
            PC   4745,
            PC   A61K31/522,A61K31/553,A61K31/65,A61K31/7125,A61K45/00,A61K48/
            PC   00,A61P9/10,
            PC   A61P35/00,A61P43/00,C07H21/00,C12N15/09,C12N15/00 CC
            antisense oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||||  ||||||  |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 1840
I25826/c
LOCUS       I25826                   20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 6 from patent US 5552390.
ACCESSION   I25826
VERSION     I25826.1  GI:1605696
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Scholar,E.M. and Iversen,P.L.
  TITLE     Phosphorothioate inhibitors of metastatic breast cancer
  JOURNAL   Patent: US 5552390-A 6 03-SEP-1996;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||||  ||||||  |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 1841
I50039/c
LOCUS       I50039                   20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5641754.
ACCESSION   I50039
VERSION     I50039.1  GI:2472259
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Iversen,P.L.
  TITLE     Antisense oligonucleotide compositions for selectively killing
            cancer cells
  JOURNAL   Patent: US 5641754-A 1 24-JUN-1997;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||||  ||||||  |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 1842
I59872/c
LOCUS       I59872                   20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 4 from patent US 5654415.
ACCESSION   I59872
VERSION     I59872.1  GI:2478504
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Smith,L.James.
  TITLE     Antisense oligonucleotides to p53
  JOURNAL   Patent: US 5654415-A 4 05-AUG-1997;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||||  ||||||  |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 1843
AR182885
LOCUS       AR182885                 20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 57 from patent US 6339068.
ACCESSION   AR182885
VERSION     AR182885.1  GI:20226092
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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Qy       2782 ATTGAAAAAAAAAAAAAAA 2800
              ||  ||||||||||||||||
Db         19 ATACAAAAAAAAAAAAAAA 1


RESULT 1834
A40129/c
LOCUS       A40129                    20 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 5 from Patent WO9423026.
ACCESSION   A40129
VERSION     A40129.1  GI:2296287
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Vasseur,M., Blumenfeld,M., Meguenni,S. and Poddevin,B.
  TITLE     STAPLE AND SEMI-STAPLE OLIGONUCLEOTIDES, METHOD OF PREPARATION AND
            APPLICATIONS
  JOURNAL   Patent: WO 9423026-A 5 13-OCT-1994;
            GENSET (FR)
COMMENT     Other publication AU 6432094 941024
            Other publication FR 2703053 940930.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              |||| | ||||||||||||
Db         19 CTTTCTATTTTTTTTTTT 1


RESULT 1835
AR065945/c
LOCUS       AR065945                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5849727.
ACCESSION   AR065945
VERSION     AR065945.1  GI:5996161
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Porter,T.R. and Iversen,P.L.
  TITLE     Compositions and methods for altering the biodistribution of
            biological agents
  JOURNAL   Patent: US 5849727-A 4 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              |||||||| ||||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 1836
AR080767/c
LOCUS       AR080767                  20 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 8 from patent US 5968909.
ACCESSION   AR080767
VERSION     AR080767.1  GI:10007497
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Agrawal,S., Temsamani,J. and Zhao,Q.
  TITLE     Method of modulating gene expression with reduced immunostimulatory
            response
  JOURNAL   Patent: US 5968909-A 8 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              |||||||| ||||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 1837
AR107646
LOCUS       AR107646                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 86 from patent US 6110664.
ACCESSION   AR107646
VERSION     AR107646.1  GI:12823133
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 86 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2265 TATTTATTTCAGATGTTTC 2283
              ||||||||||| ||||||
Db          1 TATTTATTTCATTTGTTTC 19


RESULT 1838
AR157688/c
LOCUS       AR157688                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 4 from patent US 6245747.
ACCESSION   AR157688
VERSION     AR157688.1  GI:16218662
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Porter,T.R., Iversen,P.L. and Meyer,G.D.
  TITLE     Targeted site specific antisense oligodeoxynucleotide delivery
            method
  JOURNAL   Patent: US 6245747-A 4 12-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
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DEFINITION  Sequence 1 from patent US 5962664.
ACCESSION   AR078461
VERSION     AR078461.1  GI:10005207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Friedhoff,A.J., Basham,D.A. and Miller,J.C.
  TITLE     Psychosis protecting nucleic acid, peptides, compositions and
            method of use
  JOURNAL   Patent: US 5962664-A 1 05-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2181
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 16


RESULT 1830
AX589115
LOCUS       AX589115                  27 bp    DNA     linear   PAT 24-JAN-2003
DEFINITION  Sequence 33 from Patent WO02083179.
ACCESSION   AX589115
VERSION     AX589115.1  GI:27900764
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mckerracher,L.
  TITLE     Fusion proteins
  JOURNAL   Patent: WO 02083179-A 33 24-OCT-2002;
            Bioaxone Therapeutique Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide used in the cloning of a reverse
                     HIV Tat sequence in C3Basic3"

  Query Match             0.6%;  Score 16;  DB 1;  Length 27;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||| || ||||| || |
Db          4 TCCTTTGTTTCTTCTTTTTCTTCT 27


RESULT 1831
AX394618
LOCUS       AX394618                  28 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 16 from Patent EP1186673.
ACCESSION   AX394618
VERSION     AX394618.1  GI:21065731
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 16 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1832
AX394620
LOCUS       AX394620                  29 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 18 from Patent EP1186673.
ACCESSION   AX394620
VERSION     AX394620.1  GI:21065733
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 18 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1833
AX067205/c
LOCUS       AX067205                  20 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 57 from Patent WO0100669.
ACCESSION   AX067205
VERSION     AX067205.1  GI:12544870
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barry,C., Bougueleret,L., Chumakov,I. and Cohen-Akenine,A.
  TITLE     A bap28 gene and protein
  JOURNAL   Patent: WO 0100669-A 57 04-JAN-2001;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide BAP28polyTcourt"

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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  Query Match              0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAA 2803
              ||| ||   | ||||||||||||||
Db         24 GAACTGGTTATAAAAAAAAAAAAA 1


RESULT 1825
AX043076
LOCUS       AX043076                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 642 from Patent WO0065088.
ACCESSION   AX043076
VERSION     AX043076.1  GI:11341684
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 642 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match              0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAG 2197
              |||||||||||| ||||   || |
Db          1 TTTTTTTTTTTTCAACTCATAAGG 24


RESULT 1826
AX043747/c
LOCUS       AX043747                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1313 from Patent WO0065088.
ACCESSION   AX043747
VERSION     AX043747.1  GI:11342362
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1313 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match              0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAA 2803
              ||| ||   | ||||||||||||||
Db         24 GAACTGGTTATAAAAAAAAAAAAA 1


RESULT 1827
E64577/c
LOCUS       E64577                    26 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for obtaining DNA fragment in plant and utilization thereof.
ACCESSION   E64577
VERSION     E64577.1  GI:18628519
KEYWORDS    JP 2000157277-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Hibino,T. and Koshiyama,J.
  TITLE     Method for obtaining DNA fragment in plant and utilization thereof
  JOURNAL   Patent: JP 2000157277-A 1 13-JUN-2000;
            NETSUTAIRIN SAISEI GIJUTSU KENKYU KUMIAI
COMMENT     OS   Artificial Sequence
            PN   JP 2000157277-A/1
            PD   13-JUN-2000
            PF   25-NOV-1998 JP 1998333469
            PR
            PI   TAKASHI HIBINO,JUNKO KOSHIYAMA
            PC   C12N15/09,A01H1/00,A01H5/00,C12N5/10//(C12N15/09,C12R1:91), PC
              C12N15/00,
            PC   C12N5/00,(C12N15/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAAA 11


RESULT 1828
AR164510/c
LOCUS       AR164510                  26 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 1 from patent US 6274147.
ACCESSION   AR164510
VERSION     AR164510.1  GI:16237563
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Vakharia,V.N. and Yao,K.
  TITLE     Method for generating nonpathogenic infectious pancreatic necrosis
            virus (IPNV) from synthetic RNA transcripts
  JOURNAL   Patent: US 6274147-A 1 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAAA 11


RESULT 1829
AR078461
LOCUS       AR078461                  26 bp    DNA     linear   PAT 31-AUG-2000
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RESULT 1820
AX117632
LOCUS       AX117632                  25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 2755 from Patent WO0129262.
ACCESSION   AX117632
VERSION     AX117632.1  GI:14034583
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 2755 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAA 2801
              |||  |   ||||||||||||||||
Db          1 TAGTCTCTTAAAAAAAAAAAAAAA 24


RESULT 1821
AX043286/c
LOCUS       AX043286                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 852 from Patent WO0065088.
ACCESSION   AX043286
VERSION     AX043286.1  GI:11341894
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 852 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAA 2799
              |||  |  || ||||||||||||||
Db         24 GTTCTATGTGGAAAAAAAAAAAAA 1


RESULT 1822
AX043616/c
LOCUS       AX043616                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1182 from Patent WO0065088.
ACCESSION   AX043616
VERSION     AX043616.1  GI:11342224
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1182 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2802
              || ||||  |  ||||||||||||
Db         24 AGTATTGGGACCAAAAAAAAAAAA 1


RESULT 1823
AX042714
LOCUS       AX042714                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 280 from Patent WO0065088.
ACCESSION   AX042714
VERSION     AX042714.1  GI:11341322
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 280 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-A Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAACTTTGA 2194
              |||||||||||| |  | || |||
Db          1 TTTTTTTTTTTTGTCAATCTGTGA 24


RESULT 1824
AX042891/c
LOCUS       AX042891                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 457 from Patent WO0065088.
ACCESSION   AX042891
VERSION     AX042891.1  GI:11341499
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 457 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Homozygote Primer Sequence"
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            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 115 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Homozygote primer sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAA 2801
              | |||  |  ||||||||||||||||
Db         24 TGGAAAAGGTAAAAAAAAAAAAAAA 1


RESULT 1816
AX043230/c
LOCUS       AX043230                25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 796 from Patent WO0065088.
ACCESSION   AX043230
VERSION     AX043230.1  GI:11341838
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 796 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAA 2801
              | |||  |  ||||||||||||||||
Db         24 TGGAAAAGGTAAAAAAAAAAAAAAA 1


RESULT 1817
AX042901
LOCUS       AX042901                25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 467 from Patent WO0065088.
ACCESSION   AX042901
VERSION     AX042901.1  GI:11341509
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 467 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||| ||   || |
Db          1 TTTTTTTTTTTTTATTCGGAATT 24


RESULT 1818
AX043067/c
LOCUS       AX043067                25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 633 from Patent WO0065088.
ACCESSION   AX043067
VERSION     AX043067.1  GI:11341675
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 633 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2799
              ||||||||||||||||
Db         16 TGAAAAAAAAAAAAAA 1


RESULT 1819
AX042691
LOCUS       AX042691                25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 257 from Patent WO0065088.
ACCESSION   AX042691
VERSION     AX042691.1  GI:11341299
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 257 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-A Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 2.6e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAACTT 2191
              |||||||||||| ||| |  || |
Db          1 TTTTTTTTTTTTATTTCTCCACAT 24
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DEFINITION  Sequence 88 from Patent WO0185961.
ACCESSION   AX300680
VERSION     AX300680.1  GI:17381994
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Kletzien,R.F., Reardon,I.M. and Weiland,K.L.
  TITLE     Human caspase-12
  JOURNAL   Patent: WO 0185961-A 88 15-NOV-2001;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="Primer"

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        129 GATTTAACTGGCGACTGTTTTGGG 152
              | ||||||| || ||||  |||||
Db          1 GCTTTAACTTGCCACTGGGTTGGG 24


RESULT 1812
AX394608
LOCUS       AX394608                 24 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 6 from Patent EP1186673.
ACCESSION   AX394608
VERSION     AX394608.1  GI:21065721
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 6 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1813
AX394608/c
LOCUS       AX394608                 24 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 6 from Patent EP1186673.
ACCESSION   AX394608
VERSION     AX394608.1  GI:21065721
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 6 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1814
BD187293/c
LOCUS       BD187293                 24 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Guanosine triphosphate-binding protein coupled receptors.
ACCESSION   BD187293
VERSION     BD187293.1  GI:31879582
KEYWORDS    WO 02103006-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Suwa,M., Asai,K., Akiyama,Y. and Aburatani,H.
  TITLE     Guanosine triphosphate-binding protein coupled receptors
  JOURNAL   Patent: WO 02103006-A 17 27-DEC-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            CENTER FOR ADVANCED SCIENCE AND TECHNOLOGY INCUBATION LTD, MAKIKO
            SUWA, KIYOSHI ASAI,YUTAKA AKIYAMA,HIROYUKI ABURATANI
COMMENT     OS   Artificial Sequence
            PN   WO 02103006-A/17
            PD   27-DEC-2002
            PF   18-JUN-2002 WO 2002JP006058
            PR   18-JUN-2001 JP 01P   246789
            PI   MAKIKO SUWA,KIYOSHI ASAI,YUTAKA AKIYAMA,HIROYUKI ABURATANI PC
             C12N15/09,C12N5/10,C12P21/02,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12Q1/68,A61K38/00,
            PC   A61K45/00,A61K48/00,A61K49/00,A61P43/00,G01N33/50,G01N33/15 CC
              Description of Artificial Sequence:an artificially synthesized
            CC           primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1472 GCTGATTCTAACAAAACCCTGGAG 1495
              |||  |||| ||||| | ||||||
Db         24 GCTAGTTCTCACAAAGCTCTGGAG 1


RESULT 1815
AX042549/c
LOCUS       AX042549                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 115 from Patent WO0065088.
ACCESSION   AX042549
VERSION     AX042549.1  GI:11341157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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                    /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         24 AAAAAAAAAAAAAAAA 9


RESULT 1807
AR081684
LOCUS       AR081684                  24 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 1 from patent US 5972612.
ACCESSION   AR081684
VERSION     AR081684.1  GI:10008410
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Malmqvist,M. and Persson,B.
  TITLE     Surface-sensitive detection of hybridization at equilibrium
  JOURNAL   Patent: US 5972612-A 1 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTT 2178
              |||||||  | | || ||||||||
Db          1 TTTTTTTGCATCTTATTTTTTT 24


RESULT 1808
AR140017/c
LOCUS       AR140017                  24 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 14 from patent US 6207425.
ACCESSION   AR140017
VERSION     AR140017.1  GI:14482513
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Liu,Q. and Sommer,S.S.
  TITLE     Bidirectional PCR amplification of specific alleles
  JOURNAL   Patent: US 6207425-A 14 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         16 TGCGTGTCCAGTGACCCGGACAGC 39
              ||| ||||||| ||||| | | ||
Db         24 TGCCTGTCCAGGGACCCCGCCCGC 1


RESULT 1809
BD235199
LOCUS       BD235199                  24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Voltage gate-controlling potassium channel subunit Kv6.2.
ACCESSION   BD235199
VERSION     BD235199.1  GI:33044969
KEYWORDS    JP 2002519060-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Jegla,T.J.
  TITLE     Voltage gate-controlling potassium channel subunit Kv6.2
  JOURNAL   Patent: JP 2002519060-A 12 02-JUL-2002;
            ICAGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002519060-A/12
            PD   02-JUL-2002
            PF   30-JUN-1999 JP 2000558201
            PR   01-JUL-1998 US    60/091466
            PI   TIMOTHY JAMES JEGLA
            PC   C12N15/09,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61K45/
            PC   00,A61K48/00,
            PC
            A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10//
            PC   G06F17/30,C12N15/00,A61K37/02,C12N5/00
            CC   Description of Artificial Sequence:human standard 3' RACE PCR
            CC           gene
            CC   specific pore (P) region sense primer
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1216 CATGCTATTGGCGGCCCAGCAACT 1239
              ||| ||||||| || ||| || ||
Db          1 CATCCTATTGGTGGGCCATCATCT 24


RESULT 1810
AR364668
LOCUS       AR364668                  24 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 1 from patent US 5399676.
ACCESSION   AR364668
VERSION     AR364668.1  GI:34427592
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Froehler,B.
  TITLE     Oligonucleotides with inverted polarity
  JOURNAL   Patent: US 5399676-A 1 21-MAR-1995;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
              || || |||| |||| || |||||
Db          1 TCTTTCTTTTCTTTTCTTCTTTTT 24


RESULT 1811
AX300680
LOCUS       AX300680                  24 bp    DNA     linear   PAT 30-NOV-2001
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            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         23 AAAAAAAAAAAAAAAA 8


RESULT 1803
BD245237/c
LOCUS       BD245237                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245237
VERSION     BD245237.1  GI:33055007
KEYWORDS    JP 2002532386-A/23.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 23 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/23
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         23 AAAAAAAAAAAAAAAA 8


RESULT 1804
AX394606
LOCUS       AX394606                  23 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 4 from Patent EP1186673.
ACCESSION   AX394606
VERSION     AX394606.1  GI:21065719
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 4 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1805
AX394606/c
LOCUS       AX394606                  23 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 4 from Patent EP1186673.
ACCESSION   AX394606
VERSION     AX394606.1  GI:21065719
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 4 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1806
I33155/c
LOCUS       I33155                    24 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 9 from patent US 5589622.
ACCESSION   I33155
VERSION     I33155.1  GI:1823946
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Gurr,S.J., McPherson,M.J., Atkinson,H.J. and Bowles,D.J.
  TITLE     Plant parasitic nematode control
  JOURNAL   Patent: US 5589622-A 9 31-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
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                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 1799
I79499/c
LOCUS       I79499                  23 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 6 from patent US 5707807.
ACCESSION   I79499
VERSION     I79499.1  GI:3207789
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 6 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 1800
BD187389/c
LOCUS       BD187389                23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method for testing anti-osteoporosis agent.
ACCESSION   BD187389
VERSION     BD187389.1  GI:32997128
KEYWORDS    JP 2003009871-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Furukawa,H., Matsui,H., Kawaida,R. and Otsuka,T.
  TITLE     Method for testing anti-osteoporosis agent
  JOURNAL   Patent: JP 2003009871-A 6 14-JAN-2003;
            Sankyo Company Limited
COMMENT     OS   Artificial Sequence
            PN   JP 2003009871-A/6
            PD   14-JAN-2003
            PF   14-JUN-2001 JP 2001180142
            PI   hidehiko furukawa,hideki matsui,remi kawaida,toshiaki otsuka
            CC   Description of Artificial Sequence: PCR primer DAPG1 FH   Key
                      Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 1801
BD245241/c
LOCUS       BD245241                23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245241
VERSION     BD245241.1  GI:33055011
KEYWORDS    JP 2002532386-A/27.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 27 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/27
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                      Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         23 AAAAAAAAAAAAAAAA 8


RESULT 1802
BD245233/c
LOCUS       BD245233                23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245233
VERSION     BD245233.1  GI:33055003
KEYWORDS    JP 2002532386-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 19 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/19
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
```

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LOCUS       I79497                  23 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 4 from patent US 5707807.
ACCESSION   I79497
VERSION     I79497.1  GI:3207787
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 4 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 1796
BD133515/c
LOCUS       BD133515                23 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method for testing remedy or preventive for osteoporosis or
            articular rheumatism.
ACCESSION   BD133515
VERSION     BD133515.1  GI:23228460
KEYWORDS    JP 2002051782-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Okutsu,J., Kawaida,R., Otsuka,T. and Takahashi,W.
  TITLE     Method for testing remedy or preventive for osteoporosis or
            articular rheumatism
  JOURNAL   Patent: JP 2002051782-A 6 19-FEB-2002;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002051782-A/6
            PD   19-FEB-2002
            PF   09-AUG-2000 JP 2000241413
            PI   JUNICHI OKUTSU,REMI KAWAIDA,TOSHIAKI OTSUKA,WATARU TAKAHASHI
            PC   C12N15/09,C07K14/47,C07K16/18,C12Q1/02,C12Q1/66,C12Q1/68, PC
           G01N33/15,
            PC   G01N33/50,G01N33/50,G01N33/53//C12P21/08,C12N15/00 CC
            Description of Artificial Sequence: PCR primer for molecular  CC
                 indexing
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 1797
E12393/c
```

```
LOCUS       E12393                  23 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide primer.
ACCESSION   E12393
VERSION     E12393.1  GI:3251226
KEYWORDS    JP 1996322598-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Katou,K.
  TITLE     INDEXING METHOD OF DNA MOLECULE
  JOURNAL   Patent: JP 1996322598-A 3 10-DEC-1996;
            RES DEV CORP OF JAPAN
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996322598-A/3
            PD   10-DEC-1996
            PF   12-SEP-1995 JP 1995234122
            PR   28-MAR-1995 JP 95P    69695
            PI   KATOU KIKUYA
            PC   C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .23
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 1798
E12391/c
LOCUS       E12391                  23 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide primer.
ACCESSION   E12391
VERSION     E12391.1  GI:3251224
KEYWORDS    JP 1996322598-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Katou,K.
  TITLE     INDEXING METHOD OF DNA MOLECULE
  JOURNAL   Patent: JP 1996322598-A 1 10-DEC-1996,
            RES DEV CORP OF JAPAN
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996322598-A/1
            PD   10-DEC-1996
            PF   12-SEP-1995 JP 1995234122
            PR   28-MAR-1995 JP 95P    69695
            PI   KATOU KIKUYA
            PC   C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .23
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .23
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```
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 2 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1791
AX394604/c
LOCUS       AX394604                  21 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 2 from Patent EP1186673.
ACCESSION   AX394604
VERSION     AX394604.1  GI:21065717
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 2 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1792
AX498247
LOCUS       AX498247                  21 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from Patent WO0218951.
ACCESSION   AX498247
VERSION     AX498247.1  GI:23343166
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 3 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db          1 GAAAAAAAAAAAAAAA 16


RESULT 1793
AX394605
LOCUS       AX394605                  22 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 3 from Patent EP1186673.
ACCESSION   AX394605
VERSION     AX394605.1  GI:21065718
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 3 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1794
AX394605/c
LOCUS       AX394605                  22 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 3 from Patent EP1186673.
ACCESSION   AX394605
VERSION     AX394605.1  GI:21065718
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 3 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1795
I79497/c
```

```
            KACHIKU KAIRYO JIGYODAN,PRESIDENT OF GUNMA UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002112777-A/3
            PD   16-APR-2002
            PF   03-OCT-2000 JP 2000303994
            PI   AKIRA AIZAWA,AKIKO KAWAKAMI,TOSHIHIKO KONDO
            PC   C12N15/09,C07K14/47,C12N15/00
            CC   Novel testis-specific gene
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          4 CTTTTTTTTTTTTTTT 19


RESULT 1787
BD143136/c
LOCUS       BD143136                 20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel testis-specific gene.
ACCESSION   BD143136
VERSION     BD143136.1  GI:27848894
KEYWORDS    JP 2002112777-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Novel testis-specific gene
  JOURNAL   Patent: JP 2002112777-A 3 16-APR-2002;
            KACHIKU KAIRYO JIGYODAN,PRESIDENT OF GUNMA UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002112777-A/3
            PD   16-APR-2002
            PF   03-OCT-2000 JP 2000303994
            PI   AKIRA AIZAWA,AKIKO KAWAKAMI,TOSHIHIKO KONDO
            PC   C12N15/09,C07K14/47,C12N15/00
            CC   Novel testis-specific gene
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         20 GAAAAAAAAAAAAAAA 5


RESULT 1788
AR142678/c
LOCUS       AR142678                 21 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 8 from patent US 6203988.
ACCESSION   AR142678
VERSION     AR142678.1  GI:15103964
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kambara,H. and Uematsu,C.
  TITLE     DNA fragment preparation method for gene expression profiling
  JOURNAL   Patent: US 6203988-A 8 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         21 AAAAAAAAAAAAAAAA 6


RESULT 1789
E28097/c
LOCUS       E28097                   21 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for analyzing DNA fragment.
ACCESSION   E28097
VERSION     E28097.1  GI:13018322
KEYWORDS    JP 1999196874-A/8.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hideki,K. and Senshu,U.
  TITLE     Method for analyzing DNA fragment
  JOURNAL   Patent: JP 1999196874-A 8 27-JUL-1999;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 1999196874-A/8
            PD   27-JUL-1999
            PF   14-JAN-1998 JP 1998005399
            PR
            PI   HIDEKI KAMIBARA,SENSHU UEMATSU
            PC   C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         21 AAAAAAAAAAAAAAAA 6


RESULT 1790
AX394604
LOCUS       AX394604                 21 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 2 from Patent EP1186673.
ACCESSION   AX394604
VERSION     AX394604.1  GI:21065717
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        505 GCTGCCCTCGCACCAC 520
              ||||||||||||||||
Db         16 GCTGCCCTCGCACCAC 1


RESULT 1782
AX394603
LOCUS       AX394603                  20 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 1 from Patent EP1186673.
ACCESSION   AX394603
VERSION     AX394603.1  GI:21065716
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 1 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1783
AX394603/c
LOCUS       AX394603                  20 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 1 from Patent EP1186673.
ACCESSION   AX394603
VERSION     AX394603.1  GI:21065716
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 1 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1784
AX404077
LOCUS       AX404077                  20 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 4 from Patent EP1195382.
ACCESSION   AX404077
VERSION     AX404077.1  GI:21437393
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Testis-specific gene
  JOURNAL   Patent: EP 1195382-A 4 10-APR-2002;
            Livestock Improvement Association of Japan, Inc. (JP) ; President
            of Gunma University (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          4 CTTTTTTTTTTTTTTT 19


RESULT 1785
AX404077/c
LOCUS       AX404077                  20 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 4 from Patent EP1195382.
ACCESSION   AX404077
VERSION     AX404077.1  GI:21437393
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Testis-specific gene
  JOURNAL   Patent: EP 1195382-A 4 10-APR-2002;
            Livestock Improvement Association of Japan, Inc. (JP) ; President
            of Gunma University (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         20 GAAAAAAAAAAAAAAA 5


RESULT 1786
BD143136
LOCUS       BD143136                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel testis-specific gene.
ACCESSION   BD143136
VERSION     BD143136.1  GI:27848894
KEYWORDS    JP 2002112777-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Novel testis-specific gene
  JOURNAL   Patent: JP 2002112777-A 3 16-APR-2002;
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DEFINITION  Sequence 4 from patent US 6555670.
ACCESSION   AR309844
VERSION     AR309844.1  GI:31701953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Testis-specific gene
  JOURNAL   Patent: US 6555670-A 4 29-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         20 GAAAAAAAAAAAAAAA 5


RESULT 1778
AR312356
LOCUS       AR312356                 20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2893 from patent US 6559294.
ACCESSION   AR312356
VERSION     AR312356.1  GI:31705782
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2893 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2084 CTCTAAACCCCGTGTT 2099
              ||||||||||||||||
Db          5 CTCTAAACCCCGTGTT 20


RESULT 1779
AX048445
LOCUS       AX048445                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 44 from Patent WO0071747.
ACCESSION   AX048445
VERSION     AX048445.1  GI:12225609
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 44 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTAAC 16


RESULT 1780
AX048447/c
LOCUS       AX048447                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 46 from Patent WO0071747.
ACCESSION   AX048447
VERSION     AX048447.1  GI:12225611
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 46 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              ||||||||||||||||
Db         16 TTGAAAAAAAAAAAAA 1


RESULT 1781
AX224877/c
LOCUS       AX224877                 20 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 31 from Patent WO0161030.
ACCESSION   AX224877
VERSION     AX224877.1  GI:15554950
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gray,D.M. and Bollon,A.P.
  TITLE     Libraries of optimum subsequence regions of mrna and genomic dna
            for control of gene expression
  JOURNAL   Patent: WO 0161030-A 31 23-AUG-2001;
            Cytoclonal Pharmaceutics, Inc. (US) ; University of Texas at
            Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
            Experimental Carcinogenesis, National Cancer Institute/NIH (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
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E32461/c
LOCUS       E32461                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32461
VERSION     E32461.1  GI:13018697
KEYWORDS    JP 2000037190-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 21 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/21
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1774
AR086111/c
LOCUS       AR086111                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from patent US 5985556.
ACCESSION   AR086111
VERSION     AR086111.1  GI:10012877
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kambara,H. and Okano,K.
  TITLE     DNA sequencing method and DNA sample preparation method
  JOURNAL   Patent: US 5985556-A 5 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 1775
E13189/c
LOCUS       E13189                    20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide.
ACCESSION   E13189
VERSION     E13189.1  GI:3251994
KEYWORDS    JP 1997140400-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okano,K. and Kanbara,H.
  TITLE     DETERMINATION OF BASE SEQUENCE
  JOURNAL   Patent: JP 1997140400-A 3 03-JUN-1997;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997140400-A/3
            PD   03-JUN-1997
            PF   13-SEP-1996 JP 1996242929
            PR   18-SEP-1995 JP 95P   238141
            PI   OKANO KAZUNOBU, KANBARA HIDEKI
            PC   C12Q1/68,G01N27/447,G01N33/58//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 1776
AR309844
LOCUS       AR309844                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4 from patent US 6555670.
ACCESSION   AR309844
VERSION     AR309844.1  GI:31701953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Aizawa,A., Kawakami,A. and Kondo,T.
  TITLE     Testis-specific gene
  JOURNAL   Patent: US 6555670-A 4 29-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          4 CTTTTTTTTTTTTTTT 19


RESULT 1777
AR309844/c
LOCUS       AR309844                  20 bp    DNA     linear   PAT 12-JUN-2003
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1770
E32453
LOCUS       E32453                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32453
VERSION     E32453.1  GI:13018689
KEYWORDS    JP 2000037190-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 13 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/13
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1771
E32455/c
LOCUS       E32455                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32455
VERSION     E32455.1  GI:13018691
KEYWORDS    JP 2000037190-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 15 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/15
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1772
E32459
LOCUS       E32459                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32459
VERSION     E32459.1  GI:13018695
KEYWORDS    JP 2000037190-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 19 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/19
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1773
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         18 TTTTTTTTTTTTTTTT 3


RESULT 1766
AR208425
LOCUS       AR208425                  18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 5 from patent US 6383754.
ACCESSION   AR208425
VERSION     AR208425.1  GI:21509576
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 5 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1767
AX085251
LOCUS       AX085251                  18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 5 from Patent WO0112855.
ACCESSION   AX085251
VERSION     AX085251.1  GI:13275309
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 5 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match              0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1768
E32450
LOCUS       E32450                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32450
VERSION     E32450.1  GI:13018686
KEYWORDS    JP 2000037190-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 10 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/10
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 16;  DB 1;  Length 18;
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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1769
E32452/c
LOCUS       E32452                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32452
VERSION     E32452.1  GI:13018688
KEYWORDS    JP 2000037190-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 12 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/12
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
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                     /mol_type="genomic DNA"
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  Query Match              0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1762
BD171178/c
LOCUS       BD171178                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171178
VERSION     BD171178.1  GI:27876990
KEYWORDS    WO 0250269-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 3 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/3
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15C', an artificially
            CC           synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="synthetic construct"
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  Query Match              0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1763
AX361600
LOCUS       AX361600                 18 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 18 from Patent WO0208461.
ACCESSION   AX361600
VERSION     AX361600.1  GI:18694219
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
  TITLE     A method and an algorithm for mrna expression analysis
  JOURNAL   Patent: WO 0208461-A 18 31-JAN-2002;
            Global Genomics AB (SE)
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Double-stranded product DNA"

  Query Match              0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1764
AX814932
LOCUS       AX814932                 18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 18 from Patent WO03064691.
ACCESSION   AX814932
VERSION     AX814932.1  GI:39104070
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
  TITLE     Methods and means for manipulating nucleic acid
  JOURNAL   Patent: WO 03064691-A 18 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
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                      product DNA"

  Query Match              0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1765
A14689/c
LOCUS       A14689                   18 bp    DNA     linear   PAT 28-MAR-1994
DEFINITION  Nucleotide sequence 9 from patent number WO8303623.
ACCESSION   A14689
VERSION     A14689.1  GI:513760
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   .
  TITLE     CODING DNA FRAGMENTS FOR POLYPEPTIDES CONTAINING AT LEAST ONE
            ANTIGENIC DETERMINANT OF THE PAPILLOMAVIRUS PARTICULARLY OF THE 1a
            HPV TYPE AND CORRESPONDING POLYPEPTIDES
  JOURNAL   Patent: WO 8303623-A 9 27-OCT-1983;
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="unidentified"
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Db         17 GAAAAAAAAAAAAAA 2


RESULT 1759
BD168111
LOCUS       BD168111                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168111
VERSION     BD168111.1  GI:27873923
KEYWORDS    WO 0233069-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 18 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/18
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
            A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
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            CC           anchor
            CC   primer sequence
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FEATURES             Location/Qualifiers
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  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1760
BD168112/c
LOCUS       BD168112                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination for allergosis.
ACCESSION   BD168112
VERSION     BD168112.1  GI:27873924
KEYWORDS    WO 0233069-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Saito,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0233069-A 19 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA,CHUHEI NOJIRI,NOBUO
            MATSUHASHI,KOJI NISHIZAWA, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0233069-A/19
            PD   25-APR-2002
            PF   28-SEP-2001 WO 2001JP008574
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N15/63,C12Q1/68,C12Q1/02,G01N33/53,C12N5/10, PC
            A61K39/395,
            PC   C07K14/47,C07K16/18//C12P21/02,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized

            CC           anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1761
BD171177
LOCUS       BD171177                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD171177
VERSION     BD171177.1  GI:27876989
KEYWORDS    WO 0250269-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
            Tsujimoto,G.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0250269-A 2 27-JUN-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
            MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
            GOZO TSUJIMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250269-A/2
            PD   27-JUN-2002
            PF   21-DEC-2001 WO 2001JP011286
            PR   21-DEC-2000 JP 00P   389476
            PI   YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
             TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO
            PC   C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
            PC   A61P37/08,
            PC   C12Q1/68,G01N33/50
            CC   Description of Artificial Sequence:'GT15A', an artificially
            CC           synthesized
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
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FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 3 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/3
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
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FEATURES                Location/Qualifiers
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  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1757
BD167907
LOCUS       BD167907                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167907
VERSION     BD167907.1  GI:27873719
KEYWORDS    WO 0226962-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 6 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/6
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
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FEATURES                Location/Qualifiers
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  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1758
BD167908/c
LOCUS       BD167908                  17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD167908
VERSION     BD167908.1  GI:27873720
KEYWORDS    WO 0226962-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
            Saito,H.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0226962-A 7 04-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
            SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
            NAGASU, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0226962-A/7
            PD   04-APR-2002
            PF   21-SEP-2001 WO 2001JP008247
            PR   26-SEP-2000 JP 00P   293021
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES                Location/Qualifiers
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                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
```

```
          TAKESHI NAGASU,
          PI   KOZO TSUJIMOTO
          PC
          C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
           C07K14/47,
          PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
          ,C12N15/09,C12P21/02,
          PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
           C12N15/00
          CC   Description of Artificial Sequence:an artificially synthesized

          CC            primer
          CC   sequence
          FH   Key             Location/Qualifiers
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          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
             ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1754
BD143835/c
LOCUS       BD143835                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143835
VERSION     BD143835.1  GI:27849593
KEYWORDS    JP 2002095500-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 3 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/3
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   KOZO TSUJIMOTO
            PC
            C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
             C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
            ,C12N15/09,C12P21/02,
            PC   C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
             C12N15/00
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
             ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1755
BD167835
LOCUS       BD167835                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167835
VERSION     BD167835.1  GI:27873647
KEYWORDS    WO 0233122-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
            and Takahashi,E.
  TITLE     Method for examination of allergosis
  JOURNAL   Patent: WO 0233122-A 2 25-APR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
            HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
            SAITO,EIKI TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0233122-A/2
            PD   25-APR-2002
            PF   11-OCT-2001 WO 2001JP008937
            PR   13-OCT-2000 JP 00P   314093
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
            TAKESHI NAGASU,
            PI   HIROHISA SAITO,EIKI TAKAHASHI
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
             A61K39/395,
            PC   A01K67/027//C07K16/18,C12N5/10
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            anchor
            CC   primer sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
             ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1756
BD167836/c
LOCUS       BD167836                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for examination of allergosis.
ACCESSION   BD167836
VERSION     BD167836.1  GI:27873648
KEYWORDS    WO 0233122-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
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            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1751
BD142808
LOCUS       BD142808                 17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142808
VERSION     BD142808.1  GI:23237753
KEYWORDS    WO 0224903-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 2 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/2
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1752
BD142809/c
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LOCUS       BD142809                 17 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of examining allergic disease.
ACCESSION   BD142809
VERSION     BD142809.1  GI:23237754
KEYWORDS    WO 0224903-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
            Tsujimoto,G. and Takahashi,E.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: WO 0224903-A 3 28-MAR-2002;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
            OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
            TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0224903-A/3
            PD   28-MAR-2002
            PF   21-SEP-2001 WO 2001JP008246
            PR   25-SEP-2000 JP 00P   291318
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
            TAKESHI NAGASU,
            PI   GOZO TSUJIMOTO,EIKI TAKAHASHI
            PC   C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
             C12Q1/68,
            PC   A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
            PC   G01N33/15,
            PC   G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1753
BD143834
LOCUS       BD143834                 17 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of examining allergic disease.
ACCESSION   BD143834
VERSION     BD143834.1  GI:27849592
KEYWORDS    JP 2002095500-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
            Tsujimoto,K.
  TITLE     Method of examining allergic disease
  JOURNAL   Patent: JP 2002095500-A 2 02-APR-2002;
            GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002095500-A/2
            PD   02-APR-2002
            PF   25-SEP-2000 JP 2000291316
            PI   YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
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            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1748
BD091774/c
LOCUS       BD091774                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091774
VERSION     BD091774.1  GI:22637385
KEYWORDS    WO 0073440-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC   Description of
            Artificial Sequence:Artificially Synthesized CC   Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1749
BD097334
LOCUS       BD097334                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097334
VERSION     BD097334.1  GI:22642908
KEYWORDS    WO 0165259-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 5 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/5
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1750
BD097335/c
LOCUS       BD097335                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for examination for allergosis.
ACCESSION   BD097335
VERSION     BD097335.1  GI:22642909
KEYWORDS    WO 0165259-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
  TITLE     Method for examination for allergosis
  JOURNAL   Patent: WO 0165259-A 6 07-SEP-2001;
            GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
            NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
            FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
            OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
COMMENT     OS   Artificial Sequence
            PN   WO 0165259-A/6
            PD   07-SEP-2001
            PF   23-FEB-2001 WO 2001JP001372
            PR   02-MAR-2000 JP 00P    61832
            PI   TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
              HIROHISA SAITO
            PC   G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
            PC   A61P37/08
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers
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            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1745
BD091750
LOCUS       BD091750                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091750
VERSION     BD091750.1  GI:22637361
KEYWORDS    WO 0073439-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 2 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/2
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
            Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1746
BD091751/c
LOCUS       BD091751                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  465, a novel gene related to pollen allergy.
ACCESSION   BD091751
VERSION     BD091751.1  GI:22637362
KEYWORDS    WO 0073439-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     465, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073439-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073439-A/3
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003191
            PR   27-MAY-1999 JP 99P   148784
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC   Description
            of Artificial Sequence:Artificially Synthesized CC   Primer
            Sequence
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1747
BD091773
LOCUS       BD091773                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  787, a novel gene related to pollen allergy.
ACCESSION   BD091773
VERSION     BD091773.1  GI:22637384
KEYWORDS    WO 0073440-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     787, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073440-A 2 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0073440-A/2
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003192
            PR   27-MAY-1999 JP 99P   148785
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            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/2
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES                 Location/Qualifiers
     source              1. .17
                         /organism="synthetic construct"
                         /mol_type="genomic DNA"
                         /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1742
BD011731/c
LOCUS       BD011731                  17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011731
VERSION     BD011731.1  GI:22091920
KEYWORDS    WO 0065050-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 3 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS   Artificial Sequence
            PN   WO 0065050-A/3
            PD   02-NOV-2000
            PF   26-APR-2000 WO 2000JP002734
            PR   27-APR-1999 JP 99P   120494
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC
            A61P37/00
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FEATURES                 Location/Qualifiers
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                         /mol_type="genomic DNA"
                         /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1743
BD091742
LOCUS       BD091742                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091742
VERSION     BD091742.1  GI:22637353
KEYWORDS    WO 0073435-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 2 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/2
            PD   07-DEC-2000
            PF   18-MAY-2000 WO 2000JP003190
            PR   27-MAY-1999 JP 99P   148783
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NEI YOSHIDA,
            PI   KAORU OGAWA,KEIKO MATSUI
            PC   C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC   Description of Artificial Sequence:Artificially Synthesized CC
              Primer Sequence
            FH   Key             Location/Qualifiers.
FEATURES                 Location/Qualifiers
     source              1. .17
                         /organism="synthetic construct"
                         /mol_type="genomic DNA"
                         /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1744
BD091743/c
LOCUS       BD091743                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  441, a novel gene related to pollen allergy.
ACCESSION   BD091743
VERSION     BD091743.1  GI:22637354
KEYWORDS    WO 0073435-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
  TITLE     441, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0073435-A 3 07-DEC-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS   Artificial Sequence
            PN   WO 0073435-A/3
            PD   07-DEC-2000
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LOCUS       AX692524                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5256 from Patent EP1281758.
ACCESSION   AX692524
VERSION     AX692524.1  GI:29415482
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5256 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          2 CTTTTTTTTTTTTTTT 17


RESULT 1738
AX692526
LOCUS       AX692526                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5258 from Patent EP1281758.
ACCESSION   AX692526
VERSION     AX692526.1  GI:29415484
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5258 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1739
AX692526/c
LOCUS       AX692526                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5258 from Patent EP1281758.
ACCESSION   AX692526
VERSION     AX692526.1  GI:29415484
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5258 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 1740
AX724426
LOCUS       AX724426                 17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 2113 from Patent WO03025176.
ACCESSION   AX724426
VERSION     AX724426.1  GI:30503769
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025176-A 2113 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2074 ATCTGACACACTCTAA 2089
              ||||||||||||||||
Db          2 ATCTGACACACTCTAA 17


RESULT 1741
BD011730
LOCUS       BD011730                 17 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  795, a novel gene related to pollen allergy.
ACCESSION   BD011730
VERSION     BD011730.1  GI:22091919
KEYWORDS    WO 0065050-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
  TITLE     795, a novel gene related to pollen allergy
  JOURNAL   Patent: WO 0065050-A 2 02-NOV-2000;
            GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
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AR241830/c
LOCUS       AR241830                17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 118 from patent US 6472154.
ACCESSION   AR241830
VERSION     AR241830.1  GI:27287642
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 118 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
             ||||||||||||||||
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 1733
AR266625
LOCUS       AR266625                17 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 63 from patent US 6495319.
ACCESSION   AR266625
VERSION     AR266625.1  GI:29695689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 63 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
             ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1734
AR323671
LOCUS       AR323671                17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1073 from patent US 6566127.
ACCESSION   AR323671
VERSION     AR323671.1  GI:33709479
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1073 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2180
             ||||||||||||||||
Db          2 CTTTTTTTTTTTTTTT 17


RESULT 1735
AR323674/c
LOCUS       AR323674                17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1076 from patent US 6566127.
ACCESSION   AR323674
VERSION     AR323674.1  GI:33709482
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1076 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
             ||||||||||||||||
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 1736
AX146683
LOCUS       AX146683                17 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 25 from Patent WO0134834.
ACCESSION   AX146683
VERSION     AX146683.1  GI:14285076
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 25 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
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Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1737
AX692524
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DEFINITION  Pollinosis-associated gene.
ACCESSION   E34258
VERSION     E34258.1  GI:18624263
KEYWORDS    JP 2000106879-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 2 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/2
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 1729
E34259/c
LOCUS       E34259                    17 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Pollinosis-associated gene.
ACCESSION   E34259
VERSION     E34259.1  GI:18624264
KEYWORDS    JP 2000106879-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
  TITLE     Pollinosis-associated gene
  JOURNAL   Patent: JP 2000106879-A 3 18-APR-2000;
            GENOX RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000106879-A/3
            PD   18-APR-2000
            PF   06-OCT-1998 JP 1998284610
            PR
            PI   TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI   MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI   NING NO,
            PI   KAORU OGAWA
            PC   C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 1730
AR187061
LOCUS       AR187061                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2549 from patent US 6346398.
ACCESSION   AR187061
VERSION     AR187061.1  GI:20233026
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2549 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          2 CTTTTTTTTTTTTTTT 17


RESULT 1731
AR187064/c
LOCUS       AR187064                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2552 from patent US 6346398.
ACCESSION   AR187064
VERSION     AR187064.1  GI:20233029
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2552 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 1732
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LOCUS       AX814938                 17 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 24 from Patent WO03064691.
ACCESSION   AX814938
VERSION     AX814938.1  GI:39104076
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
  TITLE     Methods and means for manipulating nucleic acid
  JOURNAL   Patent: WO 03064691-A 24 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Double-stranded
                     product DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
             ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1724
AR172076
LOCUS       AR172076                 17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 30 from patent US 6297425.
ACCESSION   AR172076
VERSION     AR172076.1  GI:17911026
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6297425-A 30 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
             ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTT 17


RESULT 1725
AR172076/c
LOCUS       AR172076                 17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 30 from patent US 6297425.
ACCESSION   AR172076
VERSION     AR172076.1  GI:17911026
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6297425-A 30 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
             ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 2


RESULT 1726
AR173367
LOCUS       AR173367                 17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 30 from patent US 6303846.
ACCESSION   AR173367
VERSION     AR173367.1  GI:17912858
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6303846-A 30 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
             ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTT 17


RESULT 1727
AR173367/c
LOCUS       AR173367                 17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 30 from patent US 6303846.
ACCESSION   AR173367
VERSION     AR173367.1  GI:17912858
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6303846-A 30 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
             ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 2


RESULT 1728
E34258
LOCUS       E34258                   17 bp    DNA     linear   PAT 31-JAN-2002
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2551 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1719
AR323672/c
LOCUS       AR323672                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1074 from patent US 6566127.
ACCESSION   AR323672
VERSION     AR323672.1  GI:33709480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1074 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 2


RESULT 1720
AR323673
LOCUS       AR323673                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1075 from patent US 6566127.
ACCESSION   AR323673
VERSION     AR323673.1  GI:33709481
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1075 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1721
AX361606
LOCUS       AX361606                  17 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 24 from Patent WO0208461.
ACCESSION   AX361606
VERSION     AX361606.1  GI:18694225
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
  TITLE     A method and an algorithm for mrna expression analysis
  JOURNAL   Patent: WO 0208461-A 24 31-JAN-2002;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Double-stranded product DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1722
AX692525/c
LOCUS       AX692525                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5257 from Patent EP1281758.
ACCESSION   AX692525
VERSION     AX692525.1  GI:29415483
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5257 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 2


RESULT 1723
AX814938
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          FT   source          1. .16
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1715
BD167414
LOCUS       BD167414                 16 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Surface-roughened slide glass and method of analyzing biological
            substance using the same.
ACCESSION   BD167414
VERSION     BD167414.1  GI:27873226
KEYWORDS    JP 2002211954-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
  TITLE     Surface-roughened slide glass and method of analyzing biological
            substance using the same
  JOURNAL   Patent: JP 2002211954-A 2 31-JUL-2002;
            TOYO KOHAN CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002211954-A/2
            PD   31-JUL-2002
            PF   30-OCT-2001 JP 2001332778
            PI   HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
            PI   KENICHI TAKAGI
            PC   C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
            PC   C12Q1/68,
            PC   G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
            Surface-roughened slide glass and method of analyzing  CC
             biological substance
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1716
BD167414/c
LOCUS       BD167414                 16 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Surface-roughened slide glass and method of analyzing biological
            substance using the same.
ACCESSION   BD167414
VERSION     BD167414.1  GI:27873226
KEYWORDS    JP 2002211954-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
  TITLE     Surface-roughened slide glass and method of analyzing biological
            substance using the same
  JOURNAL   Patent: JP 2002211954-A 2 31-JUL-2002;
            TOYO KOHAN CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002211954-A/2
            PD   31-JUL-2002
            PF   30-OCT-2001 JP 2001332778
            PI   HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
            PI   KENICHI TAKAGI
            PC   C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
            PC   C12Q1/68,
            PC   G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
            Surface-roughened slide glass and method of analyzing  CC
             biological substance
            CC   using the same
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1717
AR187062/c
LOCUS       AR187062                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2550 from patent US 6346398.
ACCESSION   AR187062
VERSION     AR187062.1  GI:20233027
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         17 AAAAAAAAAAAAAAAA 2


RESULT 1718
AR187063
LOCUS       AR187063                 17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2551 from patent US 6346398.
ACCESSION   AR187063
VERSION     AR187063.1  GI:20233028
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C12P21/02,
PC C12P21/08,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Isolation of novel aging factor gene P23
FH Key Location/Qualifiers
FT source 1. .16
FT /organism='Unidentified'.
FEATURES Location/Qualifiers
source 1. .16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTTG 1782
||||||||||||||||
Db 1 AAGCTTTTTTTTTTTG 16

RESULT 1712
BD138638
LOCUS BD138638 16 bp DNA linear PAT 18-SEP-2002
DEFINITION A novel gene and uses therefor.
ACCESSION BD138638
VERSION BD138638.1 GI:23233583
KEYWORDS JP 2002505844-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Zimmet,P.Z. and Collier,G.
TITLE A novel gene and uses therefor
JOURNAL Patent: JP 2002505844-A 3 26-FEB-2002;
INTERNATIONAL DIABETES INSTITUTE,DEAKIN UNIVERSITY
COMMENT OS Artificial Sequence
PN JP 2002505844-A/3
PD 26-FEB-2002
PF 30-OCT-1998 JP 2000519076
PR 31-OCT-1997 AU PP 0117,11-NOV-1997 AU PP 0323 PI
PAUL ZEV ZIMMET,GREGORY COLLIER
PC C12N15/09,A61K31/711,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
PC A61P1/14,
PC
A61P3/04,A61P3/06,A61P3/10,A61P9/12,C07K14/47,C07K16/18,C12P21/ PC
02,
PC C12Q1/68//C12P21/08,C12N15/00,A61K37/02
CC Description of Artificial Sequence:Synthetic
FH Key Location/Qualifiers
FT source 1. .16
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTTG 1782
||||||||||||||||
Db 1 AAGCTTTTTTTTTTTG 16

RESULT 1713
BD167413
LOCUS BD167413 16 bp DNA linear PAT 17-JAN-2003
DEFINITION Surface-roughened slide glass and method of analyzing biological
substance using the same.
ACCESSION BD167413
VERSION BD167413.1 GI:27873225
KEYWORDS JP 2002211954-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE Surface-roughened slide glass and method of analyzing biological
substance using the same
JOURNAL Patent: JP 2002211954-A 1 31-JUL-2002;
TOYO KOHAN CO LTD
COMMENT OS Artificial Sequence
PN JP 2002211954-A/1
PD 31-JUL-2002
PF 30-OCT-2001 JP 2001332778
PI HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
PI KENICHI TAKAGI
PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
PC C12Q1/68,
PC G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
Surface-roughened slide glass and method of analyzing CC
biological substance
CC using the same
FH Key Location/Qualifiers
FT source 1. .16
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 1 AAAAAAAAAAAAAAAA 16

RESULT 1714
BD167413/c
LOCUS BD167413 16 bp DNA linear PAT 17-JAN-2003
DEFINITION Surface-roughened slide glass and method of analyzing biological
substance using the same.
ACCESSION BD167413
VERSION BD167413.1 GI:27873225
KEYWORDS JP 2002211954-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE Surface-roughened slide glass and method of analyzing biological
substance using the same
JOURNAL Patent: JP 2002211954-A 1 31-JUL-2002;
TOYO KOHAN CO LTD
COMMENT OS Artificial Sequence
PN JP 2002211954-A/1
PD 31-JUL-2002
PF 30-OCT-2001 JP 2001332778
PI HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
PI KENICHI TAKAGI
PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
PC C12Q1/68,
PC G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
Surface-roughened slide glass and method of analyzing CC
biological substance
CC using the same
FH Key Location/Qualifiers

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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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  Query Match              0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1708
AX419606
LOCUS       AX419606                 16 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 11 from Patent WO0187935.
ACCESSION   AX419606
VERSION     AX419606.1  GI:21523978
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Heaney,A.P., Ishikawa,H., Yu,R., Horwitz,G.A., Zhang,X. and
            Melmed,S.
  TITLE     Methods of modulating angiogenesis by regulating the expression of
            pituitary tumor transforming gene (pttg)
  JOURNAL   Patent: WO 0187935-A 11 22-NOV-2001;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Anchored primer sequence."

  Query Match              0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1709
AX522006
LOCUS       AX522006                 16 bp    DNA     linear   PAT 24-OCT-2002
DEFINITION  Sequence 10 from Patent WO02064828.
ACCESSION   AX522006
VERSION     AX522006.1  GI:24410902
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Monk,M.
  TITLE     A method for identifying a target (gene) associated with a disease
  JOURNAL   Patent: WO 02064828-A 10 22-AUG-2002;
            UNIVERSITY COLLEGE LONDON (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo dT primer"

  Query Match              0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1710
BD073502
LOCUS       BD073502                 16 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel bone-mineralized protein, DNA, vector and expression system.
ACCESSION   BD073502
VERSION     BD073502.1  GI:22619105
KEYWORDS    JP 2001512019-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Hair,G. and Boden,S.
  TITLE     Novel bone-mineralized protein, DNA, vector and expression system
  JOURNAL   Patent: JP 2001512019-A 3 21-AUG-2001;
            EMORY UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2001512019-A/3
            PD   21-AUG-2001
            PF   29-JUL-1998 JP 2000505304
            PR   30-JUL-1997 US    60/054219,02-APR-1998 US    60/080407 PI
            GREG HAIR,SCOTT BODEN
            PC   C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P19/00,A61P43/00,
            PC   C07K14/47,
            PC
            C07K16/18,C12N1/19,C12N1/21,C12N5/00,C12P21/08,C12Q1/68,C12N15/ PC
             00,
            PC   A61K37/02,C12N5/00
            CC   Differential Display PCR Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1711
BD073877
LOCUS       BD073877                 16 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Isolation of novel aging factor gene P23.
ACCESSION   BD073877
VERSION     BD073877.1  GI:22619480
KEYWORDS    JP 2001512698-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Suishelm,K., Hosier,S. and Kubbies,M.
  TITLE     Isolation of novel aging factor gene P23
  JOURNAL   Patent: JP 2001512698-A 2 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS   Unidentified
            PN   JP 2001512698-A/2
            PD   28-AUG-2001
            PF   05-AUG-1998 JP 2000506375
            PR   08-AUG-1997 US    08/908873
            PI   KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
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